

525 Rec'd PCT/PTO 17 OCT 2000

FORM PTO-1390  
(REV 10-95)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1780

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

**09/673395**

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PRIORITY DATE CLAIMED

PCT/DE99/01174

15 April 1999

17 April 1998

TITLE OF INVENTION

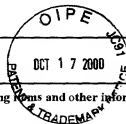
HUMAN NUCLEIC ACID SEQUENCES FROM ENDOMETRIAL TUMOR TISSUE

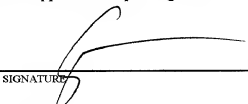
APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.

**Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:**

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
  2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
  3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
  4. ☒ A proper Demand for International Preliminary Examination was made by the 19<sup>th</sup> month from the earliest claimed priority date.
  5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
    - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
    - b. ☒ has been transmitted by the International Bureau.
    - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
  6. ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
  7. ☐ A copy of the International Search Report (PCT/ISA/210).
  8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
    - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
    - b. ☐ have been transmitted by the International Bureau.
    - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
    - d. ☒ have not been made and will not be made.
  9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
  10. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
  11. ☐ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
  12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).
- Items 13. to 19. below concern document(s) or information included:**
13. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
  14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
  15. ☒ A **FIRST** preliminary amendment.
    - ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
  16. ☐ A substitute specification.
  17. ☐ A change of power of attorney and/or address letter.
  18. ☐ Certificate of Mailing by Express Mail
  19. ☐ Other items or information.



U.S. APPLICATION NO. (if known, see 37 CFR §1.5) <b>09/673395</b>		INTERNATIONAL APPLICATION NO. PCT/DE99/01174		ATTORNEY'S DOCKET NUMBER SCH 1780	
17. <input checked="" type="checkbox"/> The following fees are submitted: <b>BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)):</b> Search Report has been prepared by the EPO or JPO..... \$860.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) ..... \$690.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO ..... \$1,000.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100.00				<b>CALCULATIONS PTO USE ONLY</b>	
<b>ENTER APPROPRIATE BASIC FEE AMOUNT=</b>				<b>\$860.00</b>	
Surcharge of <b>\$130.00</b> for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30				<b>\$0.00</b>	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	38 - 20 =	18	x \$ 18.00	<b>\$324.00</b>	
Independent claims	6 - 3 =	3	x \$ 80.00	<b>\$240.00</b>	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270.00		
<b>TOTAL OF ABOVE CALCULATIONS =</b>				<b>\$1,424.00</b>	
Reduction of ½ for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
<b>SUBTOTAL =</b>				<b>\$1,424.00</b>	
Processing fee of <b>\$130.00</b> for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
<b>TOTAL NATIONAL FEE =</b>				<b>\$1,424.00</b>	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
<b>TOTAL FEES ENCLOSED =</b>				<b>\$1,424.00</b>	
				Amount to be refunded:	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,424.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
<b>NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.</b>					
SEND ALL CORRESPONDENCE TO: <b>MILLEN, WHITE, ZELANO &amp; BRANIGAN, P.C.</b> Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333					
Filed: October 17, 2000				SIGNATURE _____  <b>Anthony J. Zelano</b> NAME	
aek:k\pat\sch\1780\natl phase transmlt				<u>27,969</u> REGISTRATION NUMBER	

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Att'y. Docket No: ALBRE-12

In re patent application of

SPECHT, THOMAS et al.

Serial No. 09/673,395

Filed: October 17, 2000

For: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents  
Washington, D.C. 20231  
**Box SEQUENCE**

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

09673395-122700

Respectfully submitted,

July 11, 2001  
Date

**HARBOR CONSULTING**

Intellectual Property Services  
1500A Lafayette Road  
Suite 262  
Portsmouth, N.H.  
800-318-3021

James A. Coburn  
James A. Coburn

09/673395-122700



09/673395

529 Rec'd PCT/PTC 17 OCT 2000

## Sequence Protocol

&lt;110&gt; metaGen Gesellschaft für Genomforschung mbH

&lt;120&gt; Human Nucleic Acid Sequences from Uterus Tumor Tissue

&lt;130&gt; 51586AWOM1XX24-P

&lt;140&gt; PCT/DE99/01174

&lt;141&gt; 1999-04-14

&lt;160&gt; 635

&lt;210&gt; 1

&lt;211&gt; 1046

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 1

tcggaacgag ggatcactaa tcaacaaacc agcttttcggg gtctgaocgg atcccttgct 60  
caggcctctc gaggtccaga cagccgcccc gccgctctg cgacgcagca gtgaatagtg 120  
tggtacctcc ttgtctcggt tcaggtccag acctccccgt cttccggctg ccttgaacct 180  
caggcgacct caggaccctg tgattggcgc ctgcgcgggc ggaccgtgac cgaggaatac 240  
cctggaggga cttgggcatt ctttgggtcc cgtgcctgtt cttcgtgctc ctttcggggc 300  
aaggatctca cattatcagt ctttgaccga cacagaatgc ctggcatttg ataatgtttt 360  
gttgaaacttg aagagacata tggacaatga atctgcataa atactgggga gagataccaa 420  
tatcatcaag ccagaccaac agaagtctct tgcatttgct cccacgggag ttccgtcttg 480  
tggaaagtcca tgacccccc ctgcaccaac cctcagccaa caagccgaag cccccacta 540  
tgctggacat cccctcagag ccatgttagt tcaccatcca tacgattcag ttgattcagc 600  
acaaccgaag tcttcgcaac cttattgcca cagctcaggc ccagaatcag cagcagacag 660  
aaggtgttaa aactgaagag agtgaacctc ttccctcgtg ccttgggtca cctcctctcc 720  
ctgatgaact cctgccttta gattgtaaga atcccaatgc accattccag atccggcaca 780  
gtgaccocaga gattgacttt tatcgtggga aaggggaacc tgtgactgaa ctcagctggc 840  
actcctgtgc gcagctcttc taccaaggca gtggcacaaa tccctggccaa cggcgggctt 900  
ttgactgtgc taatgagagt gtccctggag accctaactt gatgtggcca catgagtatt 960  
ggccttaaaag tttaccaaag ttttgcgtgt ttttgcgtgt gagcgggaag cccgggtggg1020  
agagacttcc ttttgccgaa tgtgat 1046

&lt;210&gt; 2

&lt;211&gt; 373

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 2

cgaaggcaga gttcaacagg gatcttttgt aaatgttcaa caagggccac agggaccatt 60  
tattgaattt atccatcagt taaccacagg aattaagagc acacatggaa catgaccatt120  
tccacgggta tctcgtataa cctcgaagg caagccatag tggaaocgtt gccattccac180  
gcttaaaaaat atcgttttaa aaaaggggga atatgaataa ggaccctaca acactactag240  
cacaaagtgtt attcaccctt aatttcttaa atttagataa ttaaaattcc aatcagccct300  
agaaaagcac ttttgcttaa aacctcccca ggtagcaagg ctttcagtgt tttgggaagg360  
tgttaatagt atc 373

&lt;210&gt; 3

&lt;211&gt; 1571

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 3

ctgctctggc aaccaataga agctaggaga gggcggggac aactgggtct tttgcggctg 60

```

cagcggggctt gtaggtgtcc ggctttgctg gccacgaag cctgataagc atgaagctct 120
tatctttggtt ggcctgtgggc ggggtgtttgc tgggtgcccc agctgaagcc aacaagagtt 180
ctgaagatata ccgggtgcaaa tgcatctgtc caccottatag aaacatcagt gggcacattt 240
acaaccagaa tgatctccag aaggactgca actgcctgca cgtgggtggag cccatgccag 300
tgctggcgca tgacgtggag gctactgtcc tgctgtgcga gtgcaggtac gaggagcgca 360
gaccaccacc atcaagggtca tcatgtgcat ctacctgtcc gtgggtgggtg cctctgtgtc 420
ctacactggcc ttctcgtgc tggtggagccc tctgatccga aagccgagtg ctacactgca 480
gcaactgcac aatgaggagg agaattgagga tgctcgtctc atggcgagca ctgcgtgcac 540
cctcgggggga ccccgagcaa acacagtctc ggagcgtgtg gaaggtgccc agcgcgggtg 600
gaagctgcag gtgcaggagc agcggaaagc agtcttcgat cggcacaaga tgctcagcta 660
gtggggtggt gtgtgtgtggg tcaaggcccc aacacatagg ctgcgcagctt ccaggtctgga 720
caaagcaggg ggctactctc cccctccctc ggttcacagc ttccctttaa acgctctggtg 780
catttttctc cctttctccct aactttagaa atgttgtact tggctatatt gattagggaa 840
gagggtgtgt gtctctgac tccgttgtct tcttggtgtc ttgggggtga agggaggggg 900
aaggcaggcc agaagggaat ggagacattc gaggcggtc caggagtgga tgcgtctgtg 960
ctctcctggc tccactcttg ccgccttcca gctctgagtc ttgggaatgt tgttaccctt1020
ggaagataaa gctgggtctt caggaaactca gtgtctggga ggaaagcatg gccaccatt1080
cagcatgtgt tctttctgc agtggttctt tatcacacc tccctccag cccagcgcc1140
tcagcccccag ccccgactcc agccctgagg acagctctga tgggagagct gggcccccctg1200
agcccaactg gtctctcagg tgcaactggaa gctgttccct gctgtcccc ctgcacttgal1260
cgctcgggg catggagtg ccatgcatac tctgctgcgc tgcctccac cagccccctg acttgggtgt1440
gggggtctgg cagtccccct tctccccagt gtccacagtc actgagccag acggtcggtt1380
ggaacatgat actcgaagct gagcgtggat ctgaacacca cagccccctg acttgggtgt1440
cctcttgctc ctgaactctg ttgtaccagt gcatggagag aaaaatttgt cctcttgct1500
tagagtgtg tgtaaatcaa ggaagccatc attaaattgt tttatttctc tccaaaaaa1560
aaaaaaaaa a 1571

```

<210> 4  
 <211> 1789  
 <212> DNA  
 <213> homo sapiens

<400> 4

```

agaccatgct gataaaaaatt ccaaagggaag agcaagaaga gacgtgtgca attcgtgtg 60
gttttatcat atataacaaa gtcttcacatt tctttaatgt gaagagtaat ctgggcccagc 120
ctcagatgat ggggggtgact gatgttggag aagctcttgt tctcttgttg gatggtttcc 180
ttgtcaacta tcaagaatcc caactctgtg ttcataattt gttggaccag attccagaca 240
tggtttgcaga ctctaatgaa aatgagactg tctttgctcc tctgcatccag gtcggcatgg 300
aagcactaaa ggcagcagac tgctcctggga agctgttcat ctctccattct tcttggccaa 360
ctcgtgaagc accaggaggag ctcaaaaaca gagatgacaa aaaacttgtt aatacagaca 420
aagagaagat actctttccag ccccaaaaca atgtctatga ctcaattggcc aaggactcgt 480
tggtctacgc gctgtctctgt gacactcttc tctcttccca gtccagtatgt aactgtggcc 540
tcgtctggggc tggttctcca gctcactgga ggaacccctt acaaatcaaa caattttccag 600
atgcactttg atagacaaca atttttgaac gacctcagaa atgatattga aaagaaaaata 660
ggctttgatg ctattatgag ggttcgtacc agcacaggtt tcagagccac tgattttctt 720
gggtggaatc tgatgaacaa caccacogac gtagaatagg ctgcccacag tgttgacaag 780
gcagtgacgc tggaggttcaa gcaagatgag aaactcagtg aagactgtgg agctctaatc 840
cagtgctgact tgcctttacac gacaatcagt ggtcaaagaa gacttcggat tcaaatcttt 900
gggttgtaact gcaagctctca gctagctgtc cttataaga atgtatgagc agatgctctt 960
atcaaatctt ttgccaagtc agctttttaa gcagttctcc accagccttt gaaggtctatc1020
cggggaatct tagttaactca gactgccccat atgttggcat gttaccggaa gaattgtgca1080
agtcctctgc cagcaagacca gcttattcta ccagattcca tgaaagtatt gccagtgtac1140
atgaattgtc tgttgcacaa ctgtgtacta ctacagcagc cagagatctc caactgtgaa1200
cgagcatacc atagacagct ggtcatgacc atgggtgtgg ctgactctca gcttttctct1260
taaccaaca agtgcctcat acacagctta gatgtcaaga gtatgtcaag acorgtgccl1320
gttcgttgtc ctgagtcctc tctttcagaa gaaggaatat tcttactggc taatggtctal1380
cacatgttgc ttggtcttggg agtaagcagc ccaccagaa tgatccaagg aatatttaat1440
tgcocatctt ttgacacatc caacacagat atgacatttg tgcctgaagt gggaacccca1500
tactctcaac aactcagaat gataatgggt attatccaac aaaagagccc atattcaatgt1560
aagctcacia ttgtaaagca gcgagaacaa ccagaaaatg tttccgaca gttctcggta1620
gaagacaaag gactttacgg aggtctcttc tatgtggatt tctcttgttg tgttcaacaag1680
gagatctgtc atctgtctaa ttaattggaa actcccggg gatggagggt tgcgttgca1740

```

gggggggaaa agccccctttt tggggoccaa atttgccagg gggaaaaag

1789

<210> 5  
<211> 2361  
<212> DNA  
<213> homo sapiens

<400> 5

```

ggggccagccg gctcgccccc gggccatggc agcagcggct actgcagccg aggggggtccc 60
cagtcggggg cctcccccgg aagtcaccca tctgaatgtg ggaggcgaag gattcagtag 120
ctctcgccag actctcacct ggatcccca tctctctctc tccagctcttc tgagcggagc 180
catctcgagc ctgaagaatg agaccggagc aatcttcatc gacaggggacc ctacagctct 240
cgcccccatc ctcaacttcc tgcgcaccaa agagtgtgat ccaggggtg tccacgggtc 300
cagcctctcc catgaagccc agttctatgg gtcactctct ctgggtctgc gctcgcagct 360
tcgagaggag ttggtatcgt cttctgtgtg aaacgtctct ttcaatgggt acctgccgcc 420
accagtgttc ccagctgaagc ggcggaacgc gcacagccta gtgggggcctc agcagctagg 480
aggaaggcca gccctgtccc gcgggagcaa cacgatgccc cccaaccttg gcaatgcagg 540
gctgctgggc cgaatgtctg atgagaaaac cctctctcca cccctaggga aacctgagga 600
gccccggatg gtgcgcctgg tgtgtggaca ccataattgg atcgctgtgg cctataccca 660
gtttctagtc tgctacaggt tgaagggaag cctctggcggg cagctgtgtgt ttccagccc 720
cgcctgtgac tggcccatgc gaacgactgg cgcttcacag cccgggtgca tgggtgggct 780
ttgggtgaac atgacaagat ggtggcagca gccacgggca gcgagatcct gctatgggct 840
ctgcaggcgg aaggcgggtg ctccagata ggggtcttct atctgggggt gctctgtggg 900
gctctgtctc togtcgggaa ccagctcatt gctacaagcc acacagggcg catcgggggtg 960
tggaaatgcc tcaccaagca ctggcaggtc caggagggtg agccccatcag cagttatgatc 1020
ggcgacggct ccttctctcc cttgggctgc aacaacggct ccatttacta cgtggatgtg 1080
cagaagttcc ccttgccgat gaaagacaa caccctcttg tcagcgagct cctatcggacl 1140
gcagccggag atgggggtcac cgccctcagt gtctacctca cccccaagac cagtgcagct 1200
ggaaactgga tcgagatcgc ctatggcacc agctcagggg gcgtgcgggt cactgctgag 1260
caccgggaga ctgtggggctc gggggctcag ctcttcagca ccttcaactgt gcacccgagc 1320
cctgtcacca agatcatgct gtgcggaag cactcatctc cactgtctgc gccacaacac 1380
cagctgcgga catggtctgt gactcgcttc cgccgcatga ttccaccca gcccggtctc 1440
accocactgc ctctctttaa gatcctggct ctggagtcgg cagatgggca tggcgctgcg 1500
agtgctggca atgacattgg cccctacggg gagcgggagc accagcaagt gttcatccag 1560
aaggtgtgtc ccagtgccag ccagctcttc gtgcgtctct catcactgg gcagcgggtg 1620
tgctccgtgc gctccgtgga cggctcacc acgacagcct tcacagtgtc ggagtgcgag 1680
ggctcccgcc ggctcggctc tcggcccccg cgctacctgc tcactggcca ggcccaaggc 1740
agcttgggca tgtgggacct aaccacgccc atggacggcg tcggccaggc ccttgccaggt 1800
ggcttcgagc agcaagagct gatggaacag ctggaaacact gtgagatcgc ccccgccgct 1860
ccttcagctc cctcatgggg ctgtctcccc agcccctcac cctcagcatct cctcaccagc 1920
ctcactcatc cctccagcaa cactcctctg tctggccacc gtgggagccc aagccccccc 1980
cagctcgagg ccggcgccgc tgggtggggc agccttcttg aacgctgcca ggaactgtgt 2040
cggagtgggc cagacctccc acggccaccc acaccagccc cgtggccctc cagcggtctc 2100
ggcactcccc tcacactccc caagatgaag ctcaatgaaa ctctcttttg aacaacgcag 2160
ctgcatatg cctctgggat gccctgggtc tgggggaact aggtgcctcc ctgattcctg 2220
tgggaacccc gggttcaggc caggggctc cttggaataa atggttattg ttactaggtc 2280
cccactcttc ctctttctg gaagccaaag tcaccctccc caataaagtc ctactgccac 2340
aaaaaaaaaa aaaaaaaaaa c g

```

2361

<210> 6  
<211> 1638  
<212> DNA  
<213> homo sapiens

<400> 6

```

ggctgcggat ttgcgcggaa atcccggaag tgacagcttt ggggggtttgc tgetggctct 60
gactcccgct ctgcgatggg ttgcgacggg ggaacaatcc ccaagaggca tgaactgggtg 120
aaggggcgca agaaggttga gaaggtcgac aaagatgctg aattagtggc ccaatggaa 180
tatgttactc taagtccagg aatatgaaga cgaccaatag ttgctgtgta acttggcaga 240
ctttataaca aagatgcagc cattgaattt ctcttggaac aatctgcaga aaaggctctt 300
gggaaggcag catctcccat taaaagcatt aagaatgtga cagagctgaa gctttctgat 360

```

00573395-122790

aatcctgcct	gggaaggga	taaaggaaac	actaaagggtg	acaagcacga	tgacctccag	420
cgggcgctt	tcagtgcct	cgttgtgggc	ctggagatga	acggccgcga	caggtttctgc	480
ttccttcggt	gctgcggcgt	tgtgttttct	gagcgagcct	tgaaggagat	aaaagcggaa	540
gtttgccaca	cgctgsgggc	tgccctccag	gaggatgatg	tcactcgtct	caatggcacc	600
aagggaagat	tggaagctgt	gaagacaagg	atggaggaga	gaaggctgag	agcgaattgg	660
aaaaaagaaa	aaagaaaccc	aaggcagcag	agtctgttct	aaaaccagat	gtcagtgtag	720
aaagcccaag	gccatcaaaa	gttaagacag	ggaagcctga	agaagccagc	cttgattcta	780
gagagaagaa	aaccacactg	gctcccaaaa	gcacagcaat	gaatgagagc	ttctctggaa	840
aaagctgggaa	gcctccgtgt	ggagccacaa	agaggtccat	gcctgacagt	gaagaatcgg	900
aggcctacaa	gtccctcttt	accactcaca	gctccgcmaa	gcgctccaag	gaggagtctg	960
cccactgggt	cacccacaag	tcctactgct	tctgaagccc	gcactgccac	cgctcctgcc	1020
ccagaaggtt	gttttagttc	cacgtaggca	ggtcgctttg	tgccctctgag	tgccgtgctg	1080
tgtgttctct	ctatagttct	gtgtcataaa	gctgtcctgg	ccagcctcca	agctggtgtg	1140
gcacactctg	atgtgaggcg	tgtcggttcc	aggggggaca	tgggaggggc	tgccagctgg	1200
cccaggttca	tgcttgcctc	caacctgcag	tgcatattgt	cctttccatg	gccaggaagc	1260
cctgtgggat	gcacttttta	tgcttgtagt	acaagagagc	tcacagtagt	tcaccgttgc	1320
agagtgtgca	catatttaatt	aactaaaaat	ctaattgatc	gtctacccag	ataaatacaa	1380
gtaggccaa	tgaaacttgg	ctttaaaaag	gatggatttc	aaatacactg	tgcccaactg	1440
aaagcttcgaa	gggcctcgtc	cctctgctac	agccctggga	ggagccagga	tccttgttgg	1500
tttagtctaaa	tactgttagg	ggagtgtgcc	ccatctcatc	atttcgaaga	tagcagagtc	1560
atagtgtggc	accgcgtgat	tggyttcaaa	aataaagctg	gtctgcctct	tcaaaaaaaa	1620
aaaaaaaaaa	aaaaaaaaa					1638

<210> 7  
 <211> 1034  
 <212> DNA  
 <213> homo sapiens

<400> 7

cgccctgcgcg	tcagtgcgt	gccgctccgc	cgaccgaaga	ggctggacat	gacaccagt	60
gcataatcacg	gccatggggg	ctcagcattc	cgctgctgct	cgccctctct	ctgcaggcg	120
aaagcaagaa	gatgacagg	acggtttgct	ggctgaacga	gagcaggaa	aaagcattgc	180
tcagttccca	tatgtggaat	tcacggggag	agatagcatc	acctgtctca	cgctgccagg	240
gcaggagctac	atcccaacag	agcaagtaaa	tgagtgtgtg	gctttgatcc	gcacacagtga	300
tcagagattg	cgccctcagc	gaactaagca	atatgtcctc	ctgtccatcc	tgctttgtct	360
cctggcatct	ggttttgtgg	ttttctctct	gtttccgcac	tcagtcctgt	tggaatgatga	420
cggtatcaaa	tgatgtgaa	tcacatttaa	taagcaagac	tcoccttgtaa	ttctaccatt	480
catggccacc	ctgaaaaatca	ggaactccaa	ctctacacag	gtggcagctg	ccagcctgtc	540
cagccagatt	cagtacatga	acacagtgg	gaattttacc	gggaaggccg	agatgggagg	600
accgttttcc	tatgtgtact	ttctctgcac	ggtacctgag	atcctggctg	acaacatagt	660
gatcttcatg	cgaacttcag	tgaagatttc	atacatgtgc	ctcatgacc	agagctcctt	720
ggagacacat	cactatgtgg	attgtggagg	aaattccaca	gctattttaac	aactgctatt	780
ggttcttcca	cacagcgct	gtagaagaga	gcacagcata	tgttcccaa	gcctgagttc	840
tggaagctac	ccccagctgg	gtgttaaggc	agagggaaag	aattgtttca	ctttaacttc	900
ccaggcaaac	attcctcctg	gccacttagg	gagggaaaca	ccttccctat	gggttaacat	960
ttgtgttttg	ttcaggaacc	aggcggattc	agttgcctag	gcgtgtgtgc	ccagcaatta	1020
gtttgggcat	tgca					1034

<210> 8  
 <211> 947  
 <212> DNA  
 <213> homo sapiens

<400> 8

cgaggccctg	gcattgtgcaa	agagtactga	gtgggatttc	cagcaggata	ccatcaagta	60
ctacaccatg	cacctgacca	cattgtgcaa	cagctgattg	gacaacccaa	ccagagagaaa	120
caaggatcag	ctgatccggg	cagccgtgaa	gtttctggac	accgacacca	ctgtctacagt	180
ggtggaggag	cccgagacat	tagtggaa	tcaaaggaat	gagtgggatg	caatcatcag	240
atgggctgag	aaaagatacg	gcgtggagat	cagctcctcc	accagcataa	tgggaccag	300
catcctctgc	aaaactcgtg	aggtgctcgt	cagccacactg	gcactcttaca	acacatggcg	360
tttacaaggag	attgagtttg	tagctgccca	gctcaagttc	atggtgctaa	ccttgggct	420

gattgacctg cgcctgacag tggagcaggc cgtgctctg tcaagcctgg aggaggagta480  
ccagatccag aagtggggca acattgagtg ggcccatgac tatgagctgc aggagctgcg540  
ggcccgaccc gccgggggca cctctctcat ccattctctgc tccgagagca ccacagtcac600  
gcacaagctc ctgaaggagt gaggcctggg cagagcacac tcagcaggat agaggcagtg660  
cagccacagc tccccgggcc ttcagggtct cccagcctgt ggggctggct tccttggctt720  
ttggggactc ggccctcagcg tccccctgag attccccccg agacacagtg cgtcagtagc780  
gctgtccctg ggtcagcctg atttcaaccc aggtgccccct ggccctggcca gcagtgtaatg840  
taggagatga attgtgcaag tgactttctc tcgactctga tttttatata tattttctcca900  
cctctgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 947

<210> 9  
<211> 497  
<212> DNA  
<213> homo sapiens

<400> 9

ctcgtggcga gagactgaga taaaagagca actcactgaa cacctttgtg gatcatata 60  
gcaaatgag ctccgaaagg ccaagaagtt gaggagagtg atgcaacac tagatgtagal20  
agccgatgaa gagacttttg agcttgagtg ggagggtcag agattgtctac aggaacaaagal80  
agtgaataca aggagaccag tggttctgtt agagaggcca ttccagcctg cggaggagag240  
tgtgacatta gaatttggcta aagagaacag aaagtgtcaa gaacaagctg tttccccaaa300  
ggtgatgagc cagtgtggaa attccagtag catccccctt cttagtccaa actgccccaa360  
tcaagaaggt aatgacattt cagctgcttt ggccacatga agttcttgta ttcttttgag420  
ctaattatgt attgagtaaa gtatacttt ttcagtagat catgccctga cctccaataa480  
aaacctcttt aaaaaca 497

<210> 10  
<211> 269  
<212> DNA  
<213> homo sapiens

<400> 10

cggggagagc tgggctgggc tgcaggctct ggctgtgtgc tggatcatcg cggccgtact 60  
ctgaagtttt tccctgtggc ctcccttgaga ggggttccct ctgcatcttg agaattatttt120  
gcatttcggc tcccttctct tctcgtctgc atcggtatgc ccaaataggt cctgtcccct180  
cgttgaatca gacttcggaa accgcctcgc ttcagggtca gagtccaagt acagatgagc240  
ttgagagggg ttctgaaatg caacggccc 269

<210> 11  
<211> 1717  
<212> DNA  
<213> homo sapiens

<400> 11

attctaggac caacactcct gtggagacgt ggaagggttc caaaggcaaa cagtccata 60  
cctacatcat tgaggagaac actaccacga gcttcacctg ggccttccag agggaccact 120  
ttcatgaggg aagcaggaaag tacaccaatg acgttgccaa gatctactcc atcaatgtca 180  
ccaatgttat gaatgtcgctg gctctactct gcgcctcctg tgccctagaa gccctctgat 240  
tgggtctctc ctgcacctct tgtcctgtgt gttaactatg tgaccagagt tcaggaaact 300  
gccactcttc cccccctaac acaattctga aagcccaacca gccctatggt gtccaggcct 360  
gtgtgccctg tggttccagg accaagaaca acaagatcca ctctctgtgc tacaatgatt 420  
gcacctcttc acgcaacact ccaaccagga ctttcaacta caactctccc gctttggcaa 480  
acaccgtcac tcttctgtga gggccaagt tcaactccaa aggggtgaaa taactccatc 540  
actttaccct cagtctctgt ggaaccagg gtaggaaaat gtctgtgtgc accgacaatg 600  
tcactgacct ccggattctc gagggtgagt cagggttctc caaatctatc acagcctcag 660  
tetgccaggc agtcatcatc ccccagagg tgacaggcta caaggccggg gtttctctac 720  
agcctgtcac ccttctgtat cgacttatgt ggggtgacaac agatatgact ctggatggaa 780  
tcaactcccc agctgacaatt ttccacctgg agtccctggg aataccggac gtgatcttct 840  
tttataggtc caatgatgtg acccagctct cagattcttg gagatcaacc accatccgag 900  
tcagggtcgag tccacagaaa actgtccctg gaagtttgc gtgcaccaaa acgtgctcag 960

atgggacctg	tgatggctgc	aacttccact	tctctgtgga	gagcgcggt	gcttgcgcgc1020
tctgtcag	ggctgactac	catgctatcg	tcagcagctg	tgtggctggg	atccagagaal080
ctacttacgt	gtggcgagaa	cccaagctat	gctctgggtg	catttctctg	cttgagcagall140
gagtcaccat	ctgcaaaacc	atagattttc	ggctgaaagt	gggcatctct	gcaggcacct1200
gtactgcgat	ctgtgtcacc	gtcttgacct	gtctactttt	gaaaaagaat	caaaaactag1260
agtacaagta	ctccaaagctg	gtgatgaatg	ctactctcaa	ggactgtgac	ctgccagcag1320
ctgacagctg	cgccatcatg	gaaggcgagg	atgtagagg	cgacctcacc	tttaccagcal380
agaagtcact	ctttgggaag	atcaaatcat	ttacctccaa	gaggactcct	gatggatttg1440
actcagctgc	gctgaagaca	tctcagagag	gccacagacat	ggacctgtga	gaggcaactg1500
ctgctctcacc	tgctctctca	cctctgtcatg	cacctttgca	agcctgcggc	gatttgggtg1560
ccagatcctc	gcaacaccca	ctgctggaaa	tctcttcatt	gtggccttat	catagtggtg1620
aatttcagat	ctttttttat	agagtaccca	aacctctcct	tctgcttgcc	tcaaacctgc1680
caaatatacc	cacactttgt	ttgtaaatta	aaaaaaa		1717

<210> 12  
 <211> 1419  
 <212> DNA  
 <213> homo sapiens

<400> 12

ggcagaggtg	ttacctgaaa	acttaaaaaga	aggcctgaag	gaatcttct	ggagttcatt	60
accatgtact	aaaaacagac	cttttgattt	tcattcagtg	atggaaagagt	ctcagctctct	120
caatgaacct	agcccaaaag	agagtgaaga	aataccagag	gtcactctcag	agcctgtcaa	180
aggaagctta	aacctgtctc	agtcagcaca	gtctataaat	tcaacagaaa	tgccctgccag	240
agaggactgt	ttgaaaaaag	agtgccctca	gaacctgttc	tgtcagttca	agaaaaaggt	300
gttctgtctg	aaagaaaagt	gtctctttta	gaacaggatg	tgattgtaaa	tgaagatgga	360
agaaataaag	tgaaaaaaac	aggagaaact	cccaatgaag	tctgtatgtt	ttccttagct	420
tatgggtgata	ttccagaaga	attaactgat	gtctcagatt	tccagtgctc	tctctgcatg	480
agggtgtttt	ttgagccagt	aacaacccct	tcgggacatt	cgttctgtca	gaattgtctt	540
gagcgttggt	tagatcatgc	accatattgt	ctctcttgca	aagaaagctt	aaaagagtat	600
ctagcagata	ggaggttactg	tgctcacacag	ctgttggaag	gaattaatag	tgaagtatct	660
ccctgtagaa	ctgtctgaga	gaaaaaaaat	atatgatgaa	gaaactgctg	aactctcaca	720
cttgacaaag	aattgttcca	tattttgttg	actatgtgct	taccccaactg	tgccctgccc	780
tctctctgta	tttgagccaa	gatacagatt	gatgatcgca	agaagtatac	agacttggaac	840
caaacagctt	ggcatgtgtg	tcagtgatac	acaaaatagt	tttcagcatt	atggttgtat	900
gttacaattt	agaaacgtgc	atttcttacc	ggacgggaag	tctgtgggtg	atacagttgg	960
aggaagcgcg	tttaggggtt	taaaaagagg	aatgaagaat	ggatattgca	ctgccgacat	1020
tgaatatctg	gaagatgttc	aggttgagaa	tgaagatgag	attaagaatc	tcagagagct	1080
tcatgatttg	gtttactctc	aagcctgcag	ctgggttcag	aatttaagag	acagattttg	1140
aagccaaatt	tctcagcatt	tgggatcaat	gcccgagagg	agggaaaacc	ttcaggcagc	1200
ccctaattgga	ctctgactgt	gttggtggct	ctcttgcaatt	ctccctgtag	accacagata	1260
ccagctgtgc	gtttttgtcaa	tgaagctctt	gaaagaaagg	ttgacccaag	tacagacata	1320
actgacatcat	ttttctcagag	accaattctc	agtaactaac	tctttgggat	cttccctttg	1380
aaagttgacc	ccctaattctt	ggcctgccat	ttggttggg			1419

<210> 13  
 <211> 671  
 <212> DNA  
 <213> homo sapiens

<400> 13

agcgcggtga	agcggggggtg	ggatctgaac	atggcgggcg	tggtagctgc	tacggcgctg	60
aagggcgcggt	ggggcgagaaa	tgcccgctgc	ctccggggga	ttctcgagg	agccacagct	120
acaagggtct	ctcataaacag	gacccgggccc	ctgcaaaagc	acagctcccc	agagggcaag	180
gaggaaacctg	aaccctcatc	cccgagagctg	gaatacattc	ccagaaaagag	gggcaagaac	240
cccatgaaaag	ctgttgggact	ggcctggggc	atcgggtctc	ttcttggtat	ctcctctctc	300
atcctcaccac	agcggggaagt	ggacaaggac	cgtgtgaagc	agatgaaggc	tcggcgagaa	360
atcgcggttgc	ccaacacggg	cgatgatgag	agccagaggt	tcagggctgc	ctccagagat	420
gccccgtccc	ctgatgttgg	gtctgggggtg	cagacactgag	gagcgctgtg	acctcctagat	480
gctatttgact	gttaagctcct	caggtttggc	ccagattcca	gttctgtcct	ctgaggtcca	540
ccagagggcg	catgaagccc	aggctgttgc	caaacctcac	cctgccccac	accaaggagc	600

ccaccaaaagg caaataaaagt tattgagtgt ttagtagaaa ggaaaaaaaaa aaaaaaaaaa660  
 aaaagtcgac c 671

<210> 14  
 <211> 524  
 <212> DNA  
 <213> homo sapiens

<400> 14

aagtgttctc agatgctgat gtttgaagg tcccgggtggg gccatgagga agaagaggag 60  
 ctgaagggttaa gagactcata aacaagatga ctctttgatg catgaacaag atttggaaatt120  
 ctcaagccctg taaagaatac cccctgctatt taaataaaagc tcataccaag aggttaacatt180  
 ttgccccggg ccaaatccag ggggtctagtg cccctgcatc ctttgaggca aaaaataaat240  
 gggctatgac tggttaaatg tccaaaaagg gaattctcat ttcattcaaa caaagacaga300  
 ttgctgcatt cactcaagca gaatgtggcc atgaatatc agcccttgca tacatacaaa360  
 gatgtacgca tgattccccc caccagcac acacacagtc acacacgac acacacacac420  
 atgcacacac gcgcgtgcac acacggacac atgcacacac acacgcacac gtaaacacat480  
 gcacacatgc acacacgtgc acacatgcac acacggacac actt 524

<210> 15  
 <211> 345  
 <212> DNA  
 <213> homo sapiens

<400> 15

aaactttctt tctacaaaa atcaaaagct tagctgatag atcatgaaaa tagattatga 60  
 acagtgaatt tcttgagaag gctgaaagtg cggggaacca aagcaggagg gattagcctt120  
 agtccggagg agggagaagc agatggaagt cagcagcctg ccttggtttt acgtgtaata180  
 tttaaatttg caaatgtgat tacaggaggg cctactttct gtttttatca agagtttttc240  
 ttttcttcaa agacactggg tatgggaata ttttgaaagg gtaagaaacg ctggtataaa300  
 aaggtgttgc agattaattt tgaaggtctc tacggaacca gtccc 345

<210> 16  
 <211> 1060  
 <212> DNA  
 <213> homo sapiens

<400> 16

ggcgggtccca ggcaggccca gaagctgggg agcctctgcc ggggtccggg aaaaggagct 60  
 cctgctgcca ctgctcttcc ggagcctgca gcatggggcc cctgcgcgc accgtggagc 120  
 tcttctatga cgtgctgtcc cctactcctt ggctgggctt cgagatcctg tgccggtatc 180  
 agaatactct gaacatcaac ctgcagttgc ggccagcct cataaacagg atcatgaaag 240  
 acagtggaaa caagcctcca ggtctgttcc cccgcaagg actatacatg gcaaatgact 300  
 taaagctctt gagacacat ctccagattc coactccact ccccaaggat ttctgtctg 360  
 tgatgtctga aaaaggaaagt ttgtctgcca tgcgtttcct caccgcctg aacttggagc 420  
 atccagagat gctggagaaa gcgtcccggg agctgtggat gcgcgtctgg tcaaggaaat 480  
 aagacatcac cgaggccgag agcatcctgg cggctgcaga gaaggctggg atgtctgcag 540  
 aacaagccca gggacttctg gaaaagatgc caacgccaaa ggtgaagaaac cagctcaagg 600  
 agaccactga ggcagcctgc agatacggag cctttgggct gcccatcacc gtggcccatg 660  
 tggatggcca aaccacatg ttatttggct ctgaccggat ggagctgctg gcgcacctgc 720  
 tgggagagaa gtggatgggc cctatacctc cagccgtgaa tgccagactt taagattgcc 780  
 cggaggaagc aaactcttgc tataaaaaaa gcaggccatc tgcttaaccc ttggctccac 840  
 cataaggcac tgggactcgg atttctctat ctgatagagg tattttctgt ggccctggga 900  
 gctgtctgtc ttcccccac ccccaaggat gccagggaaga cgtccacatc tagccatgtg 960  
 gcaaccctta cttctatgac tcacaagtc ctttcagaga gccccaattc tgctttccaa1020  
 caaaataaac ctaatgcatc caggcaaaaa aaaaaaaaaa 1060

<210> 17  
 <211> 1721  
 <212> DNA

0067395.12270

<213> homo sapiens

<400> 17

```
ctctctctctct tctctgtctct tctctgtctct ctctctctctt ctctctctctc tgccttccca 60
gtgcataaag tctctgtctgc tctctgtctgc tgttggcaat gcctattttt tgggtttccc 120
ccggttctctc taaactaaact atttaaagggt ctgcggtctgc aaatggtttg actaaacgta 180
ggatggggact taagtgtgaac ggcagatata ttctactgat cctcgcgggtg caaatagcgt 240
atctcgttgcg ggcgcgtgaga gcagcgggca agtgcgatgc ggtcttccaag ggcttttcgg 300
actgttttgc tcaagctgggc gacacatggc caactaccgc caggcctgga cgacaagacg 360
aacatacaaga ccgtgtgcac atactggggag gatttccaca gctgcacggt cacagccct 420
acggatttgc aggaaggggc gaaagatatg tgggataaac tgagaaaaga atccaaaaac 480
ctcaacatcc aaggcagctt attcgaactc tgcggcagcg gcaacggggc ggccgggtcc 540
ctgctccggg cgttcccggt gctcctgggt tctctctcgg cagcttttagc gacctggctt 600
tccttctgag cgtggggcca gctccccccg cgcgccacc cactactcact ccattgtccc 660
ggaaatcgag aggaagatcc attagtctct tggggacggt gtgattctct gtgatgtgta 720
aaacactcat ataggattgt gggaaatcct gattctcttt tttatttcgt ttgatttctt 780
tgcgttttat tgcctaaatgt taccaatcag tgagcaagca agcacagcca aaatcggacc 840
tcagcttttag tccgtcttca cacacaaata agaaaaaggc aaacccacc ctttttttaa 900
ttttattatt attaatcttt tttgttgcca aaagaatctc aggaacggcc ctggggccacc 960
tactatatta atcatgctag taacatgaaa aatgatgggc tcttccaat aggaaggcg 1020
ggagaggaga aggcacgggg aatgaattca agagagatgt ccacggacga aacatacgg 1080
gaataatcca cgtctcagtc gttcttcac agtatcttgt ttgtatcatt tccactgcac 1140
atttctctcc aagaaaagcg aaaggacaga ctgttggcct ttgttttggg ggataggagg 1200
gattagaggga aggggtctag gaaatctctg gggtaagagt aaaggctctc agaagacatg 1260
ctgtcatgtt cactgacggg ttactgttat ctgctgttgt tgatgcacac gtccaagctg 1320
actcgtcttt ttttccctcc tccctcttgt tttagcttgt acacacacag taatcacctg 1380
atatccaacg gtagatata caaggggggg atgttaaatg ttaattctaa atatagctaa 1440
aaaaagattt tgacataaaa gagccttgtt tttaaaaaaa agagagagag agatgtaat 1500
taaaaagattt attataaatt aaattcagca aaaaagattt tgctacaaag tagtagaag 1560
tataaataaa aagttattgt ttgaaaaaaa agtgcgtgtt gtttccatcc ccaactctg 1620
ttcttgaccg agtttccagg gaacctgaag ggacacagga aagctcacct 1680
cttcagggaag ccgcttcaag cagacctgcc accttcaagc a 1721
```

<210> 18

<211> 2367

<212> DNA

<213> homo sapiens

<400> 18

```
acctctgtgt cccgggtttc tgcagagttc acttcagaag cggaggcact gggagtcgg 60
tttgggattg ccaggtctgt gttgtgagtc agcggctgtg gcgcccaac 120
tcttcgccag catatcatcc cggcaggcga taaactacat tcagttgagt ctgcaagact 180
gggagaaact ggggtgataa gaaatctatt cactgtcaag gtttattgaa gtcaaaaagt 240
ccaaaaaaat cagtgccggt tctgtggtag agatgcaagg agatgaaatg acacgaatca 300
tttgggaatt gattaaaag aaactcattt gttcctacgt ggaattggat ctacatagct 360
atgatttagg catagagaat cgtgatgccca ccaacgacca agtcaccacg gatgctgac 420
aagctataaa gaagcataat gttggcgcca aatgtgccac tatctgcca tcatcgaaga 480
gggtataaga gttcaagttg aaacaaatgc ggaatcacc aatgtgcacc atacgaaata 540
ttctgtgtgg cagcgtcttc agagaaggca ttatctgcaa aaatatcccc cggttgtgta 600
gttgatgggt aaaaactatc atcataggtc gtcatgctta tggggatcca tacagagcaa 660
ctgattttgt tgttctctgg cctggaaaaag tagagataac ctacacacca agtgacggaa 720
cccaaaaagt gacataacgt gtacataact ttgaagaagg tgggtgtggt gccatgggga 780
tgtataatca agataagtca attgaagatt ttgcacacag ttccttccaa atggctctgt 840
ctaagggttg gcccttggat ctgagcacca aaaaacatct tatgaagaa tatgatggc 900
gtttttaaag catctttcag gagatatacg acaagcagta caagttcccg ttggaagct 960
aaaaagattg tatgtgacat aggtctatcg agcacatggt ggcccaagct atgaaatcag 1020
agggaggcct catctggggc tgtaaaaact atgatggtga cgtgcagctg gactctgtgg 1080
cccaagggtg tggctctctc ggcattgatg ccagcgtgct ggtttgtcca tagggcaaga 1140
cagtagaagc agaggctgcc ccagggactg taacccgtca ccacggctg taccagaaa 1200
gacaggagac gtccccaact ccattgtctt catttttgc ctggacagca ggggttagcc 1260
acagagcaaa gctgtataac aataaagagc ttgccttctt tgcataatgc ttggaagaag 1320
```

09673395-12700



tctctattga	gacaattgag	gctggcttca	tgaccaagga	cttggctgct	tgcattaaag1380
ggttaccocaa	tgtgcaacgt	tctgactact	tgaatacatt	ttagtctcatg	gataaaacttg1440
gagaaaactt	gaagatcaaa	ctagctcagg	ccaaaactt	agttccatacc	tgagctaaag1500
aggataatgt	tcttttggt	actaggtcta	cagggtttaca	tttttctggt	ttacactcaal1560
ggataaaagg	aaaatacaat	ttgtaatttg	tttagaagcc	agagttttac	ttttctataal1620
gtttaccagcc	tttttcttat	atatacagtt	attgccacct	ttgtgaacat	ggcaagggaac1680
ttttttacaa	tttttatttt	attttctagt	accagcctag	gaattcgggt	agtactcatt1740
tgtattcact	gtcacttttt	ctcatgttct	aattataaat	gacccaaatc	aagattgtct1800
aaaaggggt	atgatagcca	cagtattgct	ccctaaaaata	tgcataaagt	agaaaactc1860
tgcttctccc	tctgtgccat	gacctggggc	acaggggaagt	tctgggtgtca	tagatatccc1920
gttttgtgag	gtagagctgt	gcattaaact	tgacatgac	tggaaacgaag	tatgagtgca1980
actcaaatgt	gttgaagata	ctgcagtcac	ttttgttaag	acctgtctga	atgtttccaa2040
tagactaaat	actgttttag	cgcaggaga	gtttggaatc	cggaaataaat	actacctgga2100
ggtttgtctc	ctccattttt	ctctttctcc	tctgtggctg	gcttgaatat	tatactact2160
taaatagcat	atttcatcca	agtgaataaa	tgtaagctga	atcttttttg	gaacttctgct2220
ggctgtgttt	atttctttta	tataaatgtg	atttctcaga	aattgtatatt	aaacacatat2280
ttatcttctc	ctgaactgtt	gattttaatt	aaaattaagt	gctaattacc	attaaaaaaa2340
aaaaaaaaaa	aaaaaaaaaa	aaaaaaa			2367

<210> 19  
 <211> 1321  
 <212> DNA  
 <213> homo sapiens

<400> 19

cttggaaaca	agatccaaac	ccaagtgacc	ccgcccggaaa	gtgaccacgt	cagggttataa 60
aattccaaca	aaccgacgtg	aacaaataga	ccgaccaacc	aaatataaca	tccgtcaaaa 120
tacattcact	tccactacga	aaccccaaca	aaggggtgtga	atgccccccc	aggagagacg 180
gttttggttt	catcaaggtg	gtggatcgtg	atgttcgtat	gtttctccac	ctcagtgaaa 240
ttctggatgt	gaacacagctc	catattgcag	atgaagttaga	gtttactgtg	gttcttgata 300
tgtctcttgc	tcaaaagaaat	catgctatta	ggattaaaaa	acttcccaag	ggcacgggttt 360
catcttcttc	ccattcagat	caccgttttc	tggggcacggt	agaaaaagaa	gccacttttt 420
ccaatcccaa	aaccactagc	ccaaataaag	gcaaaagagaa	ggaggtctgag	gatggcata 480
ttgcttatga	tgaactgtgg	gtgaaactga	ctattgtctt	tcaagccaa	gatgtggaag 540
gatctacttc	tctctcaata	ggagataaag	ttgaatttag	tattagtac	aaacagagcc 600
ctggacagca	ggttgcaact	tgtgtgcgac	ttttaggtcg	taattctaac	tccaaaggcc 660
tcttgggtta	tgtggcaact	ctgaaggata	attttggatt	tattgaaaca	gccaatcatg 720
ataaggaaat	ctttttccat	tacagtgaat	tctctgtgtga	tgtgtgtagc	ctggaaactgg 780
gggacatgg	cyagttatag	ttgtccaaag	gcaaaaggcaa	caaaagtcatg	gcagaaaaag 840
tgaacaaaac	acactcagtg	aatggcatta	ctgagggaagc	tgatccccac	atttactctg 900
gcaagatgat	tcgccccctg	aggagtgtg	atccaacaca	gactgagtag	caaggaatga 960
ttgagattgt	ggaggggggg	gatatgaaag	gtgaggtcta	tccattttggc	atcggtggga1020
tggccaaaca	aggggtattgc	ctgcagaaag	gggagagcgt	caagttccaa	ttgtgtgtcc1080
tggggccaaa	tgcacaaact	atggccttaca	acatcacacc	ctctcgcgagg	gccacagtg1140
aatgtgtgaa	agatcagttt	ggcttcatta	actatgaagt	aggagatagc	aagaagctct1200
ttttccatgt	gaaggaagtt	caggatggca	ttgagctaca	ggcagagagat	gaggtggag1260
tctcagtgat	tcctaagagt	tcaggcggac	tggcagggtc	aggcgctctg	agatgttttg1320
g					1321

<210> 20  
 <211> 384  
 <212> DNA  
 <213> homo sapiens

<400> 20

ggctgaatcc	aaatcactca	ttgtgaaagc	tgagctcaca	gccgaataag	ccaccatgag 60
gtgtcagctg	tgtctcctga	tggtctcgtc	ggccctttgc	tgtctaccag	cccactgct120
tgtctgcoca	gtctgtcctt	ctgagatcac	agctctctta	ttcttaagt	acgtctcggt180
aaactctcaa	gttgccaaac	ttaatccacc	tccagaagct	ctctcagcca	agtttgaagt240
gaagcactgc	accgatcaga	tatcttttaa	gaacgcgctt	ctcatttgaa	aaagtctctg300
gtgggaatag	tgaaaaaatg	tgggtgtgtg	acatgtaaaa	atgctcaacc	tgggtttcca360

aagtccttttc aacggcaacc tgat

384

<210> 21  
<211> 367  
<212> DNA  
<213> homo sapiens

<400> 21

```
gggcactgggt ggtccgggttc ctcaccaaac gattcatcgg tgactatgaa agaaatgcag 60
gtaatctcta tactagacaa gtccagatag aaggtgaaac cctggctctt cagggtcaag120
acaactccagg tattcagggtc catgagaaca gcctgagctg cagtgaacag ctgaataggt180
gcatttcgctg ggcagatgct gtggtgatcg tttctccat cactgactac aagagctatg240
aactcatcag ccagctccac cagcacgtgc agcagctaca ccttgggcgc ccggctgcct300
gtgggtgttc gtggggcaca aaaagtgacc tgttgccat caaacagggt gacctcagc360
tggaact
```

<210> 22  
<211> 2621  
<212> DNA  
<213> homo sapiens

<400> 22

```
gggccttttc cgccttggc ggccggctct acgttccctg ttctgcctg cagctccgcc 60
atggctccta aaggcagctc caaacacgag tctgaggagg acctgctcct gcaggatttc 120
agccgcaatc tctcgcccaa gtctccgcg ctctctctcg gaaacgggtt catctgtctc 180
gccatcccca tctggttata ctggcgaaat tggcatatgg atcttattca gtctgctgtt 240
ttgtatagtg tgatgacctt agtaagcaca tatttggttag cctttgcata caagaatgtg 300
aaatttggtt tcaagcacia agtagcacag aagagggagg atgctgtttc caaagaatgt 360
actcgaaaac tttctgaagc tgaataataga aagatgtctc ggaaggagaa agatgaaaga 420
atcttctgga agaagaatga agttgctgat tatgaagcta caacattttc catcttctat 480
aacaacactc tgttctctgt cgtggtcatt gttgcttctt tcttcatatt gaagaacctc 540
aaccocacag tgaactacat attgtccata agtgcttcat caggactcat gcccctcctg 600
tctactggct ccaaatagac catgtcagct tcacccctcg gctttgtgtc tatgggtggc 660
ctgtggtata tggaaaagta gcagggtggt cagggtggga gacacaagat gtttttatag 720
tctagagcct ttaaaaaacc cagcagaatg taattcagta tttgtttatt ggctgttttt 780
tgacagattg ttgaaattaa atgaattgaa agggaaaactc agagtactag gactgttatt 840
aaaaggaaaa aaatgtcttg caatgtgctg taatcacaa aggagaaaaa aacttgtttc 900
cttgatctgt cagaggtctc agtaacctgg gccagagctg tattatttat tataataag 960
tagtaggaag ttaataactc gttctctgtg ttccaaagcac aatatattaca ctctctttga1020
accgttaata tcagaaatgaa tctctctccc aggggattga acagaagctt aatgtttaca1080
agtgtttgaa tttgtgatct gaaataaacac aaaaattaaaa acatgatttc tctaattttc1140
caactagagg aagagaactc tgtggaaaaa ttcttttttt tctgtttttt ttctctaaag1200
aaggcgagcc aaggtagtaa cctaaaaata gtgccaggc atatgagat ttctctacag1260
ggtaaaagaa cacactgttc cactgtatgg cttggccct gatggccag ggaggtcaac1320
ttgacctgtc oatgttggtt tgacttacta agacacagga acatgtgtt tctttgacc1380
gggtctcaca cctctggagg atgttaagta agagaagaa cctctttcct gaattattga1440
atgtaaaaga ccaagtaaat ttttctgaac ttctgcaatt ctgagaacct tccaaggaat1500
ttacagtagt tttagtgtt gtccagattt ttccatgagg accttctaac atttgactct1560
ttagtccaca ggttccattt gattgtgagc aagatattta tctcttttagc ccttggggat1620
ccagctgaga gcaactctct gcattttttt acccgtgtat gtacagatat caattcttgt1680
gtatgccatg actgaaaaaa gtttgggaag ctcttttagca atatcagcta aaaggatatt1740
aaatcacagg tctagcagtg tgcattccag taatttccca caagcagcac ccaaaaggaa1800
atatagctct aatctttact atccacttct aaatttaatt tgaattttat caatgttatt1860
agttgttttc tttataattt tataaaaaat attcatcggt agtttaacct ccaacttccat1920
gctatcggtg gtgttgggct ccatgcaaga acctggaaga aaaacaggca ggaatgcatt1980
tgcataatga cccagatcat cattttctgc actgagaat tatattttct caattgtct2040
agaagctctg aatctcttac ttttcttgg tgcatattta tctaggtgac atcactggat2100
aatgtggagt gactagagaa gtccacatct acctgaaggt acagtagagg taacctatt2160
gaggttttatt attttataaa aacttttctt gaactcctg caacatggt gaaaccccg2220
ctctactaaa aataccaaaa ttgaccaggc gtgatgggtg gtgcctgtaa tctcagctac2280
ttgggaggct gaagcaggag aactgcctga acccaggagg cagagggttg agtgaagtga2340
```

00673305-12200

```

gatcgtgcta ctactgcctg ggtggcaagg gtgagactcc atctcaaaaa agaacaacaa2400
aaaccccaaaa agttttcttt actgtgtggt aaaaaaataa gccagaccat agtttggactg2460
gtggcatgga atttggtgat caaataaaatg catttgctta ttgacaaac aaaaagtgtc2520
cactattggt gaccgaggtg gggccgtttt ttggaaaatg ggggggaaat ttgcccgctg2580
gtgggagggc ctttgtgggg ggggaaaaat tgccccttg g

```

<210> 23  
 <211> 2019  
 <212> DNA  
 <213> homo sapiens

<400> 23

```

ctgtatccta atttcttggt gaatgaactc attcttaaac agaagcaaa atttgaggaa 60
aagaggttca aattggacca ctcagtgagt agcaccaatg gccacagggt gcagatattt 120
caagattggt tgggaaactga ccaagataac ctgtatttgg ccaatgtcaa tcttatgttg 180
gagttactag tgcagaagaa gaacaactgt gaagcagaat cacatgcagc ccaactacag 240
attcttatgg aattctctaa ggttgcaaga agaataaaga gagagcaact ggaacagatc 300
cagaaggagg taagtgtttt ggaagaggat attaagagag tggaaagaaat gagtggctta 360
tactctcctg tcagtggagg tagcacagtg cctcaatttg aagctccttc cagttctcag 480
agtagtatta ttgattccac agaatacagc caacctccag gtttcagttg cagtagtgac 540
acaagaagaa agccttggtg taatagcacg ttacatcaa gacgaaaaag acttactgct 600
cattttgaag actttggagca gtgttacttt ttacaagga tgtctcgtat ctacgatgat 660
agtgcgaact caagccagtt ggatgaattt cagggaatgct tgtccaagtt tactcgatat 660
aattccagtac gaccttttagc cacattgtca tatgctagt atctctataa tggttccagt 720
atagtctcta gtattgaatt tgaccgggat tgtgactatt ttgcgattgc tggagttaca 780
aagaagatta aagctctatga atatgacact gtcacccagg atgcagtgga tattcattac 840
cctgagaatg aaatgacctg caattcgaaa atcagctgta tcagttggag tagttaccat 900
aagaacctgt ctatagcagc tgattatgaa ggcactgta ttttatggga tggattcaca 960
ggacagaggt caaagggtcta tcaggagcat cagggaagggt gttggagttg tgactttaat1020
ttgatggatc ctaactcttt ggcttcaggt tctgatgatg caaaagttaa gcgtgggtct1080
accaactctag acaactcagt ggcaagcatt gaggcaaaag ctatgtgtgt cgtgttataa1140
ttcagccctc ctccagataa ccatttggct ttgggtctga cagatcactc tgtccactac1200
tatgatcttc gtaacactaa acagccaatc atggtattca aaggacacgc taaagcagct1260
ctttatgcaa agttttgtgag tggtagaggaa attgtctctg cctcaacaga cagtcagctal1320
aaactgtgga atgtagggaa accatactgc ctacgttctc tcaagggttc tatcaaggaal1380
aaaaactttg taggcctggc ttccaattgga gattatatag cttgtggaaag tgaataaac1440
tctctctacc tgtactataa aggaactttc aagactttgc taacttttaa gtttgatacal1500
gtcaaaaagt tcttcagaaa agaccgaaaa gaagatgata caaatgaatt tgttagtgct1560
gtgtgtctgga gggcactacc agatggggag tccaatgtgc tgattgctgc taacagtcag1620
ggtaacaatta aggtgtctaga attgggtatga agggtttaac caagtcaaat tgtacttgat1680
ctcgtctgaaa tacatctgca gctgacaatg agagaagaaa cagaaaaatgt catgtgatgt1740
ctctccccaa agtcatcatg ggttttggat ttgttttgaa tatttttttc tttttttctt1800
tctcctctct gatgaccttt gggacattgg gaataccagc ccaactctcc accatcaatg1860
taactccaat gacattctgt ctcttggtag ttgtattcta tttttgtgat agggaacacal1920
attcttttga ataaaaataa ataacaaaac aataaaagtt tattgagcca caaaaaaaal1980
aaaaaaaaaa aaaaaagaaa agaaggaggg agggaaaag

```

2019

<210> 24  
 <211> 1866  
 <212> DNA  
 <213> homo sapiens

<400> 24

```

gtgggtgctg tgacaggcac tatttgaagt gctttatcat ggattaactc ttaactctca 60
gctaccgtat aaagtaggac ataaccocat ttccatgca ctacactgag acttgccctc 120
tctcccccca ctattgaagt gttctttttt cataactata tactattcca ttgcatgat 180
attctgtaat ttattttaat ccttatggat tgataattag gttcattata gatagaagtg 240
taataaacat tctgtgatcat gtatttttgt acttgtgtgg gtattttctg aggatgaata 300
actagaataa tattgtatca ggtttcacat ttgcagtttt gaaaactact accaaaaaga 360
tttcaccaat ttacaactcc atcattagta agaagtgcctg ttgtgctata gctctgccaa 420
ctcagatcct taaaaaattt tgccaactctg gtaggcaaaa tttctttgact tttctttgaa 480

```

```

attaatgagg aggaacatct tttcatgttt ctgtggccatt tgcatttctt attatgaatt 540
gcttttgccc atttttcttt ttttaattat gaaagtctaa tgcattcttt ctcatgtgat 600
aaaaaacaca gttctttgaa tagagagacc cttttctoca atgtacccaa tcacattcca 660
cttaccacag ttttaacatac atccctctagt caccctttccg tacgaatata catcacata 720
aaaaacattt ttacataaat aggtatctcat attctgtagc tttttaaaat ttgtgtctca 780
aaaaacagata acaggtctttt aaatttctttt aatgggtgaa tatgattaaa tactatgaaa 840
atgccaattat ttattcccttt aatttttttct ctctcgctat tacatgtcca aagtaaacat 900
cctattcaga tgtctttgtg catgtgtgtg aatatttctt tagtctggag tccagtaagg 960
tggatttttg gatcaaaagg ttgttctctt gtccaacttc agtcttccca aaggcttca1020
taactgtatt ttccaacagt gtatggagaa tgttcatttc cccatataac catactaca1080
cttgatagtt tttatttgtt gggcgaaaaa gaaccttttc ttattttgca ttccctgga1140
tataaaaaaa aatgggtgaga ttgggggttat ttctatgttt attggccatt atagttttac1200
tgtggattgt ttgtatccct tacctgtctt ctattggggt atgtgtggat atatgttttt1260
tatttgttca gcatctctt ccccatcttc tggtaacaca accttttatt atttgtgggg1320
aacctattcc ctgtggctta ggtgagcatg tgaccaggcc tggcctcctg agtcccacag1380
cttctagcc acagtgataa aagaatgggt atataactta agccaggcta aggaagccc1440
ttaacagAAC tctgtctgga actactggaa agaagggttt atggagatcc caggaaacca1500
ggacccatga agcctgaatt tgtgccatgt ggagagagtc tgtctgagga gaaactcgga1560
tgctagcaga aatggaaagt gaactaaagt ctgatgtcat tttttgtgag gccctagatc1620
cagctgtgcc taaagcctgc cctacctccg gactttaaag ttttgtgagc gttatttgtat1740
ctttcttgtt ttaagataat tgaattgagt ttctgttctg atttaatatg atgtactata1800
ttttcttatt gatttgtaga aaacctttgt aatttttaaa aaaaaaaa 1866
taagtttaata aaattagcat ggccttccat gaaaaaaaaa
aaaaaa

```

<210> 25  
 <211> 1189  
 <212> DNA  
 <213> homo sapiens

<400> 25

```

ctagcaagca ggtaaacagc ctttgtacaa acacacacag accaacacat ccggggatgg 60
ctgtgtgtgt cttagcagca ggcgtattaa acactcagtg tgttggctct ctgtgcaact 120
cctggaaaaa aatgaattgg gtaaggaaaca gtttaataaga aaatgtgcct tgtctaactgt 180
gcaattacca acaagaagct gccagctcct gaaggaaaaa ggctgtgccc ctgcgcgttc 240
aaacttgtca gtcaactcat gccagcagcc tcagcgtctg cctccccagc acaccctcat 300
tacatgtgtc tgtctggcct gatctgtgca tctgtctcgga gaagctcctg acaagctggg 360
aatttctcta ttctctcact ggtgcaaaaga gcggatttct cctctgtctt cttctgtcac 420
ccccctctct ctccccccag aggcctcctg atttatggta gctttggagt tgcttccccg 480
ctgtactctc ctgtactctc agaattggaag aagctgagct ggtgaaggga agactccagg 540
ccatcacaga taaaagaaaa atacaggaag aaatctcaca gaagcgtctg aaaatagagg 600
aagacaaact aaagcaccag catttgaaga aaaaggcctt gagggagaaa tggcttctag 660
atggaatcac cagcggaaaa gaacaggaag agatgaagaa gcaaaatcaa caagaccagg 720
accagatcca ggttctagaa caaagtatcc tcaggcttga gaaaagatc caagtcttg 780
aaaaagctga actgcaaatc tcaacgaagg aagaggccat ttttaagaaa cttaaagtcaa 840
tgagcggcag aacagaagac attataagat ctgtgaaagt ggaagagaga gaaagcagc 900
aagagtcaat tgaggcaatc tatgctaata tccctgacct tccaaagtcc tacataactt 960
ctaggtttaag gaaggagata aatgaggaaa aagaagatga tgaacaaaat aggaagctt1020
tatattgcat ggaaattaaa gttgaaaaag acttgaggac ttgagaaaat acagttctgt1080
cttcaatacc tgtcccatca gatgacttta aaaggtccag gattaaaagt ttatgatgat1140
gggcaaaagt ccagtgtatt cagtaaaagt ctaatcacia ttggagggt 1189

```

<210> 26  
 <211> 1418  
 <212> DNA  
 <213> homo sapiens

<400> 26

```

gagctcgcag ctccgcggcg gectgggtccc agcgcgccgg ggcgcgcgtc ccggggccaa 60
ccatggcgctc ctccgcggcg ggcgtgcgtgg tgatcgttgg cagtggagtc attggggcaa 120
gtgggccaatg ctggttgcca gtggaggctt ccaggtgaaa ctatgcaga ttgagcaca 180

```

```

gcagataagg aacgcccttg aaaacatcag aaaggagatg aagtgtctgg agcaggccag 240
ttctctgaag ggcctccctga gtgtggaaga gcagctgtca ctcatcagtg gttgtcccaa 300
tatccaagaa gcagtagaagg gtgccatgca cattcaggaa tgtgttccag aagactctaga 360
actgaagaag aagatttttg ctcagtttaga ttccatcatt gatgatcgag tgatctttaa 420
cagttccact tctgtctcca tgccctccaa gttgtttgct ggcttggtcc atgtgaagca 480
atgcattcgt gctcatccct tgaatccgcc atactacatc ccgctgggtg agctcggtccc 540
cgaccgggag acggccctta cgacagtggg cagaaccacac gccctgatga agaagattgg 600
acagtgcccc atgcgagtc agaaggaggt ggccggcttc gttctgaacc gccctgaata 660
tgcaatcatc agcgaggcct ggccgctagt ggaggaaagg atcgtgtctc ctatgacct 720
ggacctgttc atgtcagaag ggttgggcat gcggtatgca ttcattggac cccctgaaa 780
catgcatctc aatgcagaag gtatgttaa gctactgcag agatacagc aaggcataaa 840
acatgtctca cagacttttg gaccattcc agagtttcc agggccactg ctgagaagg 900
taaccaggac atgtgcatga aggtccctga tgaccgggag cacttagctg ccaggaggca 960
gtggagggac gagtgcctca tgagactcgc caagttaga agtcaagtc gccccagtg 1020
aatttcttgt aatgcagctt ccactctct cattggaggc cctatttggg aacactgcaa 1080
gccttcaatc agccctctgt gacataggt gacgccacg gagatccta gaggctgtc 1140
ttgtgtcgag cctgagtggt gtggtgcagg ccggtagtct gccctgca ctggtcatc 1200
gccttggggc tggcggcaca gcagcaettg cgttctcggg gctgtcgatt tctgagatt 1260
tgggcagata acctggagat ttccacctt tctttttcag cttgattgca tttgagatt 1320
atttgacagc cagtgattgt agttttcatg ttaatatgtg ggcaaaaat ttttgaatt 1380
attttgttaa tccctttctg agtaatctgg ggttccct 1418

```

<210> 27  
 <211> 814  
 <212> DNA  
 <213> homo sapiens  
 <400> 27

```

gcagcaacgg ggtgcggcag ggtggggaac gggggagggg gccagctccc aggaagctg 60
ctctgcgagc ggcctctgcc cggctccca gtcctcgcc gaccocggcc tcccagagac 120
ccagccgggg ctgcgcggcc cgtcccgga gtcacagct gaacctgtt ttccattgt 180
ggcccaaatg aggcacatgt ggtctccggg ttctgcccga gcccccagct catggtggct 240
ggaggcgctg tctttgtctc gccctgcac caacagatoc agagatctc tctcaacaca 300
ctgacctcta atgcgaagag tgaaaagggt tacactcgcc atggggctcc catctcagtc 360
actggcattg cctttcagag gctttcagc ccttttccc acagtcact tcccactcac 420
cctctctccc agacattaag acatcttctg gccacagct tctcaacct tgcctcgaga 480
gaagtctctc tgctagtctc atcttttcca ggcacccac ggcactctgc tctcctctcc 540
ttctttccct gaaatggaa gagcatttct gagagggtc tccctctct ctctgtttt 600
cctctgactt catgagacc ccaccacac ttctctaccc ctactctggt tacaggtaaa 660
aatccagggg cagaacaagg agatgttggc ggcccgctg cagatgttgc tggggaagac 720
ggaggctgag attgccaca ttgccctgga gacgttagag ggccaccaga gggccatcat 780
ggccacatg acttgtggga ggttgggct taga 814

```

<210> 28  
 <211> 3039  
 <212> DNA  
 <213> homo sapiens  
 <400> 28

```

gaactgagat attgtaatca aatagttaac atcaggaagt taatttggtt ggcaaaattc 60
tagggaaact tggccagaaa actgggtgtg aaggcttttg ctcatataaa caagtgcct 120
tgagtttcaa atgaccagca aatatattta gaaccttctg ttgtttatgt ctgtacctcg 180
tccacccctc aggttaatacc tgccctctac aggtacagct gtttcttggg aatcctccaa 240
c0aaatagca gttttctctaa cttgattagc ttgagctgac agactgttag aatacagtc 300
tctggccaca gctgatgagg gctttctgta ctgcacacag attgtgtact gaacccagc 360
ccaggtgact ggtaccacac cgagtgtgtc cgtgcaaaac ctgtccagta tatgcatgtg 420
gtggccctac tgacttgtag tggtttagag catttatgga ttttaagctt tgaggaaaaa 480
ccatgacttt taacaaattt ttatgggcta tatgcctaaa ccccttagcc acatagtgg 540
aaataattat gaaaaattgt ctgttctaaa ttggtaggtg ccttttggta gcaggaggca 600
taattattgg tttattatgt taattatgtg gattttttaa atgactgata atgttaaaa 660
gttttctaac agttttatctg tgcctattcc caagatatta ttgaattagg aatttttcca 720

```

```

gatgagtgtt  acatagattc  tttgaattta  gtataaaagt  actgagaatt  aagtttgtac  780
ttccataaag  ttggatttta  aacactgata  gtatctcatg  agtaaatgtg  gttttgggag  840
agggagggat  gctgattgat  attccacatt  gtatgaaata  ccgatgttga  aacctcatgc  900
aataatgtta  tgctgttgta  atccctctca  agttctcgat  ttaaaataata  ttttttcttt  960
ataggaattg  atgtatacca  tgaagtcatt  gtcagttgta  tgactctctga  tgttgaatgal  1020
gatatacatt  tttagcattc  catctttactg  actagggtag  aagaacacctt  ttcttggctal  1080
catttggagg  ataccocagg  agtcttgggt  gtcccttatc  tgggggaagca  aacattttcac  1140
tagtctcttt  ttttcatcct  ttaaatgtta  aattaaggat  tactcaagct  caccattatt  1200
caagatgtgg  actcgcttcc  cagtcgacac  tctgcctctg  ctgctattgc  tgcaaaagagc  1260
tgctgtcttg  ccaaccccaa  acggctctct  tgcattattt  ttccctttgl  ttccctttgl  1320
gtgtgtgtgt  ttcttagaag  tacgttcaga  tgcttggggg  aatgcaatgt  atgatttgct  1380
agctctctca  ccaacttaact  cactgtgagg  ataaatatgc  atgctttttg  taatttaactg  1440
gtgctttgaa  aatctttttt  aagggagaaa  aatctcaacc  aaagttaatg  tcattccagac  1500
aagctgacct  ttgagttaat  ttcagcacaa  ctattcttc  agtcctctat  gactgaaaaac  1560
aaaaaacaaa  aaaaacgaaa  catcttcaca  atgaagcttc  cagatagcac  cgttttgtct  1620
aaagatacat  tctcaattgt  ttccaacagt  gatggcttcc  acataaggtt  aaacaaacta  1680
gggtgctgta  aataatttat  tacagtttac  tctatcgcat  ttctgtaaac  tgaatgcat  1740
gcccctcttc  aggggaagac  tgtggtcaag  ttaaaaaaaa  aaaacaatat  taaaacaatat  1800
gaaactgcag  tctgtttttg  aaaatgagaa  tgtcctaagt  gattcagaag  agaggaggga  1860
agtttgtcac  tctgaaaaat  catgaaaaac  aaaggcaaaa  actagtggga  aatgtgtaga  1920
actgttaact  gagacggctt  cgagtctctc  ttctggaaat  tgttaaatat  cacaaagtca  1980
tgagggtaaa  tggagaaaaa  attctcgga  ttcaaatgaa  tghtaagccca  aattgtgaaa  2040
ttgccagtaa  cctggatggg  gaaaaagcat  tcccatagca  ctccatgtaa  tatgagtct  2100
ctgtgagatg  ttcactcagt  ttttatagaa  atggtgttgc  tgggaaacca  agtttgcacc  2160
tggaaactta  caatgcactt  tagcgcagta  agggcttgcc  atccgcttag  gaaaaaactg  2220
ctaacccagg  tttgccaaaa  ctattttgac  accaggacct  tttctctctt  tgggataact  2280
atgaacctct  cactaattgt  ctgtggagaa  catattggga  acataactgt  tagatagttc  2340
tttaaggaga  caaaacggta  atgaacagat  agcaactggg  cagaatatgc  atgcattttg  2400
taacgtccag  tgtggcgctg  aatagatgtg  tatttctccc  cctgcagaaa  ataagcacag  2460
aaaattataa  ttaggttgat  cggagctctt  tcttttgata  gaggaacacg  ccccaatgat  2520
cctggctctt  tcaactgaacg  tatcagaata  catggatgaa  ttggggtaaa  taagggttta  2580
attcagatct  agaagaaaag  attgtaactt  tgaatcgata  ttltatctca  tttttatct  2640
tagtgtttag  acatgacagg  acctatcgtt  gagggttcta  agacttacta  tgggctgtaa  2700
acctgttttt  taaaactatt  ttgaaaacct  gagaactgoc  ctgtggcat  tagtttaaat  2760
acaaactaat  gatgtcattt  gaaagagatt  cttagacctt  ttctctaaag  cttagagctc  2820
tgaatgtctt  tgaaggagg  tattaaacta  tttgcctgtt  gtacaaaaga  atgttaagac  2880
tcgttgaaga  aattactata  aggtactctg  aaataactgc  gattttgtga  gcaaaaacata  2940
cttggaaagt  cctctgtgatt  tttatgcttg  ttagtgtatg  gcaagaaaca  cagaaaatgt  3000
agttttgttt  taataaacca  aaaattgaac  ataaaaaac  3039

```

<210> 29  
 <211> 1448  
 <212> DNA  
 <213> homo sapiens

<400> 29

```

taccaatctg  aagggggaag  cggcgccgcc  atcgctctcc  ggcgtctccc  ccccgactcc  60
taagtctctg  ggccgccacc  atgtccgcct  cgtctgtctt  ctactctggc  gtttaaggga  120
agccattgat  cagccgcgac  tacaaggggc  atgtggccat  gagcaagatt  gagcacttca  180
tgccctttgt  ggtacacggg  gaggaggga  ggcgccttgc  ccgcgtcgtg  agccacggcc  240
aggtccaact  cctattgata  aaaaacagca  acctctactt  ggttggccac  acatcgaa  300
atgccaattg  ctccctgggt  tactcctctc  tgtataagac  aatagaggta  ttctgtgcat  360
acttcaagg  gctgtggagg  gagagcatcc  gggacaactt  tgtcatcgct  tacgagtgtc  420
tggcagagct  catgactctt  ggcttccccc  agaccaccga  cagcaagatc  ctgcaggagt  480
acatcatctc  gcagagcaac  aagctggaga  cgggcaagtc  aggggtgcc  cccactgtca  540
ccaacgctgt  gtccgtggcg  tccgagggtt  tcaagtataa  gaagaacgag  gtcttcatgt  600
atgtcataga  gtctgtcaac  ctgctgggtc  atgccaacgg  cgtcgtctct  ctgagcgaaa  660
tcgtgtgatt  catcaagctc  aaggtgtttc  tgtcaggaa  gccagagctg  cggctggggc  720
tcaatgacgc  cgtgtctctc  gagctcactg  ggcgcagcaa  gcaacaaatc  gtgagctcgg  780
aggaattgaa  attccaccag  tgcgtgcggc  tctctcgttt  tgacaaacgc  cgcacatctc  840
ccttcatccc  gctctatggt  gactttgagc  tcatgtcata  ccgcctctac  accagggtca  900
agccactgat  ctggatttag  tctgtcattg  agaagttctc  ccacagccgc  gtggagatca  960

```

tggctcaaggc caagggggcag ttaagaaac agtcagtgcc caacgggtgtg gagatatctg1020  
 tgccctgtacc cagcgatgcc gactccccca gattcaagac cagtggtgggc agcgccaagt1080  
 atgtgcgcga gagaaacgtc gtgattttgga gtattaaagt tttcccgggg ggcaaggagt1140  
 actgtatgcc agcccaacttt ggccctcccca gtgtgaaaaa ggaagaggtg gagggccggc1200  
 cccccatgg gggtcaagttt gagatccctt acttcaccgt ctctgggatc caggtccgat1260  
 acatgaagat cattgaaaaa agtggtttacc agggccctgc cctgggggtt cgctacattc1320  
 acccagatgg ggcgattacc aactttcggt accagctagg aagggggaga gagatggggg1380  
 ggttttaaca cgggggtttgc tttacagccc cggatgcaga tttttagaag ggagggcagg1440  
 tgccgggt 1448

<210> 30  
 <211> 1394  
 <212> DNA  
 <213> homo sapiens

<400> 30

atgaatacaa ggctgcaagt ggaacatcct gttactgaga tgatcacagg aactgacttg 60  
 gtggagtgcc agcttagaat tgcagcagga gagaagattc ctttgagcca ggaagaaat 120  
 actctgcagg gccatccctt cgaagctaga atatatgcag aagatcctag caataacttc 180  
 atgctctgtg caggccctatt agtgcacctc tctactcctc gagcagaccc tccaccagg 240  
 attgaaactg gagtacggca aggagacgaa gtttccgtgc attatgacc ctagattgcg 300  
 aagtgggtcg tgtgggcagc agatcgccag gcggcattga caaaaactgag tgacagcctt 360  
 ggtcagtaaa atattgtttg actgcccacc aacattgact tcttactcaa cctgtctggc 420  
 cccccagagt ttgaagctgg gaacgtgcac actgatttca tccctcaaca ccacaaaacag 480  
 ttgttgctca gtcgggaaggc tgcagccaaa gagtctttat gccaggcagc cctgggtctc 540  
 atccctcaagg agaaagccat gaccgacctt ttcactcttc aggcacatga tcaattctct 600  
 ccaatttcgt ctgacagtgg aagaagactg aatatctcgt ataccagaaa catgactctt 660  
 aaagatggta aaaacaatgt agccatagct gtaacgtata accatgatgc gtcttatagc 720  
 atgcagattg aagataaaaac tttccaaagt cttggtaatc tttacagcga gggagactgc 780  
 acttacctga aatgtttctg taatggagtt gctagttaaag cgaagtgtat atccctggaaa 840  
 acactattta ccaattttcc aagggaaggaa gatttgagat tgacattcca gtcccccatt 900  
 acttattctc tgtgagctca caagaaactc agggcgcccc cttagctcct atgactggaa 960  
 ccaattaaaa ggtgtttgtc aaagctggag acaaaagtga agcgggagtc tccctcatgg1020  
 ttatgatcgc catgaagatg gagcatacca taaagtctcc aaaggatggc acagttaaag1080  
 aagtgttcta cagagaagggt gctcaggcca acagacacac tcccttagtc agcttgagg1140  
 aggaagaatc agacaaaagg gaatcggaat aaactccagc aaggaaatgg ccagttaaag1200  
 agtgctctct ctctccacca aaaagaggaa gtgctccag cttttctggg ggtctgagct1260  
 agagagcttt tactaaatga ttgtatgctt atgtgaaaca ctttccatat tggagaatca1320  
 tgcatttggg tcactaatta tctcaaaaata tttcactacta ataaagtga attatttttt1380  
 attggaagcc aaaa 1394

<210> 31  
 <211> 734  
 <212> DNA  
 <213> homo sapiens

<400> 31

gccgacaaga tgttcttctg gctctctccg gctcgggggc gactagtcgt ccgacgtctg 60  
 gcgctgagac gtttccggag ccggagtctc tccaccgcga acatgacgaa gggcctgtgt120  
 ttaggaaatc attccaaaaga aaaagaagat agttgccac gatgtgccag tgcaggagag180  
 aatttttgata aattgtttat tggaaaagctg agagagactt tgaacatata tggaccacct240  
 ctgaagcgag ggaagactcg aaccttttat ggtctgcato aggaactccc cagcgtgggtg300  
 ctagtgtggc tcggcaaaaaa ggcagctgga atcgacgaac aggaaaaactg gcatgaaggc360  
 aaagaaaaaa tcagagctgc tgttgacgcy ggggtgcagc agattcaaga ctggagctc420  
 tgcctctgtg aggtggagtc ctgtggagac gctcaggctg ctgaggaggg agcggctgtt480  
 ggtctctatg aatacagatg cctaaaagcaa aaaaagaaga tggctgtgtc ggcaaaagctc540  
 tatggaagtg gggatcagga ggcctggcag aaaggagctc tgtttgtctc tgggcaagaa600  
 ctctgggcagc ccaattttgat gggagacgccc agccaaattga gattgacgcc aaccagattt660  
 tgcgaaatt atttgagaag attttcaaaa ttggtatgta gttaaaaacc aggtctctt720  
 cagaccccaa tttt 734

<210> 32  
 <211> 692  
 <212> DNA  
 <213> homo sapiens

<400> 32

```
tgcagcgcgt gcgtgctgcg ctactgagca ggcgcattgga ggactctgaa gcaactgggct 60
tcgaacacat gggcctcgat ccccggtccc ttcaggctgt caccgatctg ggctgggtcgc120
gacctacgct gatccaggag aaggccatcc cactggccct agaaggggaag gacctcctgg180
ctcgggcccg caccgggtccc ggggaagacgg ccgcttatgc tattccgatg ctgcagctgt240
tgctccatag gaaggcgaca ggtccggtgg tagaacaggc agtgagagggc ctgttctttg300
ttctaccacaa ggagctggca cggcaagcac agtccatgat tcagcagctg gctacctact360
gtgctcgga tgctcgagtg gccaatgtct cagctgctga agactcagtc tctcagagag420
ctgtgctgat ggagaagcca gatgtggtag tagggacccc atctcgcata ttaagccact480
tgcaagaaaga cagcctgaaa cttcgtgact ccttgagact tttggtgggtg gacgaagctg540
acctcttttt ttcccttttg ctttgaagaa gagctcaaga agtcttcttc tggctcacttt600
gcccccggat ttttaacaagg cttttctcat gtcagctact ttttaacgagg acgtacaagc660
actcaaggag ctgatattac ataagccggt at 692
```

<210> 33  
 <211> 517  
 <212> DNA  
 <213> homo sapiens

<400> 33

```
ctgccacgca cgactgaaca cagacagcag ccgcctcgcc atgaagctgc tgaatggctct 60
catgctgggg gccctcctcc tgcactgcta tgcagattct ggctgcaaac tctctggaggaa120
catggttgaa aagaccatca attccgacat atctatacct gaatacaaa agcttcttca180
agagttcata cacagtgtat ccgctgcaga ggctatgggg aaattcaagc agtggttctc240
caaccagatca gatagaactc tgaaaaactt tggactgatg atgcatacag tgaacgacag300
catttgggtg aatagaaga gtaattaact ttacccaagg cgtttggctc agaggggtac360
agactatggc cagaactcat ctgttgattg ctagaaacca ctttctcttc tgtgtgtgtc420
tttttatgtg gaaactgcta gacaactgtt gaaacctcaa attcatttcc atttcaataa480
actaactgca aatcacaaaa aaaaaaaaaa gtcgacg 517
```

<210> 34  
 <211> 222  
 <212> DNA  
 <213> homo sapiens

<400> 34

```
tcaagctgtg ggtgagaagc tctctagcag ggactctgac cttatggagg atcgctgttt 60
cccccatctt tctctttcac ccaaaaaagt cctgcttctg tcacctctca aacagcctgt120
gagcctaaat ttttctggcc atgggacaga caaggacccc gtcttcagct gaactaagga180
aaagtctctg gacatctttg gccatcaaac tccaacccag tcacccaacc agagcctctg240
aggaaatggc cctcttttgc gggaaacctt tacaatgggc cttctgactg atgtttcccc300
aaaacagtgc cctgtctac ag 322
```

<210> 35  
 <211> 1559  
 <212> DNA  
 <213> homo sapiens

<400> 35

```
gcacgagttg agagtgtgtg tgtgtgtgtg cgtgtgcacg tgcacacatg tgcacgggtg 60
gtgtatggg aaataaacctt ataataaggg acgtatttga gaaggaaata catagacct 120
caacttttag caaatagcag tgatgtttta ggaactgaaa tgtcacactt aaagtcttca 180
gccccagctc ttccctattt ttggcgggga gaagaggccc gattagacac tgttctggtt 240
gtgtttggcg ggaggggaat aatttttgtt cagtctctct tagtgaccaa accttaattt 300
```



ttaagaataa	tatatgtgact	tactgaactg	aagcattctg	agttgaaagg	agctccagag	360
gagtgaggct	ctgtgtgtgt	cacatgttaa	aagcttgctc	accttcagag	cagaggggaat	420
acctatcttc	agatatccgc	ccattttcat	ctcttcatta	tactcaaaac	gtgtgacttg	480
agagtggttg	tctgtgtgtc	gtattctggc	ttatgaagat	tatttgaata	agaaactctta	540
ctacatgtga	atgcagactt	ttaaaaattt	aaatattgga	ttaggcagtc	aaaaaaccaa	600
acaagcatata	aaggtcaata	agttgtaatc	ttaaaagtaa	aggtggaaaa	ctcattataa	660
atggaagaaa	agttttgatt	tccttttttg	tttgatgggc	agtatgccat	attataacca	720
aagttctttt	aaaaaatatt	tccatcaacc	atttttattt	aaaaataaca	tttgagggaa	780
gttaccagg	cagctttttt	cccaaaaagt	aacctgttcc	tccttggaa	agcacatttt	840
aggggcatgg	tttaatacctg	agatttttcc	tcagtaaatc	ctgagtgtta	ctgtgtgtaa	900
aatatcttta	agtaggattg	aaggccctctg	tgggggaata	aaatattacc	aaagtcctata	960
aaaaataatt	ttacatgttc	tccttttatga	cagagagcag	gtgtgtcttc	gttattttta	1020
aaatgaataa	ttgatttctt	gataggtgtt	taataattct	tcctcactg	ctgattctta	1080
gatagaaccc	attctttata	tttgatagac	tgctttcaga	aaaccccttat	caacaagtgt	1140
acaatactta	tctaaaaacta	tacatttaga	atggagcagt	ttataactag	attctcagaag	1200
ttttgaaaaa	tagcaaaagaa	gactggattt	ggaaagcatg	gtctacaatt	gggtgttaaa	1260
ttctgaagct	atgaagaata	aatgtttcaa	ctttggatta	tgaaccccca	tttatgattt	1320
tttaaatata	cttgaaaaata	aatgattata	actaaatttt	ggctcagtag	cattactttg	1380
cactgcataa	tcattataac	gtgtacgac	tttttttttt	gggttggaatt	aaataactgag	1440
agttttgtgt	gaagctacgg	catatctaac	cggagaattt	cggatgcctt	atacgggtat	1500
tatatataat	gggggcatatt	gtagtgcagc	ggaagacgga	atttatgcct	ttgggaaac	1559

<210> 36  
 <211> 1072  
 <212> DNA  
 <213> homo sapiens

<400> 36

cacacgtgct	gacggcgggg	acattccatc	ccataagaag	aaatctcagc	aagtggtcgc	60
gtccccagct	aaacacccca	tggacagcaa	gggggaggag	tcacaagatca	gctaccccaa	120
catctctctc	atgattgaca	gcttcagagga	gggtgttcagc	gacatgcaccg	taggggaagga	180
gagatgtgtc	gtgtggagct	gggtggctagt	gacaaaaacca	acacgttcca	gggggtcatc	240
tttccaggct	ccatccgcta	cgaggcgctc	aagaagtggt	atgacaaacg	gtgagcgtg	300
gccgcgccga	tggcacagaa	gatgtcgttt	ggcttctaca	agtacagcaa	catggagttt	360
gtgcgcataa	agggccccc	gggcaagggc	cacgcgcaga	tggcggctag	cagatgtct	420
acagggtgaca	agggccctct	tgggactgaa	gaggactcca	gccacagctc	gccactgcac	480
gagcgggtga	ccctctctcag	cagacccccc	accccagaac	ggaacaaaccg	gcctgccttc	540
ttctcccat	ccctcaaagag	gaaggtgccc	cggaaaccgga	tcgctgagat	gaagaagtcg	600
cactcgccca	acgacagcga	ggagtctctc	cgggaggagc	acggtggagc	cgatctgcac	660
aatgcaacca	acctgcggct	tcggtccctg	tcgggcacag	gacggtccct	gttcgggttc	720
tggtctgaag	tgaacagagc	agatggaaac	ttctctctct	atgcacactt	aaactacgtc	780
acgttgccgc	tgcatcggat	tttaacagac	atcctgggaag	ttcggcgaa	gcccatcgtc	840
atgacctagc	cgcgtgcgga	gcctgcgcag	agcccccggc	ggggccagcc	ctcggagtcg	900
tgccaaagtc	ctacctgtcc	accgccaccg	gggtctgcga	tgccacgcga	gtgttggaag	960
cgcagccagg	cggaggccact	cgactgcggg	ggccggggcc	gactgcacga	acaccagccc	1020
aaactgaagt	gcctctgacg	ggccctgctg	gcgctgcttc	gcgctgtgct	cc	1072

<210> 37  
 <211> 454  
 <212> DNA  
 <213> homo sapiens

<400> 37

gtgtgcatg	gagtgagtg	cggcatccac	cgtgaggagg	agaggagctc	tgataccctc	60
aggaccggcc	aggaggggca	tcacggaggg	ttctggacga	cttgagagct	tgctctgggg	120
agaaaaccgc	tcctgtgtgg	gccctgagtg	ctgagagga	agctgcgatg	cacttttccc	180
tggaattttt	tctgcatggg	tcgtctgttt	ttttgcaaat	aacatgtgtg	catgaatttt	240
tatgcatgag	gcataattca	tcactgtctg	atgctgaagt	ccccctctac	cttccaattg	300
gttgctggac	aggagagaga	gggtccaaagt	gccctacatc	gtgcgccagt	gccgtggagag	360
gagatcgagc	gccgaggcac	ggagaggagt	ggcatctacc	gcattgtctg	gggtggcgca	420
gacatccagg	gactgaaggg	agccttcaac	gtca			454

<210> 38  
 <211> 700  
 <212> DNA  
 <213> homo sapiens

<400> 38

```

cttgtcggag ccctaaccag gggatatctt gagcctgggt ggcctcccg agcgtcacat 60
cactttccga tcacttcaaa gtgggttaaaa actaatatct atatgcacaga agaaaaagat120
gtcattccgt aaagtaaaac tcatcatctt ggtcctgggt gttgctctct tcttactggt180
tttgcacat aacttctca gcttgagcag ttgtttaagg aatgaggtta cagattcagg240
aatgttaggg cctcaaaccta tagactttgt cccaaatgct ctccgcacatg cagtagatgg300
gagacaagag gagattcctg tggatcatgc tgcattcgaa gacaggcttg ggggggccat360
tgcagctata aaacagcattc agcacaacac tcgctccaat gtgattttct acattgttac420
tctcaacaat acacagcagcc atctcgggtc ctgggtcaac agtgattccc tgaaaagcat480
cagatacaaa attgtcaatt ttgacccctaa acttttggaa gggaaaagtaa agggagatcc540
tgaccagggg gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctggg600
ttccacagcg caaaggaagg cccgtttaca tggggttgat gatgttattt gtggcagggt660
ggattttttg ccctttacat tacagcagtg agggcggggc 700

```

<210> 39  
 <211> 914  
 <212> DNA  
 <213> homo sapiens

<400> 39

```

cgggctgcg gtggggcagca gctcagggtc tccaaatcat tgcgtagtto cgaataccct 60
cggccacacc tggcctttct catgctcgga ataacttctt gcagcgacca acagggtaaa120
gagggggag ggatccagca cgggtctctc ctccggcaac cagcgtggga gccggcgagg180
aaatggacat aaacccgggt gtgaaaagcc agggaaatgaa gcccgcgga gccgggaaatc240
tgggattcag ggcttcagag gacagggagt ttccagcaac atgagggaaa taagcaaaag300
gggcaatcgc ctccctggag gctctggaga caattatcgg gggcaagggt cgagctgggg360
cagtgaggag ggtgacgctg ttggtggagt caatactgtg aactctgaga cgtctcctgg420
gatgtttaac ttgacactt tctggaaaga ttttaaatcc aagctgggtt tcatcaactg480
ggatgccata aacaagaacc aggtcccgcc cccagcacc cgagccctcc tctacttcag540
ccgactctgg gaggatttca aacagaacac tcctttcttc aactggaagg caattattga600
gggtgcgagc gcgtcatcac tgcagaaagc tgcaggcaga gccaggtcag aactacaact660
acaaccagca tgcgtatccc actgcctatg gtgggaagta ctacgtcaag acctctgcaa720
agggggggag tctcaacctc ttctcggtt cccgggggtg aacctggggc tctgtcagat780
tgggtgaagt ttgtgtaagg caatttcttg caaccaacca ccgaaggccc cggaaaaagc840
actgggttcg tcaagggaag ctcttcccc cctttggggc ccagccttg tggcaggccc900
ctgggcccgg gtg 914

```

<210> 40  
 <211> 1669  
 <212> DNA  
 <213> homo sapiens

<400> 40

```

gagctgcagc agagcaggta acagctcttg cacctgtttc tcttgccacct gacgtgcagc 60
tgctctctac cactctctct ggctgagcct tgcttgatac aggcaccacct 120
tgcttcccca gctctaccct cccagggcagc tctctacact aactgctctc ctaggaaaagg 180
tctcactctc agcctggagc agtgggatt acagaaagcc ccatctcttg cttaggaggc 240
gccatgagca ctgaaatttg ttggtggaag ctgactttcc tccggaaaaa gaaatccact 300
cccaaatgct tgtatgagat cctgacacc tatgcccaca cagagggaga tgcagaaacc 360
ccgaggcctg acgtcggaag ccccaacagc gactttaaca cccgcctgga gaagatttgt 420
gacagagaga caaagggcaa gcaegtcaag gtctccaaat caggagcgtc caaggagaag 480
aagaagaatga gagccacgct ggcagagaa cctaactctt ttgatgata ccagggaagg 540
cggtcatcaa agtgaagggc tgaggaggt cgtagcactt cttggctccc tgccatcagc 600
cagatctgag accagacctt gccacgtctg cctctttggc catagctgaa gctgtggggc 660

```

09573395.122700

cagttgatac	ctcgtggcag	gaaatggctg	tttttaggt	ttgtatttat	gtgccgccac	720
ttttgtaagg	cctgggagat	cccaggggtc	tccacctcc	ccctgaccac	atacaaaagg	780
acctagttc	aagagtga	agtctcacc	aggaggaaca	gccctccttg	aagcaatggc	840
agggcgagca	gggaggtggg	catggcaggg	aatggagaga	gtgagccaga	cagacttcac	900
ctccttactg	gacacaggg	caaggcgag	tttcaattgc	tgctcccttt	actttctcta	960
cctgtgacta	ctccctggac	caatcctgag	gagggcacat	tttccagaag	ccactgtgata	1020
ggggctgggt	tctgtggagc	cagagggcaga	gacactgaac	ttgagctcac	ctcctaacac	1080
cggcagtaaa	cttctcggaa	ctttgccctc	aggtgcgagg	gggacagagg	accctggcac	1140
tctgttaggg	tgctgtagaa	gactagattg	atggtagttt	ggcctgttag	ttcctgtttt	1200
ggccatgac	tttgcagatg	gcaagtcaca	cacctcaca	gggaagctac	acgggccaal	1260
togggggagt	gggtggggaa	ttttctcttc	tccctttctc	actataaag	tatttaagac	1320
atatcagctc	cagagatgag	tctggagacc	ttgaattttg	tttaacaaaa	taattgtagg	1380
tttctctctg	taataacaac	gctggaaagg	cagagaacct	ctttttatg	catgtcttgc	1440
atttattgag	atgactgttt	ctcatgcctt	tatgttctct	catgtaaagta	aagtggaacct	1500
ttgtgtcctc	aaaaaaaatt	tcaagcttca	ggaaggggtt	cccaagggtg	gacaatgtag	1560
gaacctgggt	cactaatttt	taccatcaaa	cctagcctta	gtatggggat	ggggcaagcal	1620
gaaggagcta	gttacacctc	agtggctcag	tctctccagt	caacagaga		1680

<210> 41  
 <211> 355  
 <212> DNA  
 <213> homo sapiens

<400> 41

cggccctccc	ctcgtctgca	ggctcggggt	ccccagctcc	gcgtaaactg	cacgatttcg	60
ccctctgtct	agctcccttc	tgccccctct	ttccaagaga	gacttcacga	tccacattt120	
tcttgactga	ttttgaagct	gtctgtttgc	attctgatgt	ggaacactgg	gatcattttc180	
atcatcgcca	cagtggtgtg	aatggatgta	tccctttcca	tgaccgccac	tgtgtctatt240	
gaggggtccg	aggaaatcca	gcgtaagacc	tagcagccca	tgggtttaacg	atgtctgttt300	
tgagcacatg	gccacaaatt	acaagcttga	atttacaagca	cttgtggttt	tttca	355

<210> 42  
 <211> 2628  
 <212> DNA  
 <213> homo sapiens

<400> 42

gggtgcgcct	gctttcgccc	tcctttccca	gcgggagggg	cgcggacttc	cgcggggcgg	60
agtcgctcta	gtgctgacgt	tgccagccga	accctaaagta	gatcgaggcg	gcgggctgca	120
cattcccgct	gttgcggttcg	gtttctcttc	cttttcaactc	cgcgctcaccg	gcggcgccca	180
aagcgcgccg	gagcgcgccg	cgagaaacgac	cgcggcgccca	gttctctctcc	tcctcgccac	240
ctgcctctgt	cggctcagta	gtcggcgccc	ggcgcccgccg	ttgtgtcctac	acctcgctcg	300
tgcgcgcccc	agccccagcg	gccgtagcta	gcgtctggcc	tgagaaacctc	ggcgctccgg	360
cggcgcgccc	accacgagcc	gagcctcgca	gcggctccag	aggaggcagg	cgagtgagcg	420
agtcgagggg	gtggccgggg	caggtggtgg	gcgccggaag	atggctcgca	agcaaggat	480
cgtatggccc	acagagaagc	acagcaagaa	catccaccag	cgcggcaacg	tcgccaaagc	540
cgtgagaaat	gcccccgaag	agaaggcgct	tgtaggaccc	tgggtatttg	ctctcttcac	600
tttctgtgtc	tgtgtgtctg	caattttcca	gattattcaa	agtaacagga	tgggcatgtg	660
aagtgcactga	ccttaagatg	tttccattct	cctgtgaatt	ttactctgaa	ctcattctctg	720
attgtttgata	ccctgggtga	aaacaattca	gtaaaagcatc	ctgcctcaga	atgactcttc	780
tatcatgctt	catgtgtcat	tccaaggttt	cttcatgagt	cattcccaag	tttctagtcc	840
ataccacagt	cggctgtcaaa	aaacaccaca	tgaataaagc	aataaaaatt	gattgttaag	900
atacagtagt	ggaccctact	tattcagcta	attaagagta	agttttttta	tgtggtatt	960
aaaaacagta	gaacaattag	tctaactctg	catagacagg	gtctagattt	gtttaaccal	1020
aatgtataac	tgcagtttagc	ttaaatatac	atttgaagtc	ttgtggtttt	tatatagcta	1080
ggcactttat	tactcttttg	aaactgaaagc	acactccctt	ataggttcat	gttaactgtcc	1140
tgtataaagg	tgttataaaa	tggaaacaact	acacagccta	attttgccac	aaccttttagc	1200
atctaaaaag	ttttaaaaagc	ttctaaatgt	ctaataataa	gggagatgct	tatagccacal	1260
acatctattt	taccaaatatt	gtttccattta	cactacottg	gattttgtat	gagtgagtat	1320
agtaaccctaa	gatgccataa	aaaaaaactt	gatcgttttc	tgacttaatc	agttactgtg	1380
gtttcactaa	aagctaccgt	ggtggagatga	agtcagtcag	ggaagggtttg	tttatgttac	1440

attttatttca	ccagaactat	tttaatatat	caaagggggt	tactatgcc	aacaaaattc1500
tagggaaaaa	tactgtctaaa	aatggatgcc	tcatcagaac	atgctgttga	gtccaatgtg1560
ccataagaca	ttttagcatg	ttaaatagca	cttttaaatg	caaaaaaagg	catcatcaact1620
gcgaagttaa	ctctagtttg	caaatgcttt	ttcttagatta	atgatttttc	aattcattagg1680
gtatcagaca	ctcagcccta	aagtggcatc	tggaaattgaa	tggattttact	gataatgattc1740
agtcctttagt	cttcctcttg	ttatatgact	ttatagggtta	tgatttgata	aatttacctgt1800
ttactaatgg	taagggttgag	ggctataggg	caggtttttgg	gttttctagt	actgttgaaa1860
actgcaagta	ttgggttatt	gtataactag	ccataaacttg	gtgaaaaaaa	acctgagcag1920
tgctctatga	ttaatgcggt	ggaaagaaa	gtgctgtgtg	ttgcttttgt	gtcaccctagt2040
ggatattttc	tttaaaataa	gcgtgtttta	gaggaacaga	tcgaacattg	agaacagtaa2100
ctatcacacg	cgtgaacctc	acagggggct	tcgtataccc	ctggaattag	gaatgaatca2160
gggagcagag	tggttaagga	ctttcaggaa	cttaactatt	tgccctttctc	accaggttaa2220
actgaccttg	ggccagcagg	tttttaacta	aattgttaact	tggttaacta	attctgtttt2280
tcagtctctg	tacttgtttc	cttttttgaa	acaagtgtct	tttttagtcaa	accattccat2340
atggttgtgc	taaatccata	gcaggtgcct	tattccttgc	agttgttgtt	gtgtttttt2400
atcagaattt	tccttgggtt	actatagata	tttggtttta	tagctagcaa	tcattttaca2460
aatgtacaat	gttctgataa	atttgactgt	taaatgtcta	accaatttca	gtgtttttat2520
tatgtaaaaa	tgcatctcct	ttgtatttca	tggttaattc	tgctcttact	gatttattct2580
attcaggttg	gattatgcac	gtttaggtaa	acgaaagctg	aaaaaaa	2628
ttaaaaataa	agttccctga	atatttgaaa	aaaaaaaaa		

<210> 43  
 <211> 2535  
 <212> DNA  
 <213> homo sapiens  
 <400> 43

agttcgccac	agggggaggga	acctggccct	gggaggaggc	tggttcgctgc	tcctacagaa	60
tcocgtctctg	agaggaagag	catgttttgcg	ggcgtcccca	ccatgcgtga	gagctcccc	120
aaacagtaca	tgcagctcgg	aggcagggtc	ttgctggttc	tgatgttcat	gacctctatt	180
cacttttgacg	cagcgtctct	ttctattgtc	cagaacatcg	tgggcacatc	tcctgagatt	240
ttagtgcaca	ttggttttaa	aaaccaagctg	gctgotttga	ctcttgtgtg	gtggctgttt	300
gcacttcaacg	tataattcaa	cgctctctcg	accattccag	ctctagagcc	catgcatgac	360
ttcctgaaat	acgactctct	ccagaccatg	tcggtgatgt	ggggcttgct	ccgtgtgggtg	420
gccctggggc	ctgggggtgt	ctccatggat	gagaagaaga	aggagtgtga	acagtccacg	480
atccctacct	gcctggctaa	gacccgtggc	cgtcaaggac	tggttcgggg	tggtttcaac	540
aaaactgcc	gcttttatgt	atccctctcc	cttccccctc	cttggtaaag	gcacagatgt	600
tttgagaact	ttattttcag	agacacctga	gaatcgatgg	ctcagctctgc	tcctggagcca	660
cagctctggc	tcctgacctg	cagtgccagg	cagcctggca	gctgggaagcc	tcctccacgc	720
cggagctttg	gagtgaaacg	ccgccttggc	tggtgcctct	cagctctatt	tttgagtttt	780
tttggctggg	tacagagagg	ggccttcaag	ctgtactgtg	agcagacgca	ttgtgtattt	840
catccaagag	agtcctccct	ttatttga	gtttacattt	ttagcggaaa	ctactaaaatt	900
attttgggtg	gttcagccaa	acctcaaaac	agtttaattc	cctgggttaa	aatcacacca	960
ggggttttga	tggtttttct	gccccgcatt	gtattttata	ggaatagtga	aaacatttag1020	
ggacacccaa	agaatgatgc	agttattaaag	gggtgtgtaga	agctcgtgtt	tatgataaaa1080	
gtcatcgtgc	agaaaaatcag	cttggtattgg	tgccaagtgt	tttatttgggt	aaacccctgg1140	
gagtttttag	agcttggagg	aaggtgtgagg	ggcaagaagt	ccttggggaa	gctgtcgtgt1200	
tggtgtgctg	tggtcctcaa	gctggcagtg	ggaaagggtca	gtgagaccac	acaggggtgat1260	
ccccagcagc	agcacccctgc	aagccagcct	ggccagctgc	tcagaccagc	tgccagagcc1320	
gcagcccgctg	tggtggcagg	gtgtggcagg	agctccccgc	actggagacc	ccaggtactca1380	
accaggttac	ctcacatggg	gccttttctg	agcaagggtc	cgaaagcgca	ggccgcctct1440	
gctgagcagc	accgcccctt	ccagcgtgca	ctgcgccctg	ggcagacccc	gacacacac1500	
ttctctgagg	ctgtgcctca	ctcagattgt	ccgttttgta	tgccagattc	agcccaaat1560	
ccctttttaca	atttgtgatg	cttaccagat	ttgatcttaa	tcctgtattt	aaagttttct1620	
aaactcgcct	tataacttgt	ttctcttttt	ggggagagctt	aactgcctgt	tgctcctctg1680	
cgctcgcacc	atagttaaat	ccacaagggt	agtcgaacac	ctctctggcc	cttagacctat1740	
tgtggggaca	ggctgggtcca	gcctgtctcc	agggctgctg	cgggccagcc	ccagagcctg1800	
ctccccctct	gcctctcaac	cattggctct	gcaggggcagg	ggtagggcag	gtttctgctc1860	
ataagtgctt	ttgggaagca	cttacctttt	taacacagcc	gaactagtc	caacggcttt1920	
gcaaatattc	ccctggtaga	ctacttccct	acccccgaat	attggtagaa	tcgagcaatg1980	
gcttcaggac	atgggtttct	ttctcctgtg	atcattcaag	tgctcactgc	atgaagactg2040	
gcttgtctca	gtgtttcaac	ctcaccaggg	ctgctctctg	gtccacacct	cgctccctgt2100	

tagtgccgta	tgacagcccc	catcaaatga	ccttggccaa	gtcacgggtt	ctctgtggtc2160
aaggttggtt	gggtgattgg	tggaagtag	ggtggaccaa	aggaggccac	gtgagcagtc2220
agcaccagtt	ctgcaccagc	agcgccctcg	tcctagtggt	tgctctctgt	tctccctggcc2280
ctgggtgggc	tagggcctga	ttcggaaga	tgcccttgca	gggaggggag	gataaagggt2340
atctaccaat	tgattctggc	aaaacaattt	ctaagatttt	ttgtctttat	gtgggaaaca2400
gatctaaatc	tcattttatg	ctgtatttta	tatcttagtt	gtgtttgaaa	acgttttgat2460
ttttggaaac	acatcaaaat	aaataatggc	gtttgttgta	aaaaaaaaaa	aaaaaaaaaa2520
aaaaaaaaaa	aaaaa				2535

<210> 44  
 <211> 805  
 <212> DNA  
 <213> homo sapiens

<400> 44

ggcagagagc	gcacagagcca	tctccatccc	cggagcatct	gtatgatcca	gaagtacaac 60
cacgatgggg	aagcagggtcg	gctggaggct	tttagccaaag	gggaaagtgt	cctaaaggaa120
cccaagtacc	aggaagagct	ggaggacagg	ctgcatttct	acgtggaggga	atgtgactac180
ttgcagggct	tccagatcct	gtgtgacctg	cacgatgggt	tcctctggggt	aggcgccgaag240
gcggcagagc	tgctacaaga	tgaattacca	ggggggggaa	taataacctg	gggacctgcta300
ctctggctct	accatcgtgg	ggaggccccc	agaaacatct	atcgctctatt	aaacacagct360
tttgggtctg	tgacactgac	tgctcacagg	tcctctgtct	gccctctgtc	cttgggtggg420
agcctcgggc	tgcgaccocga	gccacctgtc	agcttccctt	acctgcatta	tgatggccact480
ctgcctctcc	actgcagctg	catcctggct	acagccctgg	tcctgcttct	tgatggccact540
cgctctgtgt	cctctccagt	ttccatgtgt	catctggctg	acatgctgag	cttctgtggg600
aaaaagggtg	tgacagcagg	agcaatcctc	cctttccctt	tggtccagg	ccagtcctct660
cctgattccc	tgatgcagct	tgaggaggcc	accccatgga	ccccactgtg	tgcatgtggg720
gagccctctg	gaacacagtg	ccttgccagg	tcagtgtgtg	tgagggggga	tagacagagc780
atgccacaca	agccacagac	ttaat			805

<210> 45  
 <211> 1279  
 <212> DNA  
 <213> homo sapiens

<400> 45

cggaaagtgc	cgcaggcatg	gcggcggtta	tgccgctgtt	gctctgctgc	tcctgtgtgt 60
cctggggccc	ggcggtctgt	gccttgcaga	accccacgc	gacagcctgc	gggaggaaact 120
gtgtcatcacc	cgctgtcctt	ccggggagct	agccgccaca	ttccagtctc	gcacgcgctg 180
ggattccggg	cttcagcggg	aaggagtgtc	ccattacagg	ctctttccca	aagccctggg 240
gcagctgac	tcacagtatt	ctctacggga	gctgcacctg	tcattcacac	aaggcttttg 300
gaggaccocga	tactgggggc	cacccttctc	gcaggcccca	tcaggtgcag	agctgtgggt 360
ctgggtcccaa	gacactgtca	ctgatgtgga	taaatcttgg	aaggagctca	gtaatgtcct 420
ctcagggaatc	ttctgcgcct	ctctcaactt	catcgactcc	accaacacag	tcactccccc 480
tgctctcttc	aaacccctgg	gcttggccca	tgacactgac	cactactctc	tgccgtatgc 540
tggtgtgtcgc	cgggaggttg	cttgcaccca	aaacctcacc	ccctggaaga	agctcttgcc 600
ctgtagtcttc	aaggcaggcc	ttctctgtct	gctgaaggca	gatcgctgtg	tcacacaccg 660
ctacactctc	caggcagctg	atatccgcct	tggtttgcaga	aatgcacgtg	gtactagcat 720
ctctctgggg	ctgaggcaga	ccctgtcagt	tgattttgat	gccttcatca	cggggcaggg 780
aaagaaagac	tggtccctct	ttccggatgt	ctcccgaaac	ctcacgggag	cctgcccccct 840
ggctctcagg	agccgagttc	atgtggacat	caccacctac	aaccaggaca	acgagacatt 900
agaggtgcac	ccaccoccca	ccactacata	tcaggacgtc	atcttaggca	ctcgggaagac 960
ctatgccatc	tatgaactgc	ttgacaccgc	catgatcaac	aactctcgaa	acctcaacat1020
ccagctcgaag	tggaagagag	ccccagagaa	tgaggccccc	ccagtgccct	tcctgcatgc1080
ccagcgggtac	gtgagtggtg	atggggctgca	gaagggggag	ctgagcaccg	tgctgtacaa1140
caccacacca	taccgggctc	ttccgggtgt	gctgtggag	acgttaccct	ggatctctgcg1200
gctgttacct	ccactaccag	cctgcccagg	acgggctgca	accccacctc	ctggagatgc1260
tgattcagct	gcccggccaa				1279

<210> 46  
 <211> 1923

<212> DNA  
<213> homo sapiens

<400> 46

gcgcaagaca caggaggccc agggccggcag tcaggacatg gcggcgattt gcagattcca 60  
atctctctgt ttctcgccggc attgaacacc caacattggc gaccgggatc gcggaaagtg 120  
atggctgtctg tcccggcgctc tctctcagga caggacgtgg gatcatttgc atactctaca 180  
attaaagaca gaataaccaca gatcttaact aagggttattg atacatttgc tgcacataaa 240  
agtgaatttt ttgagaaaca cggagagggaa ggcggtggaag ctgaaaagaa agctactctc 300  
ctcctttctta aattacggaa tgaattgcac acagataaac catttatccc cttggtttag 360  
aaattttgtg atactgatat atggaatcag taccatagaat atcaacagag tcttttaaat 420  
gaaagtgatg gaaaatcaag atgggtctac tcaccgtggg tggttggtaga atgttaccatg 480  
tatogaagaa ttcatggaagc aattatccag agtccacca tgcattactt tgatgtattt 540  
aagaatcaa aagagcaaaa tttctatggg tcacaggaaat ccatcattgc tttatgtact 600  
cacctgcaac aattgataag aactattgaa gacctagatg aaaatcagct gaaagatgag 660  
ttttttaaac ttctgcagat ttcactgtgg ggaataaagt gtgatctgtc totctcaggt 720  
gggaaagta gttctcagaa taccaatgta ctaaattcat tgggaagact aaaaccttc 780  
attttatga atgatattgga acatctttgg tcatctgcta gcaattgcaa gaaaacagaa 840  
gaaaaagctt ctgctactag agtgatatatt gttctcgata attctggatt tgagcttgtt 900  
acagatttaa tattagccga ctctctgttg tctctgaaac tggctactga gggtcatttt 960  
tatgaaaaaa caattccatg gtttgtttct gatactacta tacatgattt taattggttal020  
attgaacagg taaaacacag taatcataag tggatgtcca agtgtggggc tgaactgggaa1080  
gagtatatta aaatgggttaa atgggtttac cacaaatcata tattttggac tctgctcatt1140  
gagtatctgt caatgcctca ggttgcaact gacttatatg ctgaactaca gaaggacat1200  
ttaattttat caaagggtga tttgaattac aggaagtgtga cagggtgcagc aaaatgggag1260  
ttttctgttc catttcatca ggcctctgaat ggcttccatc ctgtaccatal320  
agaacattaa aagctgaaat tcagggttggg ctgcagcctg ggcaagggga acagctcctg1380  
gcctctgagc ccagctgggtg gaccactgga aaatatggaa tatttcagta cgatgggtccc1440  
ctttgactgt atttaggagc tctcagttgc atagaaaagt ctgggtgagca ctttttcatc1500  
ccagaaaaag gagcagctga attgagtcgc ctggcggtgc tgtacgcgct cagggaagct1560  
tagctctctg gtgcccactc acgtgcaactg gatgattttt cttttgaaca ttttgcccal620  
ctacactggt tttggggata gctgggttaa gcaagttaaa gatatttaca tttatatgtg1680  
agatttttaag caactttttt ttcaagggtaa atataaatt tcaaatgctc tttaaatggal1740  
ccttaatttt gaagtgggtta gggccaaaaa ataaagggag ggctcctttg aggtaggtaac1800  
ccttggcctt tcttaaaaag ccctcaatg ggatttagat ccgggggggt gggtgtattt1860  
tccttggttt ggccatgaaa atccttggaa ccggcttatg cctctttgaa aagggggggt1920  
ttt 1923

<210> 47  
<211> 706  
<212> DNA  
<213> homo sapiens

<400> 47

cattttacga caggcgggat tgttttgtgg ctgtcagctt tctccgtggt ctgagtttgt 60  
gggtcgattt ttatctctgg tggctctgct acggcgccgc agaaatgagg cagaagcggal20  
aaggagatct gaggccctgt gagctgatga aggagatggt attaaacacac180  
tgattgaagc ccacgagcag gggaaagaca tgcatactaaa taagggtgaaa accaagacag240  
ctgccaaaata tggcctttct gccacgcccc gcctggttga tatcattgct gccgtccctc300  
ctcagtatcg caaggtcttg atgcccgaatg tgcgtactat aggagatggt attaaacacac180  
ggatgtgctg cgtggtctgt atgtgcaaac cccacagatg tccacacatc agttttacag420  
gaaatatatg tgtatactgc cctgggtggac ctgattctga ttttgtagat tccacccagt480  
cttacactgg cttatgagcaa cctccatgag agctattccg tggccagatag ggaccccttt540  
ccttacacga caaggagacc ggatttaggaa cagtttaaaa caagtggggt tctagtggtg600  
gggttaagtg ggagtttgtt gttggatggg gtgggaactt tttggggccc ttccagagga660  
ttacagaggtt atttttattt cggaaagtta ctgtatgggt ttttcg 706

<210> 48  
<211> 749  
<212> DNA  
<213> homo sapiens

09673395.122700

<400> 48

```
gacatctcct catctgtgca aggaggagtg gccaaactct gagcccaggc tgttgcttcc 60
tggtctgggtg gtgaatcctc catagtctgg tgagtgtagt gcccaactct ggagcccagg120
atgtgtctctc ccggtctggt ggtgaatcct ccatagtctg gagatctcag cctcgtcgag180
ctgagtctga tgcataagtg agatgttatt aaacaactga ttgaagccca cgagcagggg240
aaagacatcg atctaaataa ggtgaaaacc aagacagctg ccaaatatgg cctttctgcc300
cagcccccgc ttggtggatat cattgcttgc cgtccctcct cagtatcgca aggtccttgat360
gcccaagtta aaggcgaaac ccatcagaac tgctagtggg attgctgtcg ttggtgtgat420
gtgcaaaccc cacagatgtc cacacatcag ttttacagga aatatatgtg tatactgccc480
tggtggggac ctgattctga ttttgagtat tccaccagct cttacactgg cgtatgagcc540
aacctccatg aggagctatt ccgtgccaga tatggaccct tttccttaca ggacaaggag600
accggattag gaacagttta aaacaagttg ggttcgtagt gtgggggttaa gtgggagttt660
ttttgtggaat ggggtgggaa ctttttgggg ccgttcacaga ggattacaga gttattttta720
tttcggaagt ttacgtgatg ggttttccg 749
```

<210> 49

<211> 857

<212> DNA

<213> homo sapiens

<400> 49

```
accttaccaa ggggagaaaa aaacctccca ctttggctca ctgtgggttt ggcactaaga 60
ggcagcagat ctgaaggagg tcattccagt tttaaaagta cggcagactgc tgttggaact120
gaccacaaaa atgtatttgt aaaaaaaaaa tgaaaaaccag cagtgtatttg ggtcccccgt180
aaaacctctg gaatcggagg tgggccagg aggtgtcagg acgcagcaga aatagtcaca240
gaaaggagag acgggtccatg cagcgggctt gtgctttttt gtgtgtgttt gtgtgtttta300
caccatcacat ctccaaatga agtatttatt aacaattgtc gtgtaaagcct gtgataaaaat360
agcacaaaag ttcttttaaa agtttcactt ttaaggcctc agaaaagtata atgtggcaaa420
catttttaatt aaaacatcag aagtaaattt tattttaaac tttaggcctc tgaatttttc480
cagttaaacac agtttcagcta tgtggcagg tcaatgggtg gcatctaaaa tgacttttta540
catctacaaa aaaaaataaa taaaataaag acacagcccc aaacgggtgc acctcttcgc600
ggccgctcca catgcacaga atctactagg atttgtcacg gccgggtggc acccgatttg660
tttgactcat acaacaact tttttttcaa aagtatttgt tcaggataac ttaaaaaata720
atataaaaaa aaacatggga ttgactttt cctcacaagt tgaagaagaa ggggtggggg780
gaggtgttaa ccattggcct tttttttttt ggagggggcc cattgggatt gtaaggccct840
ggggttcagg cttttccc 857
```

<210> 50

<211> 268

<212> DNA

<213> homo sapiens

<400> 50

```
ccgcgcgcgg ccccccaggca attttaataa taaatcttaa tagatggggg aagagctgcc 60
ttcatcccat acagagaata caatggtgct agactaagta gagattttat ttacagctaa120
agattctgtt tgatgtctga aattacatgt ttaggcgcca tggggaacag gactgttctt180
tagcatcagt ttcaacaatta ctttaactca ctagggttca ttcaccttat aattctgaaa240
tttcatcagc agtgggggaa agaaaagg 268
```

<210> 51

<211> 297

<212> DNA

<213> homo sapiens

<400> 51

```
ctgatgtgca ctctaggtta gtaaccattt ttgtgaaaaa tttagagaaa ttctttgagc 60
agcttccact gaaacactaa aacccaatag gcccaaggcc ccataacctg aggaaacctt120
attattgtct taatccaaca taggcatatg aagtttttag ttctctcttg tgtattagaa180
```

tttcattcct atttgttgta gagagtatag tacggggaat cagtaaatata aatgaagtaa240  
actaaagatt acacctttgc tgcctggcact aagcgaaaag caaaaccagt ggctgtc 297

<210> 52  
<211> 590  
<212> DNA  
<213> homo sapiens

<400> 52

acggtcaaaa tgaataactca tgtattttat tccaacaaca ttgggtttat aaaggaatac 60  
aaacaggcac aaaaacatggt tcagaagatt tattaagtaa acttgctaaa atattggacag120  
atacacttag cagtcacaaca gttgaatatt cattgctacc tcattaaaagt ttttgatct180  
gtattaccag gtccaaacat aaaaaccacc tctgttcaaa aaataaatgt tcagagagct240  
gtatgttctt tgttctggta tgtacatttt aaaaaaacac ctctttccag tcttgctaac300  
caagaattatt agtcatataa aagaacttag aatttttttc cccaagtaca agctatctt360  
tgctccaaaa cagttctgaa ggtttttatt atattttatc ttatcccgag ggacccaacag420  
caggcatacc tttgccagtc cttcttgtag aaagacacag agcggtaaag gcaaaaataa480  
aattgcaata aagtataagg tattgggggc agggagaacc agaaaccctc aaggggacca540  
atttttagca cgttcttttt ttagggttta cctgtggag taagaactag 590

<210> 53  
<211> 1714  
<212> DNA  
<213> homo sapiens

<400> 53

ggaaggggaa gtttcgcctc agaagcgctc ctgcctggtc cgaattcggt ggccgccagt 60  
ccgcgcgtct cgcctctctg catcgggctt tcggcggtt ccacctagac acctaacagt 120  
cgccggagccg gccgcgtcgt gagggggctg gcacggggag tcggggcggtc ttgtgcatct 180  
tggtctacctg tgggtcgaaag atgtcggaca tcggagactg gttcaggagc atcccgccga 240  
tcacgcgcta tctgtctgcgc gccaccgtcg ccgtgccctt ggtcgggaaa ctgcgcctca 300  
tcagcccgccg ctacctcttc ctctggcccg aagccttctt ttatcgcttt cagatttgga 360  
ggccaatcac tgccacattt tatttccctg tgggtccagg aactggattt ctttatttgg 420  
tcaattttata ttctttatat cagtattcta cgcgacttga aaacaggagct tttgatggga 480  
ggccagcaga ctatttattc atgctcctct ttaactggat ttgcatctgt attactggct 540  
tagcaatgga tatgcagttg ctgatgattc ctctgatcat gtcagtactt tatgtctggg 600  
cccagctgaa cagagacatg attgtatcat ttgtgttttg aacacgattt aaggcctgtg 660  
atttaccctg ggttatcctt ggattcaact atatcatcgg aggcctcggt atcaatgagc 720  
ttattggaaa tctgggttga catctttatt ttctctaact gttcagatata ccaatggact 780  
tgggagggaag aaattttcta tccacacctc agtttttcta ccgtggtctg ccagtagga 840  
gaggaggaggt atcaggattt ggtgtgcccc ctgctagcat gaggcgagct gctgatcaga 900  
atggcggagag cgggagacac aactggggcc aggggttttc acttgagagc cagtgaaagg 960  
ggcgccctgg gcagccgctc ctctcaagcc acatttcttc ccagtctggg gtgcgtctta1020  
caactgcggt ctggctaaca ctgtttggacc tgaccacacac tgaattgtag ctttcagtacl1080  
gagacaaagt tctcttaaat ccgaagaaaa atataagttg tcacaagttt tcaagattct1140  
cattcaagtc cttaactctg tgaagaacaa ataccaactg tgcaaatgac aaactgact1200  
acattttttg gtgtcttctc ttctccctct tccgtctgaa taatgggttt tagcgggtct1260  
tagtctgctg gcaattgaggt ggggctgggt caccacaacc ttcccaaaag gaccttact1320  
tcttctctgc acacatgcct ctctccactt tttcccaacc ccacatttg caactagaag1380  
aggttgcgca taaaattgct ctgcccctga caggttctgt tattattga cttttgcoaal440  
ggcttggtca caacaatcat attcacgtaa ttttccctct ttgggtggag aactgtagca1500  
atagggggag aagacaagca cgggatgaag cgttttctca gcttttgga ttgcttcgac1560  
ctgacatccg ttgtaacctg ttgccacttc ttcagatatt ttataaaaa agtaccactgt1620  
agtcagtgag ggccaacagat tggttattaat gagatacgag ggttgtgtct ggggtgttgt1680  
tccagataag tgaagaaggt agtggattga ctac 1714

<210> 54  
<211> 1340  
<212> DNA  
<213> homo sapiens

002727 365 122700



<400> 54

```
ctcgagccgc tgcagccgaa tgggctcgag ctgaaaaagg gctacctgac cctgtcagac 60
agtggggaca aggtggccgt ggaatggggac aaagaccatg gggctcctgga gtccaccctg 120
gcggagaggg ggagagggat ggagctatcc gacctgattg ttttcaatgg gaaactctac 180
tcctgtgatg accggacggg ggtcgtctac cagatcgaag gcagcaaaagc cgtgcccctg 240
gtgattctgt ccgacggcga cggcaccgtg gagaaaaggct tcaaggccga atggctggca 300
gtgaaggacg agcgtctgta cgtggggcgc ctgggcaagg agtggacgac cactacgggt 360
gatgtgttga acgagaaacc ggagtgggtg aaggtgggtg gctacaaggg cagcgtggac 420
cacgagaact ggggtgtccaa ctacaacgct ctgcccgtg ctgcccgtat ccagccgcca 480
ggtaacctca tccatgagtc tgctctgtgg agtgacacgc tgcagcgctg gttcttctg 540
ccgcgcgcgc ccagccagga gcgctacagc gaggaaggac gacgagcgca agggcgccaa 600
cctgctgctg agcgcctccc ctgacctcgg cgacatcgct gtgagccacg tccggggcgt 660
ggccccact caccgctctc cgtccttcaa gttcatcccc aacaccgacg accagatcat 720
tgtggccctc aaatccgagg aggcacggcg cagagtcgac toctacatca tggccttcac 780
gctggacggg cgcttctcgt tgcccggagc caagatcgga agcgtgaaat acgaaggcat 840
cgagttcatt taactcaaaa cggaaacact gagcaaggcc atcaggactc agcttttata 900
aaaacaagag gagtgcactt ttgttttgtt ttgttttttt tggaaactgtg cctgggttgg 960
aggtctggac agggagccca gtcccggggc ccatagtgtg gggggcactg gacccccggg 1020
ccccacggag gcgcgggtct gaaactgctt ccatgtctgc atctgttgtt gatttcggtc 1080
acttcaggca ttgactcaag gcctgcctaa ctggctgggt cgtttcttcc atccgacctc 1140
gtttcttttc ttctctatgt tcttttgttc agtgaatatc cctagagctc ctaccatgt 1200
tcaggcccta tgcctcaccg tgagaacgca gtaagcatga aggtggacct ggtttgtcgt 1260
gaaccggagg gctaaccccc tttttcttcc caaatttggg gccttgggaag aatcaggtcc 1320
agccctgaag atccttgggg 1340
```

<210> 55

<211> 765

<212> DNA

<213> homo sapiens

<400> 55

```
caggattgaa acaagatggc ggggtcgttg tgagaagccg tcaaggagta gaaattggta 60
tgcttagaag cagattctaa aagcagtttc tcttcagaac atcttttttc ataccactgt 120
ataagcatct tgaacacaca tggctgtagc tgcagtaaaa tgggtgtagt caaagagaac 180
tatcttgaag catttatttc cagtcacaaa tggagcttta tattgtgttt gtcataaac 240
tacgtattct cctctaccag atgactataa ttgcaacgta gagcttctgc tgcattctgc 300
tggcaggaca atagatgct accacccttc tgtggacatt ccatatgaac acacaaaacc 360
tactccctcg ccagatcctg tgcataataa tgaagaalca catgatcaag tgctgaaaac 420
cagattggaa gaaaaagttg aacaccttga ggaaggacct atgatagaac actctagcaa 480
aatgtctctt actactaagc accgttggta tctctcatgga cggatcacca gatgtcgtaa 540
gaatctgaat cctccaaaag acagatgatg cggaggttcc tgggggaaac aaagagaaat 600
gtgcctcatt tgccatttga gaaaatcgag tctggtgtat tcagtaatat atagtaaaat 660
aataatgata aatatctctt tcatatatta gaatgtgtac ttttatataa agtaattctg 720
gatttgacat tctcatttag ggggacctat tctttttttc gttttt 765
```

<210> 56

<211> 1647

<212> DNA

<213> homo sapiens

<400> 56

```
gcagccggag taagatggcg gcgctgaggg ctttgtgceg cttccggggc gtccggcccc 60
aggtgctgctg gcctggggcg ggagtcogag tgccgattca gccacgaga ggtgttcggc 120
agtgccagcg agatgtggaa ttgggcacag agtttggggg agctgttatg taccacaaga 180
aagaaaacag ccaactggag cctccacctt ggaatgatgt ggacctcca aaggacacaa 240
ttgtgaagaa cattaccctg aactttgggc cccaacaccc agcagcgcat ggtgtcctgc 300
gactagtgat ggaattgagt gggggagatg tgccggaagt tgatcctcac atccggctcc 360
tgccaccgag cactgagaag ctcattgaat acaagaccta tcttcaggag cttccatac 420
ttgaccggct agactatgtg tccatgatgt gtacgaaca ggcctattct ctagctgtgg 480
agaagtgtct aaacatccgg cctcctcctc gggcacagtg gaccagagtg cttgttggag 540
```

002227.565296

```

aaatcacacg tttgttgaa ccatcatggt ctgtgaccac acatgccctg gaccttgggg 600
ccatgacccc tttctctctg ctgttttgaa aaaggagaaa gatgttttag ttctcagcag 660
gagtgctcgg agcccgaatg catgctgctt atatccggcc agggaggagt caccaggacc 720
taccoccttg gcttatggat gacatttatc agttttctaa gaacttctct ctccggtctg 780
atgagttgga ggaagtgtgt accaacaata ggaatctggc aaatcggaca attgacattg 840
gggtttgaac agcaagaaga gcacttaact atggttttag tggagtgtgt ctccggggct 900
caggcatcca gtgggacctg cggaaagacc agccctatga tgtttacgac caggttgagt 960
tgtatgtccc tgtgtgttct cgaggggact gctatgatag gtacctgtgc cgggtggagg 1020
agatgcgcga gtcccgtaga attatcgcac agtgtctaaa caagatgcct cctggggaga 1080
tcaaggttga tgaatgcaaa gtgtctccac ctaagcgagc agagatgaag acttccatgg 1140
agtcactgat tcatcacttt aagtgtgata ctgaggggca ccaagttcct ccaggagcca 1200
catatactgc cattgaggct cccaaggagg agtttggggt tactctgtgt ctgatggca 1260
gcagccgccc ttatcgatgc aagatcaagg ctccgtggtt tgccccctgt gctgggttgg 1320
acaagatgtc taagggacac atgttggcag atgtcggtgc catcataggt acccaagata 1380
ttgtatttgg agaagtagat cgttgagcag gggagcagcg tttgatcccc cctgcctatc 1440
agcttcttct gtggagcctg ttccctcactg gaaattggcc tctgtgtgtg tgtgtgtgtg 1500
tgtgtgtgtg tgtgtgtatg ttcatgtaca ctgtggtgtc aggtcttctg tgcattgtct 1560
aaaaaaggag aaattataat aaattagccg tcttgcgccc ctaggctcaa aaaaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaa 1647

```

```

<210> 57
<211> 1166
<212> DNA
<213> homo sapiens

```

```
<400> 57
```

```

cgccgctctg cgccgggggga gccccagaca gaccgccgcc gggaccccga gtcgcgcacc 60
ccagcccccac cgccccccccc gcgcgccatg gaccccaagg accccaagaa gatccagctc 120
tcggtgcggcg cgcccccctag ccagctcgac ccccgccagg tggagatgat ccggcgccagg 180
agaccaaacg ctgcccgtgt gttccggctc tcagagcact cctcaccaga gggaggaagcc 240
tccccccacc agagagcctc agggagaggg caccatctca atcggaagag acccaacccc 300
tgtgcctaca caccaccctc gctgaaagct gtgcagcgca ttgctgagtc tcacctgacg 360
tctatcagca atttgaatga gaaccaggcg tcagaggagg aggatgagct gggggagctt 420
cgggagctgg gttatccaag agaggaaagt gaggaggaa agggagatgc agccagggctg 480
aagtcctgaa ggtcatcagg cagtctgctg gcaaaaagac aaacctgtgc cagggctcgg 540
aagggccctg ggaagcgcca cccctctctg atgagtcgga gagagatgga ggctctgagg 600
accaagtgga agaccagaca ctaagttagc ctggggaggga acctcagcgc ccttccccct 660
ctgagctcgg cacataggca ccagcctgc atctccagg aggaagtgga ggggacatcg 720
ctgttccccca gaaacccact ctatctccac cctgttttgt gctcttcccc tcgctgtgta 780
gggtctgcgc ttctgacttc tagaagacta aggtctggtt gtgtttgctt gtttgccac 840
ctttggctga taccagaga acctgggcac ttgctgctgt atgccccacc ctgccagtca 900
ttctccattt caccagcgg gagggtggat gtgagacagc ccacattgga aaatccagaa 960
accgggaaac agggatttgc ccttcacatc tctactcccc agatcctctc cctcggaacc 1020
aggagacca caggggagca ccctaagatc tggggaaaag aggtctctag aaatgagc 1080
tacccttaga tctttttcta cccactttcc tatggaggat tccaaagtaa cattgtctgt 1140
aacggttgtt aacagggttc aggttg 1166

```

```

<210> 58
<211> 487
<212> DNA
<213> homo sapiens

```

```
<400> 58
```

```

ctcagatcgg tggacgtgct gcctccact cggggccagg tctatgtccc ggtttccgcg 60
agtgcggggc agggcgccaa ggcggcagga ggagggtgag cggctcaagag acctccagga 120
ggagcggtct tcggctgtgt gcatcgccga tagaagaag aaaggatgca cgtccaggga 180
ggagggaact actccaact ttctatctca gaaacaaaga aaaaagatta tcaagctgtg 240
ggaggacaat tcatctccta ttgttactgg aaatacagga agtggtaaaa caactcaact 300
ccccaaatat ctatatgaag cagggttttc acaacatggt atgattgggt taactcaacc 360
acgaaaagta gctgtctatc cagttgtcca gagagttagt gaagaaatga atgcatcctt 420
gggatccaaa taggataacc aagttcgttt tgatgattgc agttcagcag 480

```

<210> 59  
 <211> 1630  
 <212> DNA  
 <213> homo sapiens

<400> 59

```

aaactgtgta atgccccatg taatccataa aattttaact tttcccccta acgtttttgc 60
tgaaaaatgt tgggaaaccc tcaacacgoc ttccctgaaa caattaaaaa accttgaaacc 120
tgtgaacgtt tcaaaaaacc ctocagggtgg gaaaagaccc ccaaaaccttc ttttaaggat 180
cattttgtctc gcccatcaca ggatctttgga aatgttttccc taggggtgtgt aaaaattaac 240
ccaggggggga atgaagcaca tttttctggc aacccaaactt gagttcccca gagaacagat 300
gcagagagac ctgctcctgc ttgcccggct acagggggcca ctgtggagtc acactgaggg 360
tgtgaccggc cataagccca ggagagcccg tggcagctgt gccgagggcg caggacctct 420
aagcgggaagc ttcccaagct aggaatggag caacactgca atgaaatgtg tccaccaagc 480
tcattgtttc tcccgggtgc ttataaagct cagatgtata gtgacgtatg gacaaaatac 540
aaaaaataaa aaaaaataaa aaaaaataaa gcctttcttt ctacaggcca taagacacaa 600
attatataat gttatgaagc acctttttacc aacgggtcagt tttttacattt tatagctgcg 660
tgocaaagggc ttccagatgg gagaccctac tctcttgtgc tccagacttc atcacaggct 720
gctttttatc aaaaaggggga aaactcatgc ctttcttttt taaaaaatgc ttttttgtat 780
tgttccatca gtcactatac atctgagctt tataagcgcc cgaggagaa aatgacgttg 840
gtggacacat ttcattgcag tgtgtgtcca ttccctagctt ggggaagcttc cgcttagagg 900
tccctggccgc tgggcacagc tgccacgggc tctcctgggc ttatggccgg tcacagcttc 960
agtggtgactc cacagtgccc cctgtagccc ggcaagcagg agcaggtctc tctgcatctg1020
ttctctgagg aactcaagtt tgggtgccc aaaaatgtgc ttcttcccc cctgggttaatl080
ttttacacac cctaggaaac atttcaaga tccctgtgat gcgagacaaa tgcactttaall140
aagaggtgtg gggcttttcc caacctgagg atttctgaaa ggttcacagg ttcaatat1200
aatgcttcag aagcatgtga ggttcccaac acgttcagca aaaaaccttag gagaaaact1260
aaaaatataa gaatacatgc gcaataacac gctacagaca cacattctgt tgacagggga1320
aaaacttcaa agcatgtttc tttccctcac cacacagaaa catgcagtat taaagcaata1380
tattttgtat tccccattga attcttcaat gttaaacagt cgagtcctct ttocgaagact1440
aagatgacca tggccctctt cctctgtaca tataccctta taaacggccc ctccacacac1500
tgccccccag tatatgcgc attgtactgc tgtgttatat gctatgtaca tgtcagaac1560
cattagcatt gcattgcagg ttcatattct ttctaagatg gaaagtaata aaatatatt1620
gaaatgtacc                                     1630

```

<210> 60  
 <211> 1272  
 <212> DNA  
 <213> homo sapiens

<400> 60

```

tgccgcgcgag cccgtgtccc cacggcgccc agcagcgccg cggcgccggc ctgaacgcgg 60
agggggcgga gggagccccc ggccggcgga gcagctacag cgaatggcg gagaccgtgg 120
ctgacacccc gcggctgatc accaagccgc agaacctgaa tgacgcctac ggagccccca 180
gcaactctct ccagatcgat gtgagcaacc cgcacaacggg gggggctcgg cgggggcgct 240
tcaccaacta cgaactcagg gtcaagacaaa atcttccat tttcaagctt aaagaattct 300
ctgttagaag aagatacagt gactttgaat ggctgcgaag tgaattagaa agagagagca 360
aggtcgtagt tccccgcgt cctgggaaa gctttttgcg tcaagtctct tttagagaga 420
tgatggaata tttgatgaca attttattga ggaagaaaa caagggtctg agcagtttat 480
aaaacaaggtc tctggtctat cctcggcaca gaacgaacgt tctcttccca tgtttttaca 540
agatgaaata atagataaaa gctatactcc atctaaaata agacatcgct gaaattttggc 600
aagaagggggc aaaaacgtga ctattaatga ttgataagca ccagtgaaag agttctaaact 660
tttagcatgc tgcacagaaa ctggataaac atgccttcag tatactaaac ctcatatgct 720
cagttttgtt tgtttttggc agttgacaag aagttaattt gcttttagtaa aaactccctca 780
ttccagcctt tctatataaa tagctcttgc ttgctgtttt aatgtgtgtg acactatagc 840
ctcacaaaac tgttatccca gtgtaactcg cagtgctcgt actaaagtta ctggcttgtg 900
cttatttgoa cagttttttg gctctgtgtg ctcttctgat ctgattaaat agaattttc 960
cttttcccc ttttaatttt tgaatgcact tgaccccat tatgtgtcag agcactaca1020
cattggtttc caatactgca acataagat acatactgt tgcgacaaag tatcttctc1080

```

caggcttgta	atacccttca	catggaagat	taatgagga	aatctttata	ttctgtataa1140
aaacaaaagc	aaatattata	actaaaatca	tttgtctaaa	aatttaagtt	gttttcaaat1200
aaaaattaaa	atgcattttc	gatatgcaaa	aaaaaaaaaa	aagaaaaaga	aaaaaaagag1260
ggcgccgcgt	ct				1272

<210> 61  
 <211> 1914  
 <212> DNA  
 <213> homo sapiens  
 <400> 61

tgcagcgct	gcgtgctgcg	ctactgagca	gcgccatgga	ggactctgaa	gcactgggct	60
tcgaacacat	gggcctcgat	ccccggctcc	ttcaggctgt	caccgatctg	ggctggctgc	120
gacctacgct	gatccaggag	aaggccatcc	ccctggccct	agaagggaag	gacctcctgg	180
ctcgggcccg	cacgggctcc	gggaagacgg	ccgcttatgc	tattccgatg	ctgcagctgt	240
tgctccatag	gaaggcgaca	ggtccgggtg	tagaacaggc	agtgagaggc	ctgttctctg	300
ttcctaccaa	ggagctggca	cggcaagcac	agtccatgat	tcagcagctg	gctacctagt	360
gtgctcggga	tgtccgagtg	gccaatgtct	cagctgctga	agactccgct	tctcagagag	420
ctgtgctgat	ggagaagcca	gatgtggtag	tagggacccc	atctcgcata	ttaagccact	480
tcgacgaaga	cagcctgaaa	cttcgtgact	ccctggagct	tttgggtgtg	gacgaagctg	540
accttctttt	ttctcttggc	tttgaagaag	agctcaagag	tctcctctgg	gaaggcagag	600
tcacttgccc	cggattttacc	aggcttttct	catgtcagct	acttttaacg	aggacgtaca	660
agcactcaag	gagctgatat	tacataaccc	ggttaccctt	aagttaacag	agteccagct	720
gctggggcca	gaccagttac	agcagtttca	ggtggtctgt	gagactgagg	aagacaaatt	780
ctcctctgtg	tatgcctctg	tcaagctgtc	attgattcgg	ggcaagtctc	tgctctttgt	840
caacactcta	gaacggagtt	accggctacg	cctgttcttg	gaacagtctc	gcattccccac	900
ctgtgtgctc	aatggagagc	ttccactcgg	ctccaggtgc	cacatcatct	cacagttcaa	960
ccaaggtctc	tacagctgtg	tcataagcaac	tgatgctgaa	gtcctggggg	ccccagtcala1020	
gggaacgctg	cgggggccag	ggcccaaaag	ggacaaggcc	ctcgatccgg	agcagggtgt1080	
ggccgggggg	atagactctc	accatgtgtc	tgctgtgctc	aactttgatc	ttcccccaac1140	
cccttgaggcc	tacatccatc	gagctggcag	gacagcacgc	cgctaaccaac	caggcatagt1200	
cttaaacctt	gtgcttccca	cggagcagtt	ccacttaggc	aagattgagg	agcttctcag1260	
tggagagaac	tgaggcccca	ttctgctccc	ctaccagttc	cgatcgaggg	cgatcgaggg1320	
cttccgctat	cgctgcaggg	atgccatcgg	ctcagtgact	aagcaggcca	ttcgggaggc1380	
aagattgaag	gagatcaagg	aagagcttct	gcattctgag	aagctttaaga	catactttga1440	
agacaaccct	agggacctcc	agctgctcgg	gcatagaccta	cctttgcacc	ccgcagtggt1500	
gaagccccac	ctggggccatg	ttcctgacta	cctggttcct	cctgctctcc	gtggcctggt1560	
acgcccctac	aagaagcggga	agaagctgtc	ttcctcttgt	aggaaggcca	agagagcaaa1620	
gtcccagaac	ccactcgcga	gcttcaagca	caaaggaaag	aaattcagac	ccacagccaa1680	
gcccctctga	ggttggttgg	ctctctcgga	gctgagcaca	ttgtggagca	caggcttaca1740	
cccttctgtg	acaggcgagg	ctctggtgct	tactgcacag	cctggaacaga	cagttctggg1800	
gcggggcagtg	ctggggccct	tagctccttg	gcacttccaa	ctgggcatct	tgccccctga1860	
caacagaata	aaaatttttg	ctgccccaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaa 1914	

<210> 62  
 <211> 608  
 <212> DNA  
 <213> homo sapiens  
 <400> 62

aatggaacca	ggaattctta	attaagcccg	aagttcccaa	gtctccttag	cggaaccggg	60
aaattgcca	aggaaagcaa	agaggagat	gaccagtgat	acctccagtg	ccagaggcca120	
ctttgtggag	ccaatgcgt	gacatggcca	gtcagagactc	ggcatctctc	gtcccccca180	
ttaatgactc	tcaggaaagga	ggatgtaatt	caaggcaagt	ttctaattcc	gaagctgct420	
gttcatgtta	acaggacttc	ttttattctg	tcaagatgta	ctggttccct	ggcaccttaa300	
gggaatacct	gataaaagcca	aaactgttga	gccatttggg	cccataaggt	cccaggagacc360	
aagctctgtg	tttcatgctt	actaccatgt	gttccgtgag	ggagaactgt	ccaggtcctg420	
caggactgtg	agtgatgtca	gaattctgca	aagctactact	gatcaaggaa	actggtgtgt480	
gattcttcaa	aaggcctgat	tatttaacct	aaacactcat	atataaagaa	gaaactctca540	
cttaaaaaaa	aaagagggga	taaatataatt	accctgttaa	ttaaagagaa	aactgtgggg600	
gaagtacc					608	

<210> 63  
 <211> 2674  
 <212> DNA  
 <213> homo sapiens

<400> 63

tgaagagaag ttaaggtgaa gagccgaaga gctctgatcg tgatgagcgt ctaagaaagg 60  
 agaagcaaga gcagagaaga gagagagaaa gaacgggaga gagaaagaaa 120  
 agggaaagac gaaggggaaga ggaagaaaga gaaaagaaaaa gggctcgtga cagagaaaga 180  
 agaaagagaa gtcggtccag aagtagacac tcaagccgaa catcagacag aagatgcagc 240  
 aggtctcggg accacaaaag gtccacgaagt agagaaagaa ggcggagcag aagtagagat 300  
 cgacgaagaa gcagaaagcca tgatcgatca gaaagaaaaac acagatctcg aagtcgggat 360  
 cgaagaagat caaaaagccg ggcacgaaga tcatataagc acaggagcaa aagtcgggat 420  
 agagaacaag atagaaaatc caaggagaaa gaaaagaggg gatctgatga taaaaaaagt 480  
 agtgtgaagt ccggtagtcg agaaaagcag agtgaagaca caaacactga atcgaaaggaa 540  
 agtgatacta agaattaggt caatggggacc agtgaagaca ttaaatctga aggtgacact 600  
 cagtcacaat aaaactgac tgataagacc tcagatcaga cagaggttag tgattgtgtt 660  
 ctcaatttga ttagggtctt ttgttactgt ttgacagtcg agcgtaagt tgacacagatg 720  
 aagatggaa taagccgagc aagaagacat acaaaaagcct ctcttgaagg aaaagacagt 780  
 gtgtgtctcg aaaaacattt gaggtacatt gttttgtctc agctattttg tagcagactc 840  
 gtgcccccat tagtgtgctt ctttggaaat tatcgccccc atttgtaata tagtcgcat 900  
 tgaagaaatg attactcctt ttttagggat ttgtgatgca tttctttttt ttttttaata 960  
 aaaaagttga actgtttttt tttttctttt tggattaa gtcactctgt ttgttgatct 1020  
 tggcagagac atatgcttta aaaaactaaa tatttcggag gcacatgttg gactactttg 1080  
 ttttaattaa actgtctagt tttctttgtc aaggatgtt gcttattttt gctttatgcl 1140  
 cttgcattct aatgcagttt gttctgtaac tcgagagcca gtatgacttt atttagtgaa 1200  
 gtgcagggtt tatgaattat tgcagctgac taccatacct cacacagcgt tgggtgtgtg 1260  
 agcgcccat gaaagcccaa attaaaaatc aaggattcag tcaaaactaa caggtactca 1320  
 tgcagagtc tcttctctct accacatacc atgtttgaat gctattgcct gtgatctta 1380  
 cgcttaactg ttgtgtatct tttttgttct ttacaagaag tgcagagggg tttttgtgt 1440  
 attgcgtgaa tctgtataaa acaaatgtta acagaatgga atttttttca aactgtatg 1500  
 agggctgcag tgggtgcca aattagatat ctttaagaaa ttttaaaata aataaacact 1560  
 tcatattat cgcctgttta cactcaatgc aattctcaag tctataagag gtatgtgct 1620  
 aatatttct actgtgttagg agaatttgca gtcagccata ggtatgtagg aatagtcact 1680  
 cactggctga tacattttaa gcagcagtg gaatagcaag gacagacacc ttcaatttgt 1740  
 gaaatcaag aactgatgca ctatataaga cgaatttggg ttttttaaga aatattaaaa 1800  
 gtttagtact gtaagtgctt ttaaaacctg taaactctat tctgtgggct agtgggtg 1860  
 gacaaaatat tcttaataag aggaagtacc aattagttag ttgtgtgtgt gcatctccct 1920  
 ttgggggaag caatgcaggg ttatgtctgt gtatgtcatt cacacttagg caagcattac 1980  
 caggcagatg gcttttaaga ccacactgat gcttgaataa ttaaaaagaa tacaagcat 2040  
 coactgtaac atgtttaata gcaagttagt actgggcca cacttttcca taaaaatg 2100  
 ccttttcat gtgtgtcata tatcattttt ccccaaat tgcgtgttag gactactgt 2160  
 cgaagatttt tggagaagaa ctgagaacgg cataaagtga agatcgacat ttaaaaatg 2220  
 aggtgaaaga aagctatagt ggcataagaa aagataaag ctcagttagt tttttatta 2280  
 ttattattat taaaagttaa ttcaggaatg atgtgacct caagatttca gaacatgtg 2340  
 taatagtata tatgccactg aaaaacttag tctgtatca tacttttttc ttaagaact 2400  
 ttttaagaa attactataa caatgggctt gctcagtggt taattgcaag ttttcaact 2460  
 tggactttga aaacagggat aaacggttag attcgtgtga atcagactaa ttggggat 2520  
 atttttcaaa ctctgcctca cttagccttt ggaattagaa gtaaaaaata agtatctg 2580  
 actttctgtt acaagttga ttgtctctgt caattgaaaag ttttagtatt aatcttttc 2640  
 taataaagt attgactctg aaaaaaaaaa aaaa 2674

<210> 64  
 <211> 326  
 <212> DNA  
 <213> homo sapiens

<400> 64

gacaaatgag ggtttggcat gcagctctgc atcttaagag ttactatctt cttgcctggg 60  
 tgtttcgcg ttccagtgc cctctctgca gaccataaag gatgggaact tgttgagggc 120

09673395.122700

tatttccatc aatttttctt gaccgagaag gagtgcgccac tctttaccaca ggagacacaa180  
 acacagctcc tgcaacaatt ccatcggaat gggacagacc tacttgacat gcagatgcatt240  
 gctttcgcta cagcagcccc actgtggggg gcttgatggg tccgacaact gcattctcgcc300  
 aggaagatgc aagtggatta agcaca 326

<210> 65  
 <211> 888  
 <212> DNA  
 <213> homo sapiens  
 <400> 65

ctcgtgcggg gatgttgagc agaagataca attcaaaaga gaaacagcca gtttgaaact 60  
 gttacccccc cagccccgaa ttgtggagat gaagaaagga agcaatggct atgggtttctal120  
 tctgagggca ggctcagaac agaagaggtca aatcatcaag gacatagatt ctggaagtcct180  
 acgacaggag gctggcttga agaacaatga tctggtagtt gctgtcaacg gcgagctctgt240  
 ggaacacctg gatcatgaca gtgtggtaga aatgattaga aagggtggag atcagactct300  
 actgttggtg gttagacaag agacggacaa catgtacaga ctgggtctatt tttctccatt360  
 tctctactat caaagtcaag aactgccccaa tggctctgtc aaggaggctc cagctccctac420  
 tcccacttct ctggaagctc caagtccacc agatactaca gaggaagtag atcataagcc480  
 taaactctgc aggtctggcta aaggtgaaaa tggctatggc tttcacttaa atgcgattcg540  
 gggctctgcca ggctcattca tcaaagaggt acagaagggc ggtcctgctg acttggctgg600  
 gctagaggat gaggatgtca tcattgaagt gaatgggggt aatgtgctag atgaacccta660  
 tgagaaggtg gtggatgaaa tccagagcag tgggaagaat gtcacacttc tagtctgtgg720  
 aaagaaggcc tatgattatt tccaagccta agaaaatccc tattgttccc tgctggctg780  
 atgccagttg acagccctgc aggtttctaaa gaaggaatag tgggtggagtc aaacctgac840  
 tcgcacattg caaagaacg ggcggctatt gcagacggct aatttatg 888

<210> 66  
 <211> 202  
 <212> DNA  
 <213> homo sapiens  
 <400> 66

atcacagggg tacaaccaga acacatacag tacttgaaaa attattttcca cttttggaca 60  
 cgacagttag cgcataatcta tcaactactat attcatggcc caaaaggaaa tgaataacga120  
 acatcaaaaag aagttgaacc tttcaacaat attgatattg aaattttctat gtttgaaaaa180  
 gggaagggtac ctaagattgt ca 202

<210> 67  
 <211> 1225  
 <212> DNA  
 <213> homo sapiens  
 <400> 67

ggcgggtgga ggcggggcgt gcggcagcga aggggaagcg ctgaggcggt gggggccaca 60  
 gccatggggg agctgtttga ggaggagctc tcggttcctgg ccgcgatttt ctgcaggccc 120  
 cagagtgagg aggtgctgag ccgctcagag acagatggga ccgtgttcag aattcacaca 180  
 aaagctgaag gattttatga tgcggatata cctctggaat tgggtgtcca tttgccagtc 240  
 aattatctct catgtctacc tggatatctg attaaactctg aacagttgac caggggccag 300  
 tgtgtgactg tgaagagaaa gttactttgag caagcagaga gccctttgtc ggagcctatg 360  
 gttctatgct tttgtctctg gattcagcag aatctcagcc atactccaga ccaaccagaa 420  
 actggcagtg gctgtgaaaa gtgtactttt tcaacaagca cgaccatgga tgatggattg 480  
 tggtaacttc ttgttcattt agatcacatg agagcaaaaga ctaaatatgt caaaattgtg 540  
 gagaagtggg cttcagattt aaggctgaca ggaagactga tggttcatggg taaaaataa 600  
 cttgatttta ctacagggag acagaaacaa cctcaagggt tacttgattc ttcaaaaaa 660  
 cttcaaaagta gatgtggact caagtggaaa gaaatgcmaa gaaataatga ttagtgtact 720  
 gtttgaacaa aaagtacaga cagaacacaa aaggtttctg gcatttgaag tcaaaagata 780  
 ttccagctgt gttgaaattc aaaaaggaaat ggaacttgca ggcatttaaga agcttttttc 840  
 cgaattttgt cttgctctgg taaaatgaaa tgggaagacg gaattcttta gtaaaatagc 900  
 agtgtttttt gttgtttttg cattggattt ggggagtggt taattgaaat agtcaatttt 960

aaagtttctc tgaagcaaaa tgaatggcat cattctaact tcaggaacaa aagccagttc1020  
 tgttttatga aaatttaaac atgaagaaaa ctgtgtatatt ctaattgttg ccagggaaagg1080  
 ctagggttcag tatgatgagac attattttaa agataaaattt aaaaagatgg taaatgaacal140  
 ctgtgtttta tagacaatat ttgtttgaaa ctatgtaatt ttctgggctaa ttttctgtal200  
 attaaatgat tttttaaaaa aagaa 1225

<210> 68  
 <211> 1093  
 <212> DNA  
 <213> homo sapiens

<400> 68

gaggggcggc ctgtttccgg ggaggcgct ggggcttgag gccgagaacg gcccttgctg 60  
 ccaccaacat ggagactttg tacctgtgct cgtttettagt gctcgaatgt cccaacctga 120  
 agctgaagaa gccgcctcgg ttgcacatgc cgtcggccat gactgtgtat gctctgggtg 180  
 tgggtgtctta ctctccatcc accggaggaa taatttatga tgttatgtt gaacctccaa 240  
 gtgtcgggtc tatgactgat gaacatgggc atcagaggcc agtagctttc ttggcctaca 300  
 gagtataatg acaatatatt atgggaaggc ttgcatccag ctctctattt acaatggggg 360  
 gtttaggttt cataatccctg gaccgatcga atgcacaaaa tatcccaaaa ctcaatagat 420  
 tcctctttct gttcatttga ttctgtctgt tcctatttga ttttttcatg gctagagat 480  
 tcctgagaaat gaaactgccg ggctatctga tgggttagag tgccttttga aagaatacag 540  
 tggatactgg atttgctcct gtcaatgaag tttttaaaggc tgtaccaatc ctctaatacg 600  
 aaatgtggaa aagaatgaag agcagcagta aaagaaatat ctatgtaaaa aacaggaagc 660  
 gtattgaagc ttggactaga atttcttctt ggtattaaag agacaagttt atcagagaat 720  
 tttttttctc gctggcctat tgctatacca atgatgttga gtggcatctt ctttttagtt 780  
 tttcattaaa atatatcca tatctacaac tataatatca aataaagtga ttatttttta 840  
 caaccctctt aacatttttt ggagatgaca tttctgattt tcagaaaatta acataaaatc 900  
 cagaagcaag attccgtaag ctgagaacctc tggacagttg atcagcttta cctatgggtc 960  
 tttgccttta ctacagattgt gtgatggtag attatttcag atattgtatg aaaaactgttt1020  
 cctgaacaat aagatgtatg aacggagcag aaataaatac tttttctaat taaaaaaaal080  
 aaaaaaaa aaa 1093

<210> 69  
 <211> 309  
 <212> DNA  
 <213> homo sapiens

<400> 69

cacaaagtga ttgtggtatg gaacaatat ggagagaagg caccagatga gttatggaat 60  
 tctctagggc cccaccctat cctctgtgac ttcaaaacac agacagcaaa caggatgaga120  
 aatgactccc aggtcttttc tgaactggaa accaatgcag tgttgatggt agatgatgac180  
 acactcatca gcaccccaga cctgtgtttt gctttctcag tttggcagca atttctgat240  
 caaattgtag ggaattgttt cctagaaaag acgtctttta ctctcattca aggtatctac300  
 agttatttgg 309

<210> 70  
 <211> 380  
 <212> DNA  
 <213> homo sapiens

<400> 70

ctcatctgat ccctttttatg gccaaatcat ccttcagagt agggaaacact cagacattct 60  
 gtgcatgttg ttcccccaaa gcatggctcat cacaaagtcc tgagtttctg ttgtgtgctcc120  
 cgctctctgg gtatacagag agaaggcagg aatcaggagt tccagaagca tatacatgtg180  
 tctaccocag caacaacagg catcctgtgc tcagataaag tgcattgttg ggaagtgttt240  
 gttctcgac gtgagggtct agtgaggatg ggcacactgc cctttgtctc agaagaaggc300  
 ttgtctggct ctaactgcat cccacactgc ccagatcatt ctatagaggt tattttctga360  
 atgtttatag atttcttata 380

<210> 71

<211> 1253  
 <212> DNA  
 <213> homo sapiens

<400> 71

```

gccccccgac tccagtttag agccttgatg ccggaggggga cagtgggtcg ccgagagcgc 60
ccggaggggaa ccgcctggccc ttccggggacc accaattttt tctggaacca ccctcccgcgc 120
gtatcctact ccctgtgcgc cgaggccatc gcttcaactgg aggggttcgat ttgtgtgtag 180
ttttggtgaca agatttgcat tcacctggccc caaaccccttt ttgtctcttt ggggtgaccgc 240
aaaactccac ctcaagtttt cttttgtggg gctgcccccc aagtgtcggt tgttttactg 300
taggggtctcc ccgcccggcg ccccagtggt ttctgaggg cggaattggc caattccgggc 360
ctgcagttgc tgggcttctc catggccctg ctggggtggg tgggtctggt ggccctgccc 420
gccatccgc agtgccagat gagctccatg ccgggtgaca acatcatcac ggcccaggcc 480
atgtacaagg ggctgtggat ggactgcgtc acgcagagca cggggatgat gagctgcaca 540
atgtacgact cgggtctcgc cctgtccgcg gccttgagg ccactcgagc cctaattggtg 600
gtctccctgg tgctgggctt cctggccatg tttgtggcca cgtatgggcat gaagtgcacg 660
cgctgtgggg gagacgacaa agtgaagaag gcccgatatg ccatgggtgg aggcataatt 720
ttcatcgagg cagggtcttgc cgccttggtg gcttgcctct ggtatggcca tcatgattgtc 780
acagactttt ataacccttt gatccctacc aacattaaat atgagtttgg ccctggccatc 840
ttatttgctt gggcagggtc tgccctagtc atccctggag gtgcactgct cctctgttcc 900
tgtctgggga atgagagcaa ggctgggtac cgtgcacccc gctcttacc taagtccaac 960
tcttccaaag agtatgtgtg acctgggac tccttgcccc agcctgacag cctatgggag 1020
tgctctagat cctgaagaagg cctggggctg agctcagcct gtggggcagg tgccgacaaa 1080
agggctcctg gtcactctgt cctgcactc catgtatagt cctgtgtggg ttgggggtgg 1140
ggggtgccgt tgggtgggaga gacaaaaaga gggagagtg gctttttgta cagtaataaa 1200
aaataagtat tgggaaacaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1253

```

<210> 72  
 <211> 439  
 <212> DNA  
 <213> homo sapiens

<400> 72

```

ctaaggggag gacaggcaga aaccaggaa gccaacttaa acctgttttg tgctctgact 60
gtttgttagt atcactctca agaataaga gaaacctcaa cctttctggt tccggccaac 120
tttattgaat ttgttttttt aaatgcagtt tacatgcagt ttctttgaaa agtcatgttg 180
aatttagatc tgtctctcga gtaagacttg gcgagtagt gaaacttgac tcaagttaca 240
ttttcttttt tctgtccccc aaacgtttcac gcttcttata ggctccact tgagggtctg 300
atgaacattc atgcacttgt gttggatgac aatgatgatt ttgctgagga agtaaaccaa 360
caagaagacc tcatgagaga ggtgggaagg actttaactc ctgtttttct ggtgggtttc 420
ctttggttgt acctttttaa

```

<210> 73  
 <211> 1252  
 <212> DNA  
 <213> homo sapiens

<400> 73

```

tggacctgac cgacgccctg ctgcccgcact tgcgccgcgt ggtggggccc aagcagctga 60
ctgtgtctgg aaacaaagt gacctctctg cccaggatgc tcttgggtac cggcagaggg 120
tgcgggagag actgtgggag gactgtgccc gcgccgggct cctgtggccc cctggcacca 180
agggccacag cgccccctga aggacgagcc acaggagcgg gagaatccga atccgcgcaa 240
ctggtccccc acagtgggtca gggagctgct gctgatcag gccaaagacc gctatggagt 300
ggaagagttt atctctgccc ttcagcgctc ctggcgctac cgtggggagc tctacttagt 360
ggggcgccacc aacgcggcga aatccactc cttaacacg ctccgtgagt cctacttagt 420
cactgcacaag ggctccgagg ccatcgacag agccaccatc tccccttggc caggtactac 480
attaaacctt ctgaagtttc ctatttgcaa cccaactcct tacagaatgt ttaaaaggca 540
tcaaaagact aaaaaagatt caactcaagc tgaagaagat cttagtgagc aagaacaaaa 600
tcagcttaat gtctctcaaa agcatggtta tgccttagga agagttggaa ggacattctt 660
gtattcagaa gaacagaagg ataacattcc ctttgagtt gatgctgatt cacttgcctt 720

```

00673305.122700



tgacatggaa	aatgaccctg	ttatgggtac	acacaaatcc	accaaacaag	tagaattgac	780
tgcacaagat	gtgaaagatg	cccactgggt	ttatgacacc	cctggaatta	caaaagaaaa	840
tgtattctta	aatcttctaa	cagaaaaaga	agtaaatatt	gttttgccaa	cacagtccat	900
tgttccaaga	acttttctgc	ttaaaccagg	aatgggtctg	tttttggggt	ctataggccg	960
catagatttc	ctgcagggaa	atcagtcagc	ttgggtttaca	ctcgtgggtg	ccaacatcct	1020
ccctgtgcac	atcacctcct	tggacagggc	agacgctctg	tatcagaagc	atgcaggtca	1080
tacgttactc	cagattccaa	tgggtggaaa	agaacgaatg	ggcaggtatt	cctctctctg	1140
ttgctgaaga	cattaatggt	taaaagaaa	gactgggggc	aacctggaag	cagtgggccg	1200
acatcaaaag	ttcctctgca	ggtaatctta	tgccaagcac	tttttaaaaa	gt	1252

<210> 74  
 <211> 695  
 <212> DNA  
 <213> homo sapiens

<400> 74

tggtcattgc	ctctcgagcg	tagtccagtt	actttcaggc	tgggggagtg	aaggcctcgt	60
tgagagaaag	tctcattcgg	tggtttggga	agagagtcgt	gtggggccag	gtatcgttagc	120
ggcgacacga	gagagacggg	cgggtgtgaca	gccttccact	acctgcacga	gtgtatttggt	180
ctgtctgcta	tcagctatgc	cgctgcccg	tgcgctgcag	accgcgttgg	ccaagagagg	240
catctccaaa	catctctgagc	ctgaaccaga	ggaagagatc	atgtccggagg	actatgacga	300
tgatctctgt	gacttcagag	ccaccaggtt	ggagggccta	gcaccaagct	ggtagaaggt	360
gttcgacctc	tctctggggc	tccttactata	ctggaatgca	gacacagacc	ttgtatcctg	420
gctctcccca	catggaaccca	actccgtggt	taccaaactg	gccaaagaag	tcagaagcag	480
taattgcagat	gctgaagaaa	agttggaccg	gagccatgac	aagtgcgaca	ggggcccatga	540
caagtccggac	cgacagcgct	agaaactaga	cagggggccac	gacaagtcag	accggggcca	600
cgacaagctc	gacagggatc	gagagcgtgg	ctatgacaag	tccaggaagc	ggattcggga	660
ccgcggtgat	gaccaagcag	accgggaaga	ggggc			695

<210> 75  
 <211> 2514  
 <212> DNA  
 <213> homo sapiens

<400> 75

cggcgacggc	gcgggggcag	ctgggaatcc	ggaatgctgc	ccgatggccc	tgggtcctcg	60
ctgtggggga	atccgggctt	gcagacagat	tttagaaga	gcgttttcgc	tacgtaaagc	120
acattcgata	aaggatatgg	aaaatacttt	gcagctgggt	agaaatatca	tacctcctct	180
gtcttccaca	aagcacaaa	ggcaagatgg	aagaataggc	gtagtggagg	gtactcagga	240
gtacactgga	gccccatatt	ttgcagcaat	ctdagctctc	aaagtgtgac	agccccaatg	300
ctgttcatga	gggtgagaga	tggctgcccc	ggctgcacgc	ctctgtcgta	ggacctgctc	360
tggttagaga	tgatgcgctg	ctcagaaatg	tccaggcatc	tttggaaagt	tcaaaaggcca	420
gggacatccc	gtttgtctac	gacgcggtga	gttgacttct	ctcctctcgt	ctcggaactcc	480
cggaaaggct	gtgcagtgag	cacggctcct	tgttctgtgc	aggatggcct	gtggtaggct	540
gctcagcagc	cggccctcat	ccatggctac	cggaaaggct	tgctcactcc	caaccacgtg	600
gagttcagca	gactgttatga	cgtctgtctc	agaggcccta	tggaacgcga	tgacagccat	660
ggatctgtgc	taagactcag	ccaagccctg	ggcaacgtga	cgggtgtcca	gaaagagagag	720
cgcgacatcc	tctccaaagg	cacagaggtg	cttgtgtgca	gccacgaagg	cagcagcggc	780
aggtgtggag	ggcaaggggga	cctcctgtcg	ggctcctctg	gcgtcctggg	acactggggc	840
ctctctgtct	gaccacagaa	aacaaatggg	tccagccctc	tcctgtgtgc	cgcgtttctg	900
gcctctgtct	tcaaccagca	gtgcaaccac	caagccttcc	agaagcagcg	tgcctccacc	960
accacagctc	acatgctcgc	cgaagtgagg	gcgccttcca	gcaagctctt	tgaaactgga	1020
gcccgccgag	accagaagta	aacaggcacc	ttggacgggg	gagagcgtgt	gtgtgatggg	1080
aaaaaccgga	ccaacgcgtg	tgctgaagcg	gtacgggtgt	tgccagattt	tcaacttgag	1140
cataaaattg	ttgccattga	gaatttaaga	gtactggaata	ttgcagcttt	tggttaaaact	1200
taattgcatt	ttggagatgt	tatggcgaca	ctaaacaaag	tattcctgaa	ctttccttatg	1260
tcctctggta	gtaactggga	agacagaaat	agaagaaatc	acatgagaat	gaagaattct	1320
tttagcagctc	aacagagatt	ctcggcctgc	tcccagatcg	gcgaagtttc	tacttgttaac	1380
tctctctgcc	ggcgcccttc	gttctctctc	tgcttccctt	ccctagattc	ctcctgacga	1440
gggagctggg	caggggtccc	cgggtgtctc	ctcagtcctc	gactgcactg	actgggtcca	1500
tcagagggct	gcttctgtct	ccagctcatc	ttcttttaaa	gtgtgtgacta	gcttgggtgt	1560

atctggctgc	tgggtgtttg	cttattgaca	tactccaggg	taatcaatga	tgactttgtt1620
tggaaccctt	tttggaggca	ccatgggaac	agaaggaaac	atgagtgcac	ctgaccctgt1680
agtgtgttgg	tggggagctc	tgagacgcct	cctgtcccac	gctctccggt	gtccgtgtct1740
acacaggggg	ccccatgata	cccacgggcc	ccagcagggc	agacccggcc	ggggacgggc1800
acgggtgaag	gctgcagcct	ggggtctgac	gtggccctca	gtgctgtctc	aggagaaggc1860
tctggaggac	ttgaggcatg	ctgggctctg	tgacgtgatg	gcgctaagga	gacccgggga1920
aagacagtat	cgtggtcacg	tatgcttagg	aagcagcaca	gcgctgtcct	tagggatgtt1980
cgctccagt	aaagacactg	gtaactgcgg	tttcagccaa	cactcttcat	ggcagtgtcg2040
acctcgggtt	agctttctgt	gtctttgtgg	atggttttcc	tgaggcggcc	tgacgtgtac2100
gtgttctctg	gtcccagtgc	ttagcggggc	atggtagcgt	ttcgtgcctg	acgcgtgcat2160
taggggtgtc	tcttatactt	tcagtagcat	ctttccacag	caagggccaa	acctcctgtg2220
ttcccttcag	agtctttttg	gcctgatgat	gactcttgag	tgataccctg	tgatgcagac2280
atgcccagga	tgattcttac	tttctttaa	actagggact	ttcaagatta	aaaaaaagat2340
tgctactact	aatttgacgc	ctaacttcag	aagcttcact	gtctacatgt	gaacttttcc2400
agaaaaactg	tgccatggac	atttttcttc	tggggaatta	acatctaat	tctggttaact2460
attaaaagac	agatctgggt	aatttaaaaa	aaaaaaaaa	aaaaaaaaa	2514

<210> 76

<211> 274

<212> DNA

<213> homo sapiens

<400> 76

cagagatctg	ctgtgattat	tcctttttac	aaaccacaat	gactctggaa	aacctggctg 60
taaaccaccg	cactgccacc	agctaaggat	ctgtgatcag	gagtgcacat	tcacggtaac120
aggcagaaga	caaaagtga	acggggctga	tgccaatcac	tgggaaactg	gctttggcac180
ctccagagaa	tgaactgttt	catagcctag	ctgaccatcc	atgaaaatgg	ctgcctggag240
aggcagtgat	cagcccatcc	cctgcaaggt	gaag		274

<210> 77

<211> 449

<212> DNA

<213> homo sapiens

<400> 77

cgggtttatg	ggcagctctt	cgggattgtt	tccattgcc	ccctaaccgt	gctggcctat 60
gaacggtaca	ttcgcgtggt	ccatgccaga	gtgatcaatt	tttctcggc	ctggagggcc120
attacctaca	tctggctctt	ctcactggcg	tgggcaggag	caactctcct	gggatggaac180
aggtaacatc	tggagctaca	cggactaggc	tgcactgtgg	actgggaatc	caaggatgcc240
aacgattctc	ccctttgtgc	tttcttattt	cttggctgcc	tgggtgtgcc	cctgggtgtc300
atagcccatt	gctatggcca	tattctatat	ttccattcca	atgcttctgt	ggtgtggaag360
atcttcagac	aattcaagtg	atcaagattt	taaaatatga	aaagaaactg	gccaaaatgt420
gcttttaatg	atattcacct	tcctggtcgc			449

<210> 78

<211> 346

<212> DNA

<213> homo sapiens

<400> 78

atataacatc	tgaattggga	gatagctcat	tgtggcctcg	gtgctggact	tttcatatta 60
agtctctgtc	tagccaaggg	agaagaatgt	aaggataaga	ccaccaatatt	cacaggggct120
gtctgagcct	ttaccttgga	ttttgtacca	ctctgtggcc	ttctggagca	atggacaccc180
aagtcagcta	tcagagttac	aaaagtgagc	ctgggttatat	gtcatccaac	agcatatggt240
ccctgcaagc	ctgtttttga	agccaatatt	ctataacctca	caggaaatcca	cttgaatctg300
atgtcttttg	aagcaatata	ttttccaggt	gttccaatgg	actacg	346

<210> 79

<211> 1329

<212> DNA

<213> homo sapiens

<220>

<223> Beschreibung für Symbol "n": leer oder Lücke

<400> 79

```
ncccccatca gttcgaattt ctgcagtgag agcatctggg gttattgtga ccaactgaaa 60
gtctcagagag gtacccacagt gctccagccc ttccctcccca gcatccttga tgggttaatt 120
cacctagcag cccaggttcag ctccagaggtc ctcaacctgg tgatggagac cctgtgcattc 180
gtttgtacag tagaccccga attcaccagca agcatggaaa gcacaaatctg ccccttcacc 240
atcgccattt tcttaaaagta cagtaaatgat cccgtcgtcg cctcactggc tcaggacattc 300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaatgag gctgattccc 360
actctgtgca gcataatgca ggccccagca gacaagattc ctgcagggtc ttgtgogaca 420
ccattgatat cctgacaaca gtagtacgaa atacaaagcc tcccctttcc cagctttctc 480
tttgccaagc ttctccctgt gtggcacagt gtacccttca cacagatgac aatgccatca 540
gtgcagaatg gcggagagtg ctgcccggcc tatgtgtcag tgaccctgga acaagtagcc 600
cagtggtcag atgagcaggg ccacaaatgga ctgtggtatg tgatgcaagt ggtgagccag 660
ctcctggacc cccgcacccc agagttcact gcggcctttg tgggcccctt tgtttccacc 720
ctcatctcca aggcaggggc ggaactcggg gagaatctag accagattct tcgtgccattc 780
ctcagtaaga tgcagcaggc agagacgctc agtgcctgag agtccctgat catggtgttc 840
ctcatctggg tgcacactca gctagaacct ctcttgagtg tctgtgtgag cctcccagga 900
cctactggca aacctgctct agagtttgtg atggctgagt ggacaagccg acagcacctg 960
ttctatggag agattgaagg caaagtcagc tctgtggcac tctgtaagct gctccagcat 1020
ggcatcaatg cagatgacaa acggctacag gatattcgtg tgaagggaga ggagatctac 1080
agcatggatg aggggacctg caccgcctct aagtcagcca aaaacccaga acgctggacall 1140
aacattctct tgtgtgtcaa gatccctaaag ctgatcatca acgagctctc caagctcatg 1200
ggaggtctaat gcgcgtccgc caggccactc ctgcagagtg ggagctcaaa gtgcggaag 1260
gcccttact tcccaggaag acttttagcc tgggcagatc aagttacaaa ttgtcaaat 1320
atccaggaa 1329
```

<210> 80

<211> 805

<212> DNA

<213> homo sapiens

<400> 80

```
gcccccatca gttcgaattt ctgcagtgag agcatctggg gttattgtga ccaactgaaa 60
gtctcagagag gtacccacagt gctccagccc ttccctcccca gcatccttga tgggttaatt 120
cacctagcag cccaggttcag ctccagaggtc ctcaacctgg tgatggagac cctgtgcattc 180
gtttgtacag tagaccccga attcaccagca agcatggaaa gcacaaatctg ccccttcacc 240
atcgccattt tcttaaaagta cagtaaatgat cccgtcgtcg cctcactggc tcaggacattc 300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaatgag gctgattccc 360
actctgtgca gcataatgca ggccccagca gacaagattc ctgcagggtc ttgtgogaca 420
cccattgata tcttgacaac agtagtacga aatacaaaagc ctcccctttc ccagctttctc 480
atctgccaag ctttccctgc tgtggcacag tgtaaccttc acacagatga caatgccacc 540
atgcagaatg gcggagagtg cttgcgggcc tatgtgtcag tgacacctgga acaagtagcc 600
cagtggtcag atgagcaggg ccacaaatgga ctgtggtatg tgatgcaagt ggtgagccag 660
ctcctggacc cccgcacccc agagttcact gcggcctttg tgggcccctt tgtttccac 720
ctcatctccc aaggcagggc gggaaactcg ggagaatcta gaccagattt cttcgtgcca 780
tctctcagtt aagatggcag gaggt 805
```

<210> 81

<211> 420

<212> DNA

<213> homo sapiens

<400> 81

```
accagggtcaa gctcacccca aactattacc ttgatgcat gtgtgtgcat accctgtgga 60
gatctccaaa gtcaaaaagca actgtcagac tcagagaagt atctgtgccc cttaagata 120
aaaggctccc cctatcaaga ccttgtgtcc ttaacgaatg caggaaaaa ggtctgcca 180
```

agctggaatg	aggtgggtgtg	gacaactgaa	tatcaaggct	ggacctcgct	aaccgggtggt240
tgtatgctct	taaaaccata	cattcattcc	actaaagaaa	gtacccccca	taattgcag300
tataaccaat	gtaatccagt	gcaaaattct	attctcattc	caactctcac	tgaccctcaa360
cctacttttaa	gttgcggtat	atggcatggg	agccgaaata	gcagggggcac	atcttatgg420

<210> 82  
 <211> 2143  
 <212> DNA  
 <213> homo sapiens  
 <400> 82

cggcgccct	ttttttttt	ttttttaagt	tgaacagaac	attttatttc	tcagcaattc	60
tatgcgtaca	aattaaacat	gagatgaata	gagactttat	tgagaaagca	agagaaaatt	120
cctatcaacc	ccaaggagga	ctcaaatgta	ggctggaaga	ggacttagaa	gagtatgaaa	180
gtactctaag	attttatcta	agttgccttt	tctgggtggg	aaagttaaac	cttagtgact	240
aaggacatca	catatgaaga	atgtttaagt	tgagggtggc	aacgtgaatt	gcaaacaggg	300
cctgcttcag	tgactgtgtg	cctgtagtcc	cagctactcg	ggagtctgtg	tgaggcgccg	360
gggtccagcg	accagcctag	atgctctgta	actcttaggc	ccccatttcc	cctctgaaaa	420
taagagggtt	ggatcaaacg	atctctgggg	ccttagcattc	tcaaatctgt	tggaatctcc	480
tacttcccc	ttagagagcc	ttactgggaa	gtcagtcatt	aatgatgtgt	ccagtttatt	540
cgagatggta	agagcctatt	taccataaat	aatactaaga	accaactcaa	gtcaaacctt	600
aatgcacttg	ttatttgtga	ttaggattaa	gtagtaattt	tcaaaattca	cattaacttg	660
atttttaaat	cagtttttgt	agtcatttac	cacaagctaa	atgtgtacac	tatgataaaa	720
acaaccattg	tattctctgt	tttctaaaca	gtcctaattt	ctaaccactg	atatatcctt	780
cgacatcaat	gaacttttgt	ttcttttact	ccagtataaa	agtaggcaca	gatctgtcca	840
caacaaactt	gcccctcat	gccttgcttc	tcaccatgct	ctgtccagg	tcagccccct	900
tttggcctgt	ttgttttgtc	aaaaacctaa	tctgtctctt	gcttttctgt	gtaatatata	960
tttgggaag	atgttgtctt	gcccacacac	gaagcaaatg	aaataaagag	cacaaatgtt	1020
caaatcttaa	gccacttaaa	agcgttttgt	acattaaaaa	tgacaagggt	tattatgacaa	1080
gtagcctttt	aaaaaattct	cacacagaac	agcttttgtat	tgaacttaa	agctgtgtct	1140
actttctctg	tgacgtttgt	gttaacagtc	agtgctctag	gatgttgttt	gtatttgtt	1200
cagaatcaga	agtgactaca	caagagcatt	agccagactt	ttcagtgaga	acaggtaacal	1260
ggctgcgacc	agcacttggt	acagcacgtg	gacagggaca	cggaacccag	agttctctgt	1320
ctctccttca	cagcagatgt	actcttctat	aggtggctgt	taatttacac	aaagttatat	1380
tccagaatca	ggaagcccg	gtgcgccaac	acttgaagga	gaactatgtt	ccagttttgg	1440
tgttgaactt	ctcacgaaat	acctactacc	aaaaattgtg	acaccttatt	agacacttcc	1500
aaagtacccc	ccaaaagctg	tttaaaagac	cattccattt	tttctacac	aaagtgcatal	1560
ctaaaatttc	acaataatca	tcttcagatg	tacattttat	ttagtacatt	tcacagtttt	1620
cagttatcag	tcctctcatg	acattttata	gtcatctctt	cggtccctgt	gtgaaatatg	1680
tgattccagtg	tcaattcaga	gtgtatgatt	ccgcttttca	cgctgatcaa	gtaaatttat	1740
gggtgtctct	ttctgatctt	caacattaaa	aadatctatg	ttctgtctat	tcctgtccag	1800
ggctgtctgt	ttgtctgtct	cagattctgc	ttcattttca	tcactgttgt	agtcattctc	1860
ttctctcagt	ttctgtctgt	ttctcctctc	ccggcgagct	ttctgtctct	cctctgtccc	1920
ctcggggatg	acaaagctgt	ctcgtccagg	gccccctatc	ttctggattt	ctgggtcac	1980
tgacaggcca	gctctcaact	gtggggctgt	gccccagttt	ccggctcccc	cgaagcctct	2040
ttcaccttca	ggctgtctct	caacacctgc	ttcccgctgt	ctcctctcgg	cagcctgtcc	2100
ctctgaggtt	ccgatcaaca	ctgatctcat	ggttcccttc	cca		2143

<210> 83  
 <211> 450  
 <212> DNA  
 <213> homo sapiens  
 <400> 83

tttttttaaa	gccagctttt	cttcagattt	ttttgggtgg	caggtctgtga	aagacaggtg	60
aggaagtaga	tcttgggtct	agcatgcctc	taaaagata	atttcttttt	ttttaatgtg	120
aaagaaatgc	ataactctgt	ttctgttctt	gtccccctct	gtgcctctgt	ggtgcctgag	180
atactgggga	ttccacagct	ggggccactc	agaggctacc	aggaacgctt	ccagtttgca	240
tttggctgtt	agtgccacga	ccagaaacct	acagacctct	ctcagacctc	cctgaccctg	300
atgtccctga	agcctggaa	gtgtccacac	aatgaagcag	aattgagtga	tgggggtgtt	360
tgtggaaacc	agtgaaactg	tgttaacaca	gtggaactgt	gttaattttg	agtggaaagt	420

caagttccgt ggagttcatt gggcccgttt

450

<210> 84  
<211> 408  
<212> DNA  
<213> homo sapiens

<400> 84

tgcaactgtg caccagactt gccagatttt tccccattac acccccagtg tggcatatcc 60  
ttggtcccca gaggcacacc ccttgatctg tggacctcca ggcctggaca agagggctgct120  
accagaaacc ccaggcccct gttactcaaa ttcacagcca gtgtggttgt gcctgactcc180  
tcgccagccc ctggaaccac atccacctgg ggaggggctt tctgaatgga gtctgacac240  
cgcagagggc aggcctatgcc cttatccgca ctgccaggtg ctgtcgcccc agcctggctc300  
agaggaggaa ctccgaggagc tgtgtgaaca ggctgtgtga gatgttcagg gctagtcca360  
accaagagtg tgcctccagat gtgttggggc cctaacttgg cacagagt 408

<210> 85  
<211> 311  
<212> DNA  
<213> homo sapiens

<400> 85

tacagttttt atcagtgtac acatttttagt gtaatacatg aaactgagge ttgatagaaa 60  
acaggagaga aggcagtgtg gcatggggta catagggaga tgaggggcaag catcaccaag120  
gagcggcagt gagatagacg ctctcatgga ctgctgtctt acaacctccc tggagagcaal180  
tttaaaaata tgaatcaaga tcctttttagt ccaactaatca tccagaaatc tacacagaaa240  
tatgcacaaa aatatgtgtgg catccattga ctttccaacc tcttctcttt ccagggggaa300  
tattccttaa a 311

<210> 86  
<211> 487  
<212> DNA  
<213> homo sapiens

<400> 86

gtcttttgaa atctgttttc actacagcta tggtaagtc tatcagccgg tgctaccagg 60  
agtcactgcc agggctgccc ttctcttgaa cccagtggtc cagaatcata agccctgacc120  
ccatccctag aaagatgagg tcccagcaat ggccagagca tttctcacca gttctgtgag180  
atagcacata aaaatagagt tctttggcca aaacttttgg gaagcaatgc atctcatcatg240  
ggctgatatt cagcctgagc tgttctcaag agggaggtgg taactggcagt ttatggctga300  
aatccattct gattgtgttg agtctatgct ataccagttg ttaaacattt tgagtatcac360  
tcttgcaatac tgtttactatt atattctct tatatataga cagaaaggcc atttttagga420  
tattaaaggc tatgaaaatt tctgcagtag acccaactga aggttctatt aaggcaggggt480  
tcctaaa 487

<210> 87  
<211> 1902  
<212> DNA  
<213> homo sapiens

<400> 87

gaggaaaaag aacaatgaac agcaacgac ttgactgtgc aactcagaca ttcttcgaga 60  
aaagacatat gtgtctttac aagaaggcca aagaactatg gggccttccc agcatttgac 120  
tgttcattgc atagatagaa ttaaatatcc agttacttga atgggataaa cgcgatgaatg 180  
tgtgtatttta ttaggggccat ctgccaatcc tctcactgtg gtctctcttc tgacttttgc 240  
tgttcatcat ctaaggaggc tagatccttc gctgacttca ccatctctca aacctgtgaag 300  
ttttcactct cttccaaatt ggctttggct ctttcttcaa cctttccatt caagagcaat 360  
ctttgctaag gagtgaagtga atgtgaagag taccacactac acaattctca cagataatta 420  
gtggattgtg tttgtttgtg agagtgaagg tttcttggca tctgggtgct gattaaggct 480

00673395-102700

```

tgagtattaa gttctcagca tatctctcta ttgtcttgac ttgagtttgc tgcattttct 540
atgtgctgtt cgtgactctg agaacttaaa gtaatcgagc tatgccaact tgggggtgga 600
acagagbtact tcccaccaca gtgttgaaag ggagagcaaa gtcttatgga taaacctctc 660
ttctcttttg ggacacatcg ctctcaactg agaagctcac ctgtgctgaa tgcctccatg 720
ctactcaaac atgtttatct taaacccccc gtgtgctgga ttgaaaaggg ctctctctta 780
ttaggttttc atgggaaacat gaggcagcaa atctattgct aagactttac caggctcaaa 840
tactctgagg ctgatagata ttgacttgg taagacttaa gtaaggtctc ggctccagg 900
ggcataagca acagtttctt gaatgtgcc a tctgagaagg gagaccagg ttgtgagttt 960
tccattggaac acattggtct ttctcaaaag ttctgcctt gctagactgt tagctctttg1020
aggacacgga ctatgctcta tcaatcacta ttattttcct gttacctagc atgggacaag1080
tacacaacac atatttgtgt agtcttctaa aagactcctc tgattgggag accatatctt1140
taattgggat gtgaatcatt tcttcagtgg aataagagca caacgggcaca acctccaagg1200
acattatttc tactatgaac attttactgt gagactcttt attttgctt ctacttgcgc1260
tgaaatgaaa ccaaaacagg ccgttgggtt ccacaagtca atatatgttg gatgaggatt1320
ctgttgctct attgggaact gtgagactta tctggatga gaagccagta ataaaccttt1380
gacctgtttt aaccatgaa gattatgaat atgttaatat gatgtaaatt gctatttaag1440
tgtaaaagcag ttctaagttt tagtatbttgg gggatctgggt tttattattt tttctcttt1500
tgaaaaatac tgagggatct ttgtataaag tttagtaatgc atgttagatt ttagttttgc1560
aagactgttg tttttcaaat atatacagta tagaaaaagg taaaaacagt aagaaggaag1620
gcaattatat tattctctct tagttaagca aacacttgtt gactgctctc tatgtgcaag1680
gcattggccc atatgtgtga ggagcttgct taattatgta gatctcggtal740
ttactgatat gggcagatgc ttactgtatg aatgaagaa atcacacagta atcacaaat1800
cagagctgag ttatccccc tgtagcttgc ttggggattc cagtcttcgg gaacgagagt1860
tagggccatt ttatttaaaa gaaactcccc gttgagaccg gt 1902

```

<210> 88  
 <211> 1048  
 <212> DNA  
 <213> homo sapiens  
  
 <400> 88

```

ctcacccgtg ttctaacccg gtctctacgg ctgctctctg ttgtaocatca cgtgcagctc 60
tggctgtgtg tgcgtttacc ccacaagcgg ctcaagctacc agtgcgtctt ctctttctc 120
tgcctcttct gggcctcccc ggggacccgc ctcttctcct tctacttcaa agacttctg 180
gggcccaatt cgtctagccc ctctgctctc ttggtgctct actgctcccc ttgtgtcctg 240
cagtttttca cctccacgct gatgaacttg tacttcaagc aggtgatttt caaagccaag 300
tcaaaatatt ctccagaatt actcaaatac cggttgcccc tctacctggc ctccctcttc 360
atcagccttg ttttctgtgt ggtgaattta acctgtgctg tctctggtaaa gacgggaaat 420
tgggagagga aggttatcgt ctctgtgcga gtggccattat atgacacgct ctctgtgctg 480
tggtgcgtct ctctctccat ctgtctctac aaaaactctta agatgtcctt agccaacatt 540
tacttggagt ccaagggctc ctccgttgtt caagtgaact ccatcggtgt caccgtgata 600
ctgcttttca cctctcgggc ctgctacaac ctgttcaatc tgctattttc tgcagaacaag 660
agcgtccatt cctttgatta tgactggta aatgtatcag accaggcaga tttgaagaat 720
caggtgggag atgtcgata cgtattattt ggagtgggtt tatttgtttt ggaactctta 780
cctaccacct tagtcttata ttcttccoga gttagaaatc ctacaaagga ccttaccac 840
cctggaatgg tccccagca tggattcagt cccagatctt tatttcttg acaacctctg 900
aagatatgac agtgatgatg accttgctg gaacattgcc ctccagggaac ttcagggaa 960
gttttgcctc agattactat gagtgggga caacaaacta acagcttctc ggcagagca1020
gggacttttg aaagctctaa agtttggga 1048

```

<210> 89  
 <211> 804  
 <212> DNA  
 <213> homo sapiens  
  
 <400> 89

```

gcccccatca gttogaattt ctgcagttag agcatctggg gttattgtga ccaactgaaa 60
gtctcagaga gtaccacagt gctccagccc ttcttcccca gcatccttga tggcttaatt120
cacctagcag cccagttcag ctcagaggtc ctcaacctgg tagtggagac cctgtgcatt180
gtttgtacag tagaccgga attcacagca agcatggaaa gcataatctc cctctcacc240
atcgccattt tcttaagta cagtaatgat ccctgcgtcg tccaggaactc300

```

```

ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgc aaatagag gctgattccc360
actcttggtca gcaaatgca ggcgccagca gacaagattc ctgcagggtc ttgtgcgaca420
gccattgata tcttgacaac agtagtacga aatacaaaagc ctcccccttc ccagcttctcc480
atctgccaaag ctttccctgc tgtggcacag tgtacccttc acacagatga caatgcccacc540
atgcagaatg gcggagagtg cttgcgggcc tatgtgtcag tgaccctgga acaagtagcc600
cagtgccatg atcagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag660
ctctcggacc ccgcgacctc agagttcact gcggcccttg tgggtccacc720
ctcatctcca aggcaggggc ggaactcggg gagaattctag accagatttc tctgctgcat780
ccttcagtta agatggcagg aggt
804

```

```

<210> 90
<211> 581
<212> DNA
<213> homo sapiens

```

```

<400> 90

```

```

tctttgatca gatttagtgt cttaggtaat taaatcagaa agtctattta gctattctag 60
aagtgtatgt gtaggatttg ggtggttggg gttctttgag cgaacttgtc agaaactcca120
tctttaacat cagaatccagg gcaggatgga aaacattgtg ctgtggtatt gaaatttgcta180
taacatctat tgcagaaaaat gataggtcag atggaatgca ataataatta tatatcagat240
cttagtaaca aaattaccaa gctttatcta gtggatatat gtaaaagaat atttttaaat300
ctgcagcatt gatgtatttt ctttaagaat tattacagta ctttgggaat360
acagtaataaa aacataaaatt ttttcgtatt ttttaatttt tttatttttt tggccaagga420
tgaatccctc cctgtaaaaat attgatcttc gcctaaattt cggggttttc ctggcacata480
atagcactgg ccccaacttc ggagatggcg gatgcgggta aaaagccaaa aggatggatg540
gggatccgga aatacgtggt ggaatggaag cgaatccaat a
581

```

```

<210> 91
<211> 2042
<212> DNA
<213> homo sapiens

```

```

<400> 91

```

```

tggagatatt agtcagtttc tttagtata tttgtttcct tgatgtgcct ttttgtttt 60
ctttgggggt tttggaatcc ggatgtgtgt gaagggcaat agcagactcc tccagctaag 120
agacaggaca tgttctttgag ccactgtatg tgttgaagct ggacaccaga ccgtccctat 180
aacccccccc ccaggccata gctgtgatgc atgtgcactt ccacccacag aggggggtgt 240
gaagccttga gaacctcaag aaagggctgg attctgcact acctttgggt ctaccttggg 300
actgtcgtgt gccaacgtgt caaccagcct gtgttccctg ccacccacag acttgcgtag 360
ctgtggctga ggacagaatca tttgaatggg tgcattccaa gaggtcaggg ccctgtcttg 420
agaagaataa ctttagatc atgaaaggga aagaacgtgc acttcccttt ttttcttta 480
gtgaatgcaa gatttaataa aagtgaataa tgagcttccc ctttgggagt ggagcccgat 540
gcagctcact gacaggggtgt acatcagtat gatgtgttgg actgaaactg tatgtctgta 600
ggtagtgtgt tgccttttag ggcagaccac ggtggccacc ccatttctcc aaggtgtgtt 660
acctagctgt tgtatatttag acattgccac cctcaccctt ggccaaaaat tcttgattta 720
aaaagaaaaa tctatttttg taacgcaggg ctctgttgtg ttgtgttacta tcccaagcct 780
ggattttttt atttatttta aagtatttta atttccatatt tggctttatt ctaatcccat 840
ccatccctgt ggaagctgcag agcatcttca tgtgagtaga cggatggaca taatatgatt 900
ctatgctcatt taggaagctg ggaatttcgt gaagctgagg gtgagttcct gtgattcttg 960
ttcgtctcaa caaaaagtgg gagaccaagt ttttatagca aaagaccaaa tagctgtag1020
agtccttgaat gcagaaaaaa attaccctag ctttcttagc acttaggggt ttgtggagat1080
tcagtgttta gcacagtgct tggcacatag taagccctag taatgtgttaa atattgttat1140
tagtgttttg taaaacttga gaaatagagc tgagctcatt cccttctctg tgaattcaaa1200
ataataccta caatgaaaca tgattccaag ttgattgaa ttgttaggaa tactgtgttt1260
agagtagccc agttcttcggc ctacctctgt ggttgggatt ttaactgtatt ctgaattgaa1320
ctctgtttgaa aatatgccag acttcagccc ccaagggaaa aaggctgcac gaatttatga1380
actccagctg gaaaaggtaa aggtgacctt tggctagcca catactggac ctatccccac1440
tgacgtctct cagaacattc caaggggttt cctcaaggaa catttttgag ctagaaaaat1500
aaatgggtct tctggtgcag tcgacccctt gaggctaaagt taacagattt ccttgaagt1560
caataataga ggtctttctg cgttaaggga gaaggaaatga ccaattgaac ttacacattc1620
cccaggcagg tccctttgccc ggccctcaca ggtcgggggtg gccctcctctg tccctcaggga1680

```

tcagactccc	agactgggta	gttctgcatg	tttccatcaa	attaaagggt	attccctggc1740
cgctctctgg	agaaaaccaa	ccccaccctg	ccagctgggg	gcaatggggc	agggattttg1800
gcctctcaga	acagctccta	gaggctgctc	atgactgaat	gttttcccaa	atcacctaaa1860
tatcggtttg	ctttttgttt	tgggggagag	ctgttagcct	cttacttccc	tgatggattc1920
aaagtgttat	ctatctcctt	atctcctgct	ctgttctggc	acaactctgg	atagattgca1980
gggtggaat	ttgctgggag	ttggtggctc	cccaaattcc	ttgatctgtc	cgcaagaga2040
ag					2042

<210> 92  
 <211> 430  
 <212> DNA  
 <213> homo sapiens

<400> 92

gttaaaaacc	tagtattcat	tttttttttt	cctgtaccaa	aacaatcctc	ttcctttatt 60
tttcttgagg	cggggaagagg	agagtggaga	agaaggggaag	aatgcacaaagt	gtcactttgal120
acttctcggt	caccacacac	gtgggagctc	actcatgtca	gcagcctccg	tgacagggcc180
ccaggtgaaa	gaagaatga	ggtctagttg	gaccagctaa	cactgcctgc	cttgttttta240
cgaaagggcag	ctgcctctgt	gggtgtgattt	cagggggagcc	agacagggccc	ggggccacga300
acctgcaccc	tgcctcctaa	gcacctattt	gccatgcggt	gaggcttaac	ttgggaaact360
tcaatttgc	tggtgtgagc	attagctttc	caaatctattg	tgatgtctcat	gcttgacttc420
ccaaggactt					430

<210> 93  
 <211> 592  
 <212> DNA  
 <213> homo sapiens

<400> 93

aattaaaaata	aatagaataa	tacggagatt	cttttatgtt	ggatttatta	tacccctcac 60
cattttggctc	cctgaaaagg	gaaaagatac	acggtcgagt	agtacaggta	tgtgtttccc120
actacacatt	atggctataa	tggagttgaa	ttgcaaacag	taaaattttg	ttttgattg180
gtttccctctg	atccccccag	acaggagctt	cctctcccac	cctacctgcc	tgccccaaag240
ttgtgtccta	ttaaaactgga	cacaaatctc	acgggctttt	agtctataaa	ttgaactata300
gctacacacg	gtgacaccag	aatagtactt	tgttttttta	tgttaccagt	gagttaactg360
tttatcctctg	tatgtagaaa	ctaatttcac	catgatcaca	gatctgtgta	acatctctag420
ttttgaatttc	cacacaattt	taaaatgtct	actagggaaa	cttacacctt	tttgttccaa480
gggtgtctctt	catctattaa	aaccgtgggg	gcatacttcc	agtggtgtctt	ctgagggccaa540
aattttgtggtg	gtcgtggggg	acaattttgt	attaacatac	gttattttgt	aa 592

<210> 94  
 <211> 674  
 <212> DNA  
 <213> homo sapiens

<400> 94

aaggccgcgc	aagtgcactt	gcgtgtcacc	gttaccgtag	cgactgggct	tctggactgt 60
atatcctagc	tgctctgtca	acatcttcga	gcactcggcag	ctccggaggc	cggggttaact120
ggcagcaggt	aggaaactat	gtgaaagaat	ctcctgatgt	cataatttcc	gggtgtcacc180
ggaaacattg	atcatatctc	ctttggcaat	tcacgccttc	tgtggaaagg	ccagtagaaa240
gcattgattt	attcaccctt	acaggaaatc	gactcagcct	cttttggttt	tcagtgaagt300
atgccttttc	aattttggaac	ccaggccaag	aggtttccag	tggaaggagg	agattctca360
attgagctgg	aaactgggct	gagctccagt	gctgcctgta	atgggaaggga	gatgtccaca420
accaggcaac	tcggagggtg	ccctggaagt	cattgcttga	caataactga	tggtcccgct480
actgttttat	caagcacagag	aaagccacct	gcacaaagca	gcaaggaaat	gcattctaaa540
tgcaccattt	agactctttt	tcaaggtctg	actaggtcaa	gggttaatgga	ccagtatcat600
ctggtgatct	ggtaaaacaaa	taaaagtggt	ggcaccttta	gatgatgaaa	aaaaaaaaaa660
aaaaaaaaaa	aaaa				674

<210> 95

00573395.122700



<211> 324  
 <212> DNA  
 <213> homo sapiens

<400> 95

```
gttctttttca ttccatcact ttaggtgatg ggtaagattt ttgaaagcct tatatttttt 60
gattttgttg tctagtttaa tctacacctt aatagttgtg ttgggtaaaa ttcccacttg120
aatgtgacac tgataataat tctatctgct ttagcatct cttataggaa tcaaagttta180
ttaaagttac agagaggatt gaaaaatgta tatcactcaa tttttatcta aggagggata240
gggtataaag ggaggtagct aataagctca aataatggat ataactcttt ttcccataac300
catttgggat gcttttaaggc aatt
```

324

<210> 96  
 <211> 709  
 <212> DNA  
 <213> homo sapiens

<400> 96

```
ggatgcggca ctataacatc ccgctcagag tgtgtgagga gaccagtcta tgagagacgc 60
atgctcctga cagcctggcg acgtggcgaa gatgcacagg tggctcctgg gcttgggctg120
caggttttggg ggtctctaa aacaatctct gagaagaacc cttgggcccc tgggagccaa180
gttggacagg tgactcctga gactagcttt tgataagaga aattaaccaa gtctttcccc240
tcatcatgga tgcaatata ttcatgtggg gccttcagag cacacctgtt ggacggtgca300
aaccatatac tctccagaag gcaataactt ttgtatcaga ggaactcag ttttggagag360
gaatatgttc tttatatctc aaatcaaaac tctctctaag ggtaactcgg cttctaat420
ttttaagtac agtatatttt tttcccttt agtagtaacg ggtttctata gatcttcta480
tacagtctcg tttaaactcag gaccttgaga ttatgagact gaactgtctg ccactgcact540
gagggggctt cttaacagtct gctttaagtg gtataattct gggatagatc tgttactggc600
atagtcatga caacctctgg taactctacc ttctctcttt tatgaaggga agagcaatgg560
tttgacctta catctaaatt aaggctattt taagcagatt gttttgcaa 709
```

<210> 97  
 <211> 562  
 <212> DNA  
 <213> homo sapiens

<400> 97

```
gtccagatgg aatgactccc atcctctcct catctccctt ttgacgagcc tcaaaactgct 60
cagctcatca aagagccatt gccaaacttc gtatgtgggt ctgggtccca gggagccttg120
gaaccttgga cctctggggtg gtttaattcc ggcacagag cattcctgct tctcaaggga180
cacagtggcc tgcatgggac agcatggacc ctgggctgat catgtgcatt cctgctttct240
tggggacaca gtgggcccac atgggcccag atggacctgt ggctagagca agcacatctc300
catctctctc acctcaggca gtgtggctcc agatgtcagg agggactgac ctgaggacct360
tccaggttcc tctgtgccag gaatgagagg ccaggcccga tcttaccacc tgccttgac420
cctgaagtca gagcaggcca gccaaagcagg aagcacactg ttttaatttt tgcattggaaa480
gttaattgtg actttgatag ggttaaaata tggctctttt taagtgtgct aacccataa540
tttgagccat tgccttgctt aa
```

562

<210> 98  
 <211> 1948  
 <212> DNA  
 <213> homo sapiens

<400> 98

```
gataccaaag acacacaaa tagaccttgg gctcccagag aagaaaaaga agaagaaagt 60
gttccaaagaa ccagagactc gatactcagt tttaaacaa gatgattact ttgctgatgt 120
ttctcccttta agagctacat cccctcttaa gagtgtggcc catggggcagg cacctgagat 180
gacctctagt aagaaaaaga agaagaaaaa gaagggtgtc agcacccttt gcgaggaga 240
tgtagaacct gagaccacgc tgctctctag acggacagag aagtcaccca gcttcaggaa 300
```

0067396-122700

```

gcagggtgttg  ggccactttg  agttcctcag  tggggaaaaa  aaaaataaga  agtcacctct  360
agccatgtcc  catgcctctg  gggtagaaac  ctcccagac  cctagacagg  gtgaggagga  420
aaccagagtt  ggcaagaagc  tcaaaaaaca  caagaaggaa  aaaaaggggg  cccaggaccc  480
cacagccttc  tcggtccagg  acccttggtt  ctgtgaggcc  agggaggcca  gggatgttgg  540
ggacacttgc  tcagtgggga  agaaggatga  ggaacaggca  gccttggggc  agaaacggaa  600
gcggaagagc  cccagagaac  acaatgggaa  ggtgaagaag  aaaaaaaaaa  tcccacagga  660
gggagatgcc  ctcccaggcc  actccaagcc  ctccaggtcc  atggagagca  gccctaggaa  720
aagaagtaaa  aagaagccag  tcaaaagtga  ggctccggaa  tacatcccca  taagtgtatga  780
ccctaaggcc  tccgcaaaaga  aaaagatgaa  gtccaaaaag  aaggtagagc  agccagtcab  840
cgaggagcca  gctctgaaaa  ggaagaaaaa  gaaggagaga  gagagtgggg  tagcaggaga  900
cccttggaa  gaggaaacag  acacggactt  agaggtgggt  ttggaaaaaa  aaggcaacat  960
ggatgaggcg  cacatagacc  aggtgaggcg  aaaggccttg  caagaagaga  tcgatcgcca  1020
gtcaggcaaa  acggaagctt  ctgaaacagg  gaagtggacg  ggaacccagt  ttggccagtgt  1080
ggatactgct  ggttttgaga  acgaggacca  aaaaactgaa  ttcttcagac  ttatgggtgg  1140
cttcaaaaac  ctgtcccttc  cgttcagccg  ccccgccagc  acgattgcaa  ggcccaacat  1200
ggccctcgcc  aagaaggcgg  ctgacagcct  ctgacagaa  ctgcagcggg  actacgaccg  1260
ggccatgagc  tggaaagtaca  gccggggagc  cggcctcgcc  ttctccaccg  cccccaacaa  1320
gatcttttac  attgacagga  acgcttccaa  gtcagtcagg  ctggaagatt  aaactctaga  1380
gttttgtccc  cccaaaaactg  ccaacaattgc  ttgtattatt  ccatttatgc  tggagattac  1440
aaattttttt  tgtgaaaaaa  tcagatcttg  gtgaggacct  cgagcagtaa  gatataaata  1500
actcccataa  gcttgatcgt  ccagtaatgg  aacactaggg  ataaatgggt  tattcagttg  1560
tgcaaatgaa  agccatctga  cagttggctc  acattgaaca  cctgtggaga  ttaaggacga  1620
ggacaactat  attgatggcg  ttggatgaac  tggggcaggg  cagctcatat  ttccgggagc  1680
agggaacaga  gtgagtgcga  aaacctcctg  ttttctgtgt  taaacattcc  gtccctgttt  1740
gagacatcag  tatgtacagt  taacttttgt  tgagtgttta  cgaggtagta  gggacatact  1800
agtggtttcc  ttaattgtat  taactctcat  aattatgaaa  tgggtgctat  tattagcccc  1860
atcttataga  tggagcgaat  gaggttcagg  gataaagtaa  taaaattgcc  tggggtcacc  1920
cagccactaa  aaaaaaaaaa  aaaaaaaa

```

1948

<210> 99  
 <211> 483  
 <212> DNA  
 <213> homo sapiens

<400> 99

```

aatttatggg  gtctatcttt  gaccacgtga  taccacttac  ctgattctat  gtactgatta  60
atgtatctaa  cgtgtttata  gtgaagtata  tttttaaaaa  agtatatttg  tggctatttc  120
tatttttccc  cctttgctgt  acaagttaat  ttttactcat  ttttctgtgt  acaaaattaac  180
ttcatcaat  acaaaataaga  ggctagtgtt  aatgcatttt  atttgcctat  agcccaggaa  240
taactaaatt  ctataaagta  atgtattaaa  atagtacact  taaaaaatta  ttttctctct  300
ttttttctct  ttaattttta  agaccatcat  aataaattat  cattacaaga  tcaaacatac  360
tatatactac  tatcagtcga  tggggaaaaa  atagctccat  atgtttttat  gttaaaatgc  420
tgtataagat  tgggattgtc  caatttgctt  tgaaaaaaat  cacagcagtt  ttaggtttcc  480
cct

```

483

<210> 100  
 <211> 437  
 <212> DNA  
 <213> homo sapiens

<400> 100

```

cccgttgtag  gcgtaggggg  tggcgctctc  cgttcggcgg  cgctcccatg  gcgcacatta  60
ccatataacca  gtacctgcag  cagggtgtacg  aagccatcga  cagcagagat  ggagcatctt  120
ctgcagagtt  gtcgtctttt  aaacatcctc  atgttgcaaa  cccacgactt  caaatggcct  180
ctccagagga  gaagtgtcaa  caagtcttgg  aaccccttta  tgatgaaatg  ttgacagctt  240
atttaagggt  cacttatgca  gtggggaatc  atgacttcac  agagggcatac  atgtggcaga  300
ccgtgatatg  ccaatcattc  ttgcgagcat  tccaggccca  caaagaagaa  aactgggctc  360
tgctgtcatg  tatgcagtag  cgcttgacct  ttcagtggtt  tgccaataat  gcagttcaac  420
cagttgggta  aggaag

```

437

<210> 101

<211> 359  
 <212> DNA  
 <213> homo sapiens

<400> 101

```
cagatctagg ggcttcagct gtgtgcagac cccatgccac ttcagggaag tgacacaggc 60
ctgtgtcctc tcgctttggc agcaggtggg tggccttcct caggggaggga ggtggcctga120
gatgtgtttc aggtctttga cccatcactc cctacacaca cgacgtgaac accactcctg180
gagcatcttc agaatggaga tttgaattcc atgtggcagc ttctcacaca caaacctgcc240
atcattcccc acacaccacac tcacgacatt caacagccat gagccaaaag aagttccttg300
tttcagattt gaagggttta tgaatccact tcttcgggat gtgactcttt aatgatttt 359
```

<210> 102  
 <211> 501  
 <212> DNA  
 <213> homo sapiens

<400> 102

```
tggcgctcac atctctgagtc ggcctctctc cgaggcggag cggacatgca ggctccccgc 60
ggcacctctag tcttcgccct ggtgatcgcg ctgctccccg tcggcccgga accctctagc120
caaggatctc agagtgtcttt acagacatat gagctgggaa gtgaaaaacgt gaaagtcctc180
atttttgagg aagatcacacc ctctgttatg gaaattgaaa tgggaagagct tgataaatgg240
atgaacagca tgaatagaaa tgccgacttt gaattgttac ctaccttgaa ggaagagaag300
gaatcaaaat acaaccacaag tgacagttaa tcttaaacct gaattggcgt catgttttcc360
aagagaagca gcccctgagg gagtctgtct aggtctccaa agaggatga agagataga420
aatttaatta atttcaaatc aacatagaca caagaacctt ttgctgtttc tccaacgcc480
cactcttcct aatgatggca t 501
```

<210> 103  
 <211> 1102  
 <212> DNA  
 <213> homo sapiens

<400> 103

```
cgggatcttc cgaagggaatt tacgggggatt cctcggacca ttactctcag gcaagaaaca 60
aaaccaaact tggactctcg tgcagaaaaat gttagccatt accacatgta gccttggaga 120
cccaggcaag gacaagtaca cgtgtactca cagagggaga gaaagatgtg tacaaagat 180
atgtataaat attctattta gtcatcctga tatgaggagc cagtgttgca tgatgaaaag 240
atggtatgat tctacatatg tacccattgt ctgtgtgttt ttgtactttc ttttcaggct 300
atttacaatt gggagatttc agaaacattc ctctcaccat catttgaaa tggtttgct 360
taattggagac aatgacagat cctgtatgat ttccagtaga catggccttt taacttaagg 420
gtctaagact gattgattct agcatttact gtagtggag catggagatg ctatgatgga 480
agcatatcca ggggtggcctt tagcacagta ttagtaccat ttatttgtct gccgtcttta 540
aaaaataccc attggctatg ccacttgaaa acaatttgag aagttttttt gaagtctttc 600
tcactaaaaa atggggcgaat tgttagcctt acatgttgtg tagacttact ttaagtttgc 660
acccttgaaa tgtgtcataat caatttctgg attcataata gcaagattag caaaggataa 720
atgcogaagt cacttctatc tggacacagt tggatcaata ctgattaaat gaaaaatcca 780
agcttttgctt gagaactttt gtaacgtgga gtagtaaaag tatcggtttt attctttgtc 840
gatgtctctt ctgcttgaaa taacagtcac catcacgcta aaggagagga gttctcttcc 900
ttctaagtag gcagaaaatgg tatcattatg ttgcccgtct ccaattctcc agagctcgct 960
ctctagagaa tcaccttctt tcgcgttttt tttttttttt gagggtagga gtctcactat1020
gttgcoccaa gactaggcct gggaaactgtt ggggggcaa ggggattgct cccgtccccg1080
aggcctcccc agtaggccgg ga 1102
```

<210> 104  
 <211> 306  
 <212> DNA  
 <213> homo sapiens

<400> 104

gaccaacacctt cccctgccatt tatacggcat aaaacccctca atctcaccag tatggctacc 60  
 aaaattatag gtccaccctga aacaaagtgg attgatgcaa ctctctggaat ttacaactca120  
 gaaaaatctt caaatctatc tgtaacaacat gatttctccg aaagcccttca gagttctaat180  
 attgaatcca aagaaatcaa tgggaattcat gatgaagca atgtcttttga atcaaaagca240  
 tcttgaatcc atttttttttg aaaaacctta aaaaaggcgga tcacaattttt tttgaacaag300  
 ggatcat 306

<210> 105  
 <211> 2042  
 <212> DNA  
 <213> homo sapiens

<400> 105

tggagatatt agtcagtttc tttagtata tttgtttcct tgatgtgcct ttttgttttt 60  
 ctttgggggtt ttttgaatcc ggaatgctgt gaagggcaat agcagactcc tccagctaag 120  
 agacaggaca tgttctttgag ccaactgtagc tgttgaagct ggacaccaga cgctccctat 180  
 aacccccccg ccaggcccata gcgtgtatgc atgtgcactt ccaccccacag aggagggtgt 240  
 gaagccttga gaaacctcaag aaagggctgg atctctgccat accctttgggt ctaccttggg 300  
 actgctgtgtt gccaacgtgt caaccagcct gtgttccctg caaccaccgc acttctgtgag 360  
 tgtgtggccta gggagaatca tgtgaatggg tgcattccaa gaggttcaggg cctgtcttgg 420  
 agaagaaata ctttagcatc atgaaaggga aagaacgtgc acccctttttt tgtttcttta 480  
 gtgaatgcaa gatttaataa aagtgaataa tgagcttccc ctttggggagt ggagcccgat 540  
 gcagctcact gacagggttg acatcagtat gatgtgttgg actgaaactg tatgtctgtga 600  
 ggtaggtgtg tgccttttag gccagaccac ggtggccacc ccatttctcc aaggtggttt 660  
 acctagcttg tgtatatatt acattgccac cctcacctct ggccaaaaat tcttgattta 720  
 aaaagaaaag tctattttgt taacgacagg ctctgttcta tgtgttacta tcccaagcct 780  
 ggattatttt atttatttta aagattttta atttccatat tgggtttatt ctaatcccat 840  
 ccctccctgt ggagctgcag agcatcttca tgtgagtaga cggatggaga taaatagatt 900  
 catgctcatt taggaagctg ggaatttctg gaagctgagg gtgagttcct gtgattcttg 960  
 ttcgtctcaa caaaaagtg ggagaccaag ttttatagca aagaacaaa taagtctgtag1020  
 agtcttgaat gcagaaaaaa attacctagc ctttcttagc acttaggggt tbtgtgagat1080  
 tcaagtgttta gcacagtgct tggcaatag taagccctag taaatgttta atattgttat1140  
 tagtgttttg taaaacttga gaaatagagc tgagctcatt cccttctctg tgattcaaaa1200  
 ataataccta catgaaaaca tgattccaag ttgattgaat ttactgggaa ttactgtgtt1260  
 agagtagccc agttctcggc ctacctgctt ggttgggac ttactgtatt ctgtaatgca1320  
 ctggtttgaa aatatgccag acctcagccc caagggaaac aaggtcgcaa gaatttatga1380  
 actccagctg gaaaaggtaa aggtgacctt tggctgacca catactggac cttacccccc1440  
 tgacgtattt cagaaacatt caaggggtttt cctcaaggaa catttttgag ctgaaaatta1500  
 aaatgggttc tctggcgagc tgcacccctt gaggtaaaat caagtagatt cctttgaagt1560  
 caataataga ggtttttctg cgttaaggga gaaggaaatg ccaattgaac ttacacattc1620  
 cccagcgagc tccctttgcc gccccctaca ggcctgggtg gccctcctg tctccagggaa1680  
 tcagactccc agactgggta gttctgcagt ttccatcaa attaaagggt attccctggc1740  
 cgctctctgg agaaaaacaa cccacccctg ccagctgggg gcaatggggc agggattttg1800  
 gcctctcaga acagctccta gaggctgctc atgactgaat gttttcccaa atccactaaa1860  
 tatcggtttg cttttgtttt tgggggagag gatttagcct cttaactccc tgatggattc1920  
 aaagttttat ctatctcctt atctcctgcc ctgtcttggc acaactctgg atagattgca1980  
 ggtgtggaat ttgtctggagt ttggtggctc cccaaattcc ttgatctgtc cgcaaaagaga2040  
 ag 2042

<210> 106  
 <211> 320  
 <212> DNA  
 <213> homo sapiens

<400> 106

aatcttttta ccatgaaatt tcttccagaa ttttccccct ttgacacaaa ttccatgcat 60  
 gtttcaacct tcgagactca gccaaatgct atttctgtaa aatcttcccc gagttctccal20  
 agcagtaatt tgcctctccc tagagtttact ctgccatttt gtgcacattt gaggtaacagt180  
 agcatgttat tttacaattg tgactctctc gggagctctg gggacatata aagtggctcaa240  
 tagtctttgc tgcctctgaga gtggaatgac atttctctcc tggtttggta ttactgtaga300

tttgcgatcat tcttttggtta

320

<210> 107  
<211> 506  
<212> DNA  
<213> homo sapiens

<400> 107

gtcgaacagc aaagccaaga cttgttaaaa aggtttgaag aggaaggacc ataacaattg 60  
aaaggggtgaa attataagat acagtaaaatt cctcttcaaa gatttagcct gttgacttcc120  
ttattctttg ttctcaaaact cgacttcctt gttgtccatg cctccttgct cctagttaact180  
gtgaacaacc ttccccaccg ttctaatacaa taactcaccat ctgctccctt gggtacccac240  
tctgcaccca ttcttcccac tgaactgca cttcccacca ctgtaacctca catccccctt300  
cccttcttta tttggaaaag tattcaca aa tagccaatcg ggtcaactta gaatgagcgg360  
tccaaaccga gccctctggg gagtgacaca gaggtaggga ctgtgttagg gataaaaaacc420  
ttttcctttt tttgttcagt gtgctgctgt gatcatgatt gatgcaggca gcagcctttt480  
tgcagaagta aattgccttg ctgagg 506

<210> 108  
<211> 1276  
<212> DNA  
<213> homo sapiens

<400> 108

gcgcggccgg cgctctcgagg gcgagagggg cggggcgagg ggaagctac gtcccgagg 60  
tgcggtgttg ggcaccgggc ggggcccggg gaaccggcgc cccacggagc tgctgctgtc 120  
agacccaacc cgggccccca tcatcactgc gcgcgcgttt cagggcgcga gaactaccgt 180  
tcccgcatg ccatgaaatt ggctcggcg ctgaggcggg gtccggcctc ccaccgcctc 240  
ccgcgcggcg cgaatcgagg tgcgagcca tggaggaggga ggcctcgctc ccggggcttg 300  
gtctgcagca gcgcgacctg gagaagctga cctgggcat cagcgcatc tagaattctt 360  
ccccagtggt gactgaggtg accatcatag aaaagcctcc tgctgaactc catatgattt 420  
cttccctggga acaaaagaat aactgtgtga tgctgaaga tgtgaagaa ttttacctga 480  
tgaccaatgg cttccacatg acatggagtg tgaagctgga tgagcacatc attccactgg 540  
gaagcatggc aattaacagc atctcaaaac tgactcagct caaccagctc tccatgtatt 600  
cacttcttaa tgcaccact ctggcagacc tggaggagca tacacatgaa gccagtgtat 660  
atcagccaga gaagcctcac tttgactctc gcagtgtgat atttgagctg gattcatgca 720  
atggcagtg gaaagtttgc cttgtctaca aaagtgggaa accagcatta gcagaagaca 780  
ctgagatctg gttcctggac agagcgttat actggcattt tctcacagac accttactgt 840  
cctattaccg cctgctcatc acccactctg gctgcacca gtggcaatat gcccttacca 900  
gctatggcat tagccacag gccaaagcaat ggttcagcat gtataaacct atcacctaca 960  
acacaacact gctcacagaa gagaccgact cctttgtgaa taagctagat ccagcaaaag1020  
tgtttaagag caagaacacg atcgtaatcc aaaaaagaa agggcctgtg cagcctgcag1080  
gtggccagaa agggccctca ggaccctcgc gctccctcac ttccctcact ttctaaatcct1140  
cctctggctc tgggggaacc ccaccggga agtgaggga cctctcctc caatttgcct1200  
aaccagtttc caggagtggg gtgggttttt ccgtggcaca ggttggggcc ttaggggggg1260  
ttggacgttc catttt 1276

<210> 109  
<211> 373  
<212> DNA  
<213> homo sapiens

<400> 109

aaatacattt atgtttcttg aaatgtgta agtggccttt gtcaagggtt ttataataga 60  
agagtatata aaaaatgaatt tctctagaga tgcagcatac tctaagatc catcattagat120  
taattaaaaa tatgttaagt atgctaacat ttccatata aatatggagaa cattaactct180  
cctactgttt agttataaaa taccaaattt tgtaattatc ctatctggaa ttacactata240  
ctgcaaaaat gccagttact tcaattttaa atttgacaa ttatgtgtatg aattataaaa300  
tttaaatagcc tacatctttt cctccttgta tccaaatttc tccggacatt aatgctttaa360  
ccttttgggt acc 373

09573395.122700

<210> 110  
 <211> 492  
 <212> DNA  
 <213> homo sapiens

<400> 110

```
gtcttttgaa atctgtttcc actacagcta tggtaagtc tatcagccgg tgctaccagg 60
agtcactgac agggctgccc ttctctgaa cccagtgagg cagaatcata agccctgacc120
ccatccctag aaagatgagg tcccagcaat ggccagagca tttctcacca gttctgtgag180
atagcacata aaaaatagagt tctttgggca aaacttttgg gaagcaatgc atccacatg240
ggctgatatt cagccctgagc tgttctcaag aggagagtgg tactggcagt ttaggtgctg300
aatccattct gattgggtgg agtctatgct ataccagttg ttaaacattt tgagtatcac360
tcttgcatat tgtttactatt atatttcttc tatatataga cagaaaggcc attttaggaa420
tatttaaaagg gctcttggaa attttctggc attagaccca actgaagggt ctattaaaggc480
agggttcccta aa
```

<210> 111  
 <211> 1678  
 <212> DNA  
 <213> homo sapiens

<400> 111

```
gcctcagcag actccttggg cggtagcagg gagatgggtgc aacggcccca gctgcacag 60
gaaccagagca ggcctggatc tgccaaccat agacacggga tatgattccc agcccccagga 120
tgtctcgggc atcaggcgagc tggaaaaggcc cctgccccctc acctccgtgt gtaccacca 180
ggacctcccc agacctctca ggtccaggga gttccctcag tttgaacctc agaggtatcc 240
agcatgtgca cagatgctgc ctcccaatct tccccacat gctccatgga actatcata 300
ccattgtctc ggaagtccc atcaccaggt gccatattgg catgactacc ctgcagcagc 360
ctaccagcaa gtgatccagc cggctctgctc tgggcagccc ctgcccggag ccagtgtgag 420
aggcctgcac cctgtgcaga aggttatctc gaattatccc agccccctggg accaagaaga 480
aggcccgcga cagagagact gctcctttcc ggggcttcca aggcaccagg accagccaca 540
tcaccagcca cctaatagag ctgggtgctcc tggggagtcct ttggagtgcc ctgcagagct 600
gagaccacag gtccccagc ctccgtcccc agctgctgtg cctagacccc ctagcaaccc 660
tccagccaga ggaacctcaa aaacaagcaa tttgccagaa gaattgcgga aagtctttat 720
cacttattcg atggacacag ctatggaggt ggtgaaattc gtgaactttt tgttggtaaa 780
tggcttccaa actgcaattg acatatttga ggatagaatc cgaggcatg atatcataa 840
atggatggag cgctacctta gggataagac cgtgatgata atcgtagcaa tcagcccca 900
atacaaacag gactgtgaag gcgctgagtc gcagctggag gaggtgagc atggcttaca 960
tactaaagta attcatcgaa tgatgcagat tgagtccata aaacaaggaa ccatgaattt1020
cagattctac cctgtgctct tcccaaatgc taagaaggag catgtgcgcca cctggcttca1080
gaacactcat gtctacagct ggcccaagaa taaaaaaac atcctgtgctc ggctgctgag1140
agaggaagag tatgtgctc ctccacgggg gcctctgccc acccttcagg tggttccctt1200
gtgacacagt tcatccccag atcactgagg ccaggccatg tttggggcct tgtttctgacal260
gcatctctggc tgaggctggt cggtagcact cctggctggt ttttttctgt tctccccgag1320
gaagccctct ggccccagc aaacctgttg tgcagagatt tcccccgag accctccacal380
accctggctt tgaagtggag tctgtgactc ctctgcatc tctgtttta aaaaaaccat1440
tgcaggtgccc agtgtcccat atgttctctc tgacagtttg atgtgtccat tctgggctct1500
tcagtgccta gcaagttagt aatgtaaggg atgtggcagc aaatgggaaat gactacaaac1560
actctcctat caatcactta aggtactttt fatgagttag ccagatgctt gtgtatcctc1620
agaccaaact gattcatgta caaataataa aatgtttact cttttgtaaa aaaaaaaa 1678
```

<210> 112  
 <211> 866  
 <212> DNA  
 <213> homo sapiens

<400> 112

```
gtgcgccatga ctgccaaagg ctgctccatc atgattgcac tgtctccctg tctgcaggat 60
gccagctctg atcaaaaggcc tgtggtccct tcatcgaggt ccaggtttgc cttttcctg120
```

00673395-122700

tctgtgctgg	accttgacct	caagccctac	gagagcattc	cccatcagta	taaactggac180
ggcaagatcg	tcaactatta	ttcaaaagact	gtacgtgcc	aagacaacgc	cgatgatcg240
actcgggttca	aggaagcgca	agattgcaca	ttagttctcc	acaaggtcta	actctttccc300
tcgagtgctc	ttgaaacttg	aacataatgt	gaaggctgaa	tgatagagat	attttctgtt360
tggttgggtg	gtgttgggtt	gtgaatgttt	ttgcttttaa	ccctttttaa	gggtgggttg420
cctcttgagg	acatggaatt	gaagagcact	agaaacaact	tctctggaca	ggaatgtagg480
aagtgaagtc	tggtgtccag	gaagctgctc	acactcttaa	aatggaagtg	tcctgttaagc540
cctgggaaga	cgttctggat	agttctctct	tcccaaccag	ggctcatgtc	tgatctctca600
atcgcaaaag	ccttatttca	agacccaagg	tttgagctcg	ctaccaccag	actcctaaca660
tagaaaactt	gaattgtcac	atatacttta	cagtttggag	ttttaagaaa	acatggatac720
tactgggaac	ttccccccag	tgagttacat	gggcactttt	tcagtgcaag	ccacatatca780
acacaggggt	ttaaggtggg	tgctcggtcg	cacacgtgaa	ccccgtggcc	ccccagatgc840
cgattctgag	ccagtgtaga	cccagg			866

<210> 113  
 <211> 1434  
 <212> DNA  
 <213> homo sapiens

<400> 113

gcgcgccggg	cgctcgccgg	gagagagggt	cggggccaag	gggaagctac	gtcccggagg 60
tcggtgttgg	ggcacccggc	ggggccggcg	gaaccggcgc	cccacggagc	tgctgtgtgc 120
agaccaaaccc	cgggccccca	tcatactgc	gcccgcgttt	caggcgccga	gaactaccgt 180
tcccggcgat	ccatgaaatt	ggcctcgccg	ctgagcgagg	gtccggccct	ccaccgcctc 240
cgcgccggcg	cgaaatccgg	tcgcgagcca	tgaggaggga	ggcatcgctc	ccgggggtcg 300
gctgcagcaa	cgccgacactg	gagaagctga	ccctgggcat	cacgcgcata	ctagaattct 360
ccccagtggt	gactgaggtg	accatcatag	aaaaagcctcc	tgctgaacgt	catatgattt 420
cttctctggga	acaaaagaat	aactgtgtga	tgctgaaga	tgtagaaga	ttttacctga 480
tgaccaatgg	cttcccatg	acatggagtg	tgagactctga	tgagacatc	atttccactg 540
gaagcatggc	aattaaacagc	atctcaaaa	tgactcagct	caccagctct	tcctgtattt 600
caacttctcta	tgacccaact	ctggcagacc	tgaggagacga	tacacatgaa	gccagtgtatg 660
atcagccaga	gaagcctcac	tttgactctc	gcagtgatga	atttgagctg	gattcatgca 720
atggcagtg	gaagatttgc	cttgtctaca	aaagtgggaa	accagcatta	gcagaagaca 780
ctgagatgtg	gttctctggc	agagcgttat	actggcattt	tctcacagac	acccttactg 840
ctctattacc	cctgctcatc	accacactgt	gctgcccaca	gtggcaatat	gccttcacca 900
gctatggcat	tagcccacag	gccaagcaat	ggttcagcat	gtataaacct	atcacttaca 960
acacaaacct	gctcacagaa	gagaccgact	cctttgtgaa	taagcttagat	cccgcaaaag1020
tgtttaagag	caagaacaag	atcgtaatcc	caaaaagaa	agggcctgtg	cagcctgcag1080
gtggccagaa	agggccctca	ggacccctcg	gtccctccac	ttctccact	tcctaaactc1140
cctctgcttc	tggaacaccc	accgggaagt	gagcacccct	cctcccaact	ccctaccagc1200
tcagagtggt	tggtttccat	gcacagatgg	ccctagggggt	gacctccagt	tttgctgtg1260
gaccgttagc	ctcttctctg	ttgaatgacc	aaaattgtaa	ggcttttagt	ccaccacacal320
ttagccaggc	tcgtagttag	gcctccagag	caggttgtgc	tgtccccctg	ctctggaagc1380
aatggggaat	tgggaaatcaa	gacaatgcc	aaaaaatatt	taatgcagct	ggtc 1434

<210> 114  
 <211> 914  
 <212> DNA  
 <213> homo sapiens

<400> 114

ttggcagcgg	ggagagggaa	agaggaggaa	atgggggttg	aggaccatgg	cttacccttc 60
ctgcctttga	cccatcacac	ccatttccct	cctctttccc	tctccccctg	gccaaaaaaa120
aaaaaaaagg	aaacgtttat	catgaatcaa	cagggtttca	gtccttatca	aagagagatg180
tggaagagac	taaaagaaac	accctttgtt	cccaactcca	ctttaccat	attttatgca240
acacaaaacac	tgctcttttt	ggtccctttt	ttacagatgg	acctcttgag	aaagaattat300
gtattccacg	ttttttagccc	tcagggtaac	aagataaata	tatgtatata	taacctttat360
tattgtctata	ttctttgtgga	taatacatc	aggtgtgtct	gggtgattta	tttaaatctg420
aaacctagta	tatccttttg	tcttccacag	tcattgttag	gtgggctccc	tggtatggta480
aaaagccagg	tataatgtaa	cttcccccca	gcctttgtac	taagctcttg	atagtggaata540
tactctttta	agtttagccc	caatataggg	taatggaaat	ttcctgcctc	ctgggttccc600

cattttttact attaagaaga ccagtgataa ttttaataatg ccaccaactc tggcttagtt660  
 aagtgagagt gtgaactgtg tggcaagaga gctcacacc tcaactaggtg cagagagccc720  
 aggccttatg ttaaaatcat gcacttgaaa agcaaacctt aatctgcmaa gacagcagca780  
 agcattatcac ggtcatcttg aatgatccct ttgaaatttt ttttttggtt ggtttggttt840  
 aaaaaccaagc ctgaggtctgg gtggaacacg tagcctaca caccccaat tgggggtggt900  
 ccocgggggaa tgtt 914

<210> 115  
 <211> 685  
 <212> DNA  
 <213> homo sapiens

<400> 115

gaaaatccag ggggtgaagaa tagatctgtg gtggcagggg tgggaaaggc ggggaggatt 60  
 tgcttaactga ggggcagcac aagagaattt tgcggggcga tggatctgtc tgtatcttga120  
 ccatagtgtat gatacatgac tgtgcatttg tcagaactca caggactgaa tgaagaagaa180  
 agtgaattttc actgcctgtg aattgtttaa ataaattgcta gacagtattt taaaaatcaa240  
 gccagatcttc tgcaagacat tatggctccc caccagaagg ggaaagagaa300  
 gtgtccccaac agttaaaccca cgttccctgg gacccacctc cctcccccact gccacttccc360  
 accagcgtcca cgcacggggc agggcccttcc ctttgcagct cagacgcccag cagatgttag420  
 gtgagaatgc gtcccccac ttgactaaaag gtttacagcc agcaggggtgg gaaatgaacc480  
 agatatttaac acccccctct ccatgcccct cccaccttct gggccagttac cagtgaaggc540  
 aggaagccac ttctcccacc cccaggtctg tccaaaagcc ctggaagaac ccaaggaaag600  
 gcaggagcca agttgggagt tgaccttgat gaccaggggc cagttggccc agtttccctt660  
 gtttagttgg ggggagggaa ccctt 685

<210> 116  
 <211> 2646  
 <212> DNA  
 <213> homo sapiens

<400> 116

ttaatttaaat agctttcatg tgattaaaaa tagctaacta gactcaagga ttcacaatat 60  
 ttagggtgat tttaaatacc tccagaaaagg aaacctcagt taatcagagc aaatagtttc 120  
 agtcttcaat tgagactgtc ttccatctct aaaaaataac tcttagtagt ttggagtgaa 180  
 gatagcaagg ttttgaagca tatttgtctc atccacagat gacacttttt atcttccagg 240  
 agcactccta ggagggtccc tgctaatca atgttgactg ctttgcagat ctcaagggaa 300  
 taaaatgaca aaagcagggg aagttacaga ttcaaacagc attttaactc atgttgatct 360  
 ggataattaa tcttttctaa agatgtgtag ttcttggaaa aacagtgata tcaactgatt 420  
 aaaaattacat ttttatcaac ataattgtct ggaaagata agcccccctaa ttttctacca 480  
 gttgactttt attcattaga tacagaaggt gcagttattac acatcacccag ctgcttttgt 540  
 gaatggctca ctacacagcc attgggttac aactgtgtgc atggggcagaa acagcaagtg 600  
 cctcattgtt ggtcattggg tggggagtg cttttgtcaa ggagtctgca ggaattggct 660  
 tatttctcta tgccaaagt atcaacacac caaagtctct gccataaaga atgtggtctc 720  
 tctgatctgt ccatcctggt actctggccc cagtaatttg atgtaactgt ctgattgtac 780  
 tagagcaagg agtataccca gcttattcat aatcaagtaa agagaactcag attagatttg 840  
 attttttgat tctctctaga gccaatcagg cagttaagag taataaagaa aaagggtttg 900  
 gtcaaaaacc ctaccattat ctggagatta ctctctgtgt cactcctgtc ttgccatgca 960  
 gctcttgccc cctcaccttt gctcagccta gcagtctact tcaactttat gcccttgtaa1020  
 tgtcagggct cctggggcgt ctggaaaaaga caggagacca gggcctctca cccctactgg1080  
 taacaggtcca ttgctgggtg cacaagaggg aggtgatttg catcatggtc atgtctgatct1140  
 ggcttcaact ggatgtctgtt aaacaccaga gggcccaacc tatcagaata ccagcagcaa1200  
 aggaaaaactc agatttttaga ggctttttac aataaagtag cgtaaactca ggtcatgatt1260  
 gatttcaaat gctgcccatg aatgattttg aagtaattat gtaggatcca tcaaaagcagt1320  
 attgtaggct tttagaattgt cccagtgagt ccgggaacccc atttcactgt ctctcttgat1380  
 cgtgttaatg atgcatcag agttcaagac agggcccatg agactctgact cactctctc1500  
 ggagaaatga atttcttccc actgaaggaa actctttctc attcgcagct aagacgggag1560  
 tgcctatgtt cctctcttca ctctctgagt actgctctgt gaagcgggtc tcaacttctc1600  
 tctagtacct ctctctctct ctgaagtgtg tgaactatct ctagtgttta aatttggcag1620  
 ttaactgcga tgtatgtcag catagaaaag gaaatgtttt tacccttatc ctgtgatgtal1680  
 tgatagaact taaaagaagt gtcattttgt tttcatagcc caccagcaga aaactcctct1740



catagattaa	atgtgctgct	gtggacagga	gggaaaaaaa	aacctctac	atattgaaag1800
gcacaaaatg	taatatctga	cactgttaag	atgccccaaa	gagcaaaagt	gtagtggagaa1860
tgcagggtca	tttccccatg	ccatccacag	tgtttgttag	tgagtccacg	gctgacttgc1920
agtgataaag	aaaagccatg	agctgtgtct	gcagacaatg	gtggctgcat	ctgtaaagtg1980
cttcagagcg	agcagccctg	gggaaattga	tgggtgtggc	agtggacaga	tgaagaggga2040
gaatctagcc	ttcagccctg	ccagtgttaa	ccactagaga	aactgagcgt	tatatccctt2100
tttaatgctc	gtgaatttta	gcattattga	acattagagc	aaatactcag	gggactctt2160
attaaacatc	cctcagataa	tttagctata	tatcattaga	aaggggaaagc	tatcatcttt2220
attttaaaac	taaaacaaagc	catcttataa	actgtcacca	aagctctccc	ttttttattg2280
catgtgtgcc	ttgaatttca	taaaaacatta	attccacaatg	ggggtcagaa	ctgactctgc2340
ttgaacaact	tcttgtacca	ttttatgttc	atattatggt	tgagagggtga	aaaaattgat2400
agcagcttaa	ctgaagtaga	actattcatg	atgcttttca	cacatctgtg	cataagatgt2460
aaagttttga	attaatgtta	attttotgtgc	atttttaatat	tcttttataa	ttattaatgt2520
taattttctg	gcatttttaat	attcttttat	aattatgagc	attttataaa	attcatcttt2580
acaaaacaata	aaaaaaaaaa	aaaaaaagga	ggaaggggaaa	aggaagaaag	agggggggaag2640
aggaag					2646

<210> 117  
 <211> 2667  
 <212> DNA  
 <213> homo sapiens

<400> 117

ttatcttgga	agtctgtgta	tcaaaatgaa	gaattcagat	ggtaggagggt	tctatagtcc 60
ttttaaagct	gactcttgag	tgtcagttga	atatccatta	aattggattt	gggaaataacc 120
tgaggaaaagt	attatgaatt	cgatctgcac	agatgcctct	tagctgatag	gtggcaggccc 180
tgtgggtgtt	gggtctccct	cttttctctg	gaacatatga	caattccaga	ttaaagaaaa 240
tgtcttttta	ataaaacccc	ttggctcttc	tcttagtcac	cttttaggta	gatatttgtga 300
ttttctggag	tatatgtatat	cgtgtctctc	gtgtctctag	tttactatag	gcataaataac 360
ttctctttga	ctattgtact	gaagtgattt	gatattaaagt	aaaacagttta	atgtttgaat 420
ataggcatata	tttatgggttt	tttcgctccc	cccccaaccc	acccttttta	aaaaattct 480
acaaagccct	tgtttgagtc	tcatcatgca	catcaaatca	tggagttagg	tcttctctga 540
gctcaggggga	acacaagtgc	acagagagag	atgtcttgag	ggctactacc	aaagaattac 600
cctcattgtc	cctcactcag	ccatgtgtga	catgcgatgc	tgtctgagtgt	gctgggggtgc 660
gtggtgagtc	cgtggctccc	ccagagcact	tcttaactgg	caagctggga	gaaccattac 720
tgggtgaactt	tgtgaaatt	agaactgtat	cttttacata	atcttggcat	attacatttc 780
ataataaaaa	catcatttta	gttgcattgt	acatcaatat	tgattttata	ataattttct 840
taagcttcaa	ccatgtttta	taacctattt	cgttacatca	tatattttga	atgtgtaata 900
tgaactcttt	tgtctttaag	tcttttttta	aaatgtgaa	gtttctaaac	ttagaaggca 960
attgaatgta	tattgatgaa	aatgtgaatg	ttttgtctgt	tctcatgaca	aagatcacagg 1020
gctagtggac	atttgaataa	ataattaaag	ctagagctct	gtatgtcttt	tctttgaaag 1080
agttcttaacc	ttgtaaatgt	agaatgactt	cagagaattt	tgtattaagaa	aacattcaaa 1140
tctttaaccgc	cacaaaacact	ccaatttttt	tcaactgtgaa	gcgcacagca	atttttttct 1200
ttttcttttc	aaaagcctgc	ctctcgaatt	tatttcttgt	ttaactcatt	cagagagggt 1260
agtaaaagaa	atctattttc	ggtagtcata	tgcgttgaaa	ggatattggta	aatgtgtttt 1320
catgctgtac	catctggaaa	gtgaacagtg	ttggcaaaaa	taaccagtaa	aatcatgctt 1380
ttcaagatgc	tcttgccttg	ggatatcctt	cctaggggaga	aaaaaaataa	gtagtttaac 1440
aattgtgaa	tcattcttct	atttcagttt	ctgctgcagt	aatgggttcc	cacccattat 1500
aattccccag	ctttatgttc	tgttgtatcc	tccccttagc	ccagtaacat	ttttatctaa 1560
taccocattc	ccccatgct	gagacagatt	gaccocctac	tcattatgtg	gctctatgtg 1620
aattttaaaa	tgtggaatat	tgggcttgca	ggcagtagga	gctgcacaa	tcggtagagt 1680
ggagtgtgga	gttaaatgggt	agtatgttaa	taaggggaaa	ctgtctctga	cagaaattca 1740
gtaatgttta	ccaaaacatg	tctttctaca	ctgtgttaga	taaatgatgc	taccctgtag 1800
ctcagctaca	ggctgcagtg	caaaactttc	ttccatccag	agaaagcaga	attccctcct 1860
agtaaacctca	ttacaataac	tgttaactaga	agggcatgtg	ctctctctga	ccttcagtaa 1920
tattttgtcc	atctctttgat	gactgatgac	ctggaatgag	tatttctatg	aagggtcttc 1980
ttaggccctc	tacatcacga	agaggggtgc	tctagtgcga	tacagttagt	tcacagggaag 2040
gacacaggga	gaagtattac	ctagggctac	ttagcagctg	atcactccctg	tttctgcaca 2100
gtttctctga	actggccatc	agggcctctg	aggaactcaa	atcagttttc	ttttagcatgt 2160
cccccatcag	tgtgggtctc	actgttagtg	aggaatcggg	tctggtttga	tgtttttcta 2220
ggcaaaatgc	taagtgttgc	tgtttatgct	attcattcat	acgatgttgc	aaatttgcct 2280
aaaagggaat	tttcatgatt	tgatttagat	tagtattttaa	atatctgctt	tagatagcaa 2340

09673395.122700

```

ttaattttat tgtaaaaata aggaaaaata tgtgaatatg tgaatttttt aagcctgaga2400
gatgatagaa tgtttccata tttttcttgt aaagaaaaata atattttaac ttacacatcc2460
tgtagaaaaat accacctttt ccccttgtat tacagtacaa tgtttacatt actatactgt2520
caagctgaaa gtataaaaaa tgtacatata cattttgagt tatgtatcct ttttttaaaa2580
aaaggtgcgg ggctgtggca ctgggtcgga catgactaaa gtgtgacagag gctatgctag2640
atttataatc actagttctg ggaacttg

```

2667

<210> 118  
<211> 544  
<212> DNA  
<213> homo sapiens

<400> 118

```

catctgtgca tggatgagtg gccgactttg gagcccaggc tgttacttcc tggctctggg 60
gtgaatcctc catagtctga gactaagatc ctgtactctg gctcagcatg gaacatctgg120
cacacagtat gcaactgagga aatacttgtt ggaataatca gtgaatcata gatgaaaact180
taaccttgga attaatatg agactgctca gaggaagaga atggggagaca aaggacctgg240
tgattagacc cccaagcac tgggtgtgtc gctgtgtctc cgggttgaac aggccagcg300
agagctctta gggcgagaac tcaaggaatt tattgagcca tggcaaacag gcagtaaacac360
gccactcttg gctgtgtgat tgaagaagaga atgtgtgtga cagatataga agcatggaaa420
cctgataggg ctattgcaat cactcagaaa agaggcgatg gcagcttgga cctgttgaag480
cagtagagtg ctttccaggg agggagaaagg acctgaaggt taatttgatc accatgggcc540
atga

```

544

<210> 119  
<211> 1340  
<212> DNA  
<213> homo sapiens

<400> 119

```

gtttgatact ttccctgact taggtttgtc ctattcttca tttattcaga ctaggataga 60
aaatttttga atcagaaaaat agatccagtg tttagctaca tacaactctag tacaagttaa 120
ttttttattc taaacatagg tgtgttggtc ctttttttaa aagatgcgct ctacctgaaa 180
aggaaaattg attttagaac tggatgtggt gcagtgaagt attttaggcc caggtctgtg 240
tacacatttt atagaagaaa tgaagtaact tgaagtattt tgggtgcctt ttcatttcaa 300
ctgtgttttg aattctgtcag atcacacata tattgtgtta ttgggcgctg tggatctctt 360
tataaaacct cttgcttgtg tgcaaaagtt cctaaaaagg aacacaaagta atgcctatcc 420
attactagca tgctatgctg catgctttac tggcattgct gtatgcttta ctgtctttgt 480
aaaaatcccc ctctcccctt ttctggtaac tggaaaaagca tgctaaaaat agtcttatat 540
tttcacccca taagtgcaga atcagtaatt ccttggtcta aagctcttat ataataca 600
ttattgggtg taaataccaa gtttggatc tcatagctat ctttttttaa agaaattaa 660
ttcttgaaaa tttagccaaa tcccgtttta tgggaatgct ctttagaatt catttgttc 720
agcccttttg ttctatggtt gagaatactg aggccttac aaggttaaga gaactttccc 780
cgtgtctcac aggttagtgat aggcagagct ggaactagat atctggtctg ttgactctag 840
ctcagtgctc tctgtaact gttgaaaatt gtcttagttt gagagatggc tgaaaaaatg 900
aacataaaat gctatttata ataacaagta tatgtgaaat ttotatttgt aagactacta 960
ccggcttact gttgaaatgt ttggttatag tgtttaggct agaaaatgct cccacattgg1020
taataaaacat tacaaaaatc aatgtatttt taggtaggca ttttataaaa tgcattatgc1080
catggttgct tttgagatg attgtagtct gggtagcatc tttaaaaatg atgtgggctt1140
aacgtgttgt catatcagga gatgctctga ttgtatatgt gagactctgt tctgttat1200
tttaattgct gtaatgaaat tgatcagatt attttactac caacagttat agtttgaag1260
tccaactgta ttaattgact gataatatga taatatagag attaaaaatt ttgtcttcat1320
tccttaaaaa aaaaaaaaaa

```

1340

<210> 120  
<211> 2376  
<212> DNA  
<213> homo sapiens

<400> 120

```

ggatatgaat aaattgttaa tataaagtc tacagaaatt aatttatgaa atttctctaa 60
atcacacaaa acttaataatc agatgactac taccctgaga ctgaaaaata tgttctaatt 120
tatagtgtcta tttttgggca gttttgggtg atcaaacacat tctttttttta 180
taggagaaaaa aaggatgtct acataacaat ttgtaaaagt ataaaatcca ttagtttttta 240
agtcctctgta tgcctctggc tattataaga aacaagtatt tgcctctcgt tttaacggga 300
taataatgtc atgtctacat aaaatgattt ctaccacott aaatagctca ctgtagaatt 360
tcattgtataa atgggaacct atagtacata catatcatc tcttagtgct ggcaaatatt 420
tgagggtccat ccatattttta tattcactca tcagtagttg taaacacatt cttaaagtag 480
cattttcaga tatgaataag cagggatgaa ataagtatta gggtaaggga aatggttgag 540
gtcttccctaa gtgaagtgtg aaaaccacag ttttcttttt atggggtagt ctaatatgca 600
tttatctcgt caagcatttt aagattttcca tgaanaatgtc ctgaaaaatc aagattcttc 660
attgaggggt aggatctccc aatggggagac tgctctgaaa agagcatgtg ctttttgaat 720
tagataacct actataatca tggatgttct tgaataactta gcaaacatcc cagcatccca 780
aagtcaccaa gataaacctt cctactccaa catcacatga tcttctaatt ctacctgtaa 840
aaaaaagcat aacaatttat tagaataataa ttaogttata tacattactc cacctagaaa 900
aaaaaatagt tcattatgta gagaatgct ttttttagta catagagaaa taaaaatac 960
agataactcac tagtgaacaa aaaatgtcca aagccagcca caacagatcc taatgaacca1020
tacaatattg aatgcggggc gcagggagta ttttcaacat ctaaaaatcc taggagctta1080
agggactaga atgaaaaaaa agaaccctaga ttgagtaaga aagtatttca ttttgggggt1140
ctttggccaaa atgagacaata caccatttct tttctctgag ttgaggggtt aaactagagt1200
atgtggcacg tgacaaacct aatcagcttg cgtgtctctt gtccaccttt ggtagcaggt1260
ctgaattctt aaatccgaaa accttacaata ttggaccggga aaacctctaa gcagtaggggt1320
aacttggagc tgtattctaa ttgtctaact aactgacttg gaaataggat aattcatttt1380
atgagctctt taaatgagtt tatttgggaa tatgcctatc attggaattg aaagcagcat1440
agcttgcctc agtaactcca ataatttggg aagcagaaat ggaaaaagta atttgagtaa1500
ctgtttgctta tgtatgtccg tttaaaaatc cctagtaaat tacccttcat attttat1560
ctagggttaac atcaactgtg ttgttaagag taaatgtttc accttaagat aaacatgggc1620
aataatattaa actctagctc gtcttcttgc ctgtgaagt aggtctgact tgattatatt1680
tgattctcttg ttctgtaaac atggggaacga cagctaaagt tgggtgaaaa cgcggggatc1740
caaaagagctg gattttttat tcagatctgc cgtcaacttt tgtatcctat aggtacttt1800
tatttctatg gtctcaactc ataacatgaa tgggttgggt taaatgact aggttctctt1860
aagtcctaaa attctttttt tacagttctt attggaatta tgtatttctt atctctaata1920
tgctttaact ggaatgtctg cactctaggg cggcaagaca gacattttaa agtaacagct1980
acactgctga actggcattt ctgttaacac aaaagtttag aaaaactcac gtaactgtta2040
ctgtatttaa gttatataaa aattttcagt aaggctgctt ttaaaaaggaa ccaactgtcca2100
tttaaagggt tcatagtatt ctccaatggg ttagtattgt ttggggcagg acattaaact2160
agaagggatt ctataggatg aggtgatacc tagaaggtaa tatattgtaa ggcaaaagag2220
attagaagaa atggggggaa aggatagtaa aaggcaagtc agattaaagg gttgaaacat2280
gaagataacc ccatgttatt cgggcccatt gtttgccctt tttggctcca gcatcgtgt2340
tggaagagcc caatgtgcgc ttggctcccta ataaag

```

2376

<210> 121  
 <211> 225  
 <212> DNA  
 <213> homo sapiens

<400> 121

```

cagttgtgaa gttttgtaaa atggtcaccc aacttaaaac taggaaatta cgaagaagag 60
aaaattgtccc ggtatctgtt aaggtctgccc tbtagatctg ctgtagggct tgtcaccatt120
ggaagcaagg tcctacttca gtggcagatc tbtgtggcct tbgatggctg aagaccacca180
ccctgcacag ggtcggggcc atgcaaggc atccttccct acctt

```

225

<210> 122  
 <211> 1967  
 <212> DNA  
 <213> homo sapiens

<400> 122

```

acggggcggcg cccgcgctcg caggccactc tctgtctgct cccgtccccc gcgctcctcc 60
gaaccgcctcc agtcgcctcc gctcggccccc gcgcgcgcgc tcaacatgat ccgctgcggcg 120
ctggcctgcg agtgcgctcg ctggatcctg cccctgctcc taactcagcgc catcagctcc 180

```

gacatcatcg	cgcgtggccgg	cgcgggctgt	ttgcagctcta	ggcaccacgg	ccagacgtcc	240
tcgctgtggt	ggaaatgctc	ccaagagggc	ggcggcagcg	ggctcctacga	ggagggcgct	300
cagagcctca	tggagatcgc	gtggggtaga	gcagcggctg	ccatgctctt	ctgtggcttc	360
atcatcctgt	tgatctgttt	catcctctcc	ttcttcgccc	ctgtgggacc	ccagatgctt	420
gtcttcctga	gagtgatggg	agggtctcctt	gccttggctg	ctgtgttcca	gatcatctcc	480
ctggtaattt	accocgtgaa	gtacacccag	acottcacc	ttcatgccc	ccgtgtgctc	540
acttacatct	ataactgttc	ctacggcttt	gggtggcgag	ccacgattat	cctgatccgc	600
tggtcctctt	tcttctgtcg	cctccccaac	tacgaagatg	acottctggg	caatgccaa	660
cccaggtact	tctacacatc	tgcttaactt	gggaatgaat	gtgggagaaa	atcgctgctg	720
ctgagatgga	ctccagaaga	agaaactgtt	tctccaggcg	actttgaacc	cattttttgg	780
cagtgctcat	attattaaac	tagtcaaaaa	tgctaaaaata	atttgggagg	aaatattttt	840
taagttagtt	tatatgttca	tgtttatctt	ttattatggt	ttgtgaagtt	gtgtcttttc	900
actaattacc	tatactatgc	caatattttcc	ttatatctat	ccataacatt	tatactacat	960
ttgtaagaga	atatgcacgt	gaaacttaac	actttataag	gtaaaaatga	ggtttccaag	1020
atttaataat	ctgatcaagt	tcttgttatt	tccaaataga	atggactcgg	tctgttaagg	1080
gctaaggaga	agaggaagat	aagggttaaaa	gttgttaatg	accacacatt	ctaaaagaaa	1140
gtcaaaaata	aagttttattt	taagcctctc	gaactatttta	aggaagaacaa	aatcatttcc	1200
taaatgcata	caatttgtga	gaatttctca	ttaatatcct	gaatcattct	ttttagctaa	1260
ggcttcatgt	tgactcgata	tgtcatctag	gaaagtacta	tttcatggct	caaacctgtt	1320
gccatagttg	tgaaggcttt	cctttaaagtg	tgaatatattt	agatgaaatt	ttctctttta	1380
aagttcttta	taggggttagg	gtgtgggaaa	atgctatattt	aataaatctg	tagtgttttg	1440
gttttatact	ttcagaacca	gagtagactg	gattgaaaga	tggaactggg	ctaatttatc	1500
atgactgata	gatctgggta	agtgtgtgag	taaagcatta	ggagggtcat	tctgttcaca	1560
aaagtgcac	taaaacagcc	tcaggagaat	aaatgacttg	cttttctaaa	tctcaggttt	1620
atctgggctc	tatcatatag	acaggcttct	gatagtgttg	aactgttaag	agaaacctac	1680
atatagttaa	aatcctggct	tttcttggtt	aacagatttt	aaatgtctga	tataaacat	1740
gccacaggta	ttactcggga	tttgagtttc	tcggaatagc	atatatatga	tgcatcggat	1800
aggtcattat	gattttttac	catttcgact	tacataatga	aaaccaattt	atttttaata	1860
tcagattatt	attttgtta	ttgtggaaaa	agctaattgt	agttttctat	atgaagtttt	1920
cccaataaac	caggtattct	aaacttgaaa	aaaaaaaaag	tcgacgc		1967

<210> 123  
 <211> 612  
 <212> DNA  
 <213> homo sapiens

<400> 123

cctagctgtc	ccccagagat	gaagaaagag	ctccctgttg	acagctgcct	gccccgtca	60
ctcgagcttc	accctcagaa	gatggatccc	aagagacagc	acattcagct	cctgagcagc	120
ctgactgagt	gcctcagcgt	ggacccctcc	agtgcacgag	cttgaggcca	ctgtaccctt	180
aagcacctgt	cacagctcag	ccttctgtgt	gagcacttgc	tcagctcctg	ggagcagatt	240
cccaagaagg	tacagaagtc	tttgcaagaa	accattcagt	ccctcaagct	taccaaccag	300
agggctgctg	ggaagggtag	cagtaacaa	caggatgtcg	tcacctgtga	catggcctgc	360
aagggctcgt	tgcagcaggt	tcagggtcct	cggctgcctc	ggacgcctgt	cctcctgttg	420
ctgtggtctt	tgcgtgttag	cttcctgtgc	catgacctcc	ggctcacacg	ctccttccag	480
cctccctcta	ttgacggggt	gcttcgatca	ctgtgctctc	tcactgcctg	ccacaacgcg	540
tgttccaagt	tactctctac	agctctcaag	gttacaggtt	ggttggggga	gaaatgccgt	600
tttgggggtc	ca					612

<210> 124  
 <211> 1183  
 <212> DNA  
 <213> homo sapiens

<400> 124

tttcggcaca	gcattgaatg	ctgcgagaag	gacagctcgt	ccacagattc	tgctaacgaa	60
aaaccagccc	ttatccctcg	tgagaaaaag	atctcgatgc	ttgaggaacc	ttcaaaaggca	120
cttctgtggg	tcacagagccc	aaatatgtag	aaatcagtg	aggatttgc	acgctgcacc	180
gtttctctaa	ctgatgatcg	cgtcatgttc	aaggaagaag	tggtatagtt	cgtgaagaag	240
atcaaaagctg	cctttgtctga	attacacaa	tgcatcattg	acaaagaagt	ttcatttaag	300
gcagaaatg	ataaagttaa	agaagaagcc	atggaaatcc	tgactgctcg	tcagaagaaa	360

gcagaagaac	taaagagact	cactgacctt	gccagtcaga	tggcagagat	gcagctggcc	420
gaactcaggg	cagaaattaa	gcactttgtc	agcgagcgta	aatatgacga	ggagctcggg	480
aaagctggcc	ggttttccgt	tgacatcgaa	cagctgaagg	cccaaaatcat	gctctgcgga	540
gaaattacac	atccaaagaa	caactattcc	tcaagaactc	cctgcagctc	cctgctgcct	600
ctgctgaatg	cgacagcagc	aaactctggg	aaacagagta	actttttccc	aaaatcatcc	660
actcacaaat	agccctctga	aggcaaaagc	gcaaaaccaca	aaatgggtgag	cagctctcccc	720
agcagccggc	accctctcca	ccagaccatg	ccggcccaaca	acagaaatgg	atcttctaac	780
caaagacgga	gattttaatc	acagtatcat	aacaacagggc	taaatggggc	tgccaaagtc	840
caggggcagt	ggaatgaagc	cgagccactg	ggaaaaggga	acagcccgcca	cgaacacaga	900
agacagccgc	acaaaggctt	ccggcccaaaa	aaacaaaggc	gtgccaaaaa	tcaagaggct	960
tcctttggga	tgaagacccc	cgaggccccc	gcccattctg	aaaagccccc	gcgaaggcag	1020
gcagcgtgca	ggacacctcg	ggaggggcag	gggcctttcc	ggggtttagt	tcgggttagg	1080
gggtttcaca	gttgcatatt	tttgccccc	cgaggagatta	ggaagttttt	ccacagatgg	1140
caggcatatt	ttttgagttc	cccggttttt	gacgttttgg	ttg		1183

<210> 125  
 <211> 891  
 <212> DNA  
 <213> homo sapiens

<400> 125

Cggaggcagc	ggaaagccga	gccaggcgcc	tgcgcgctgg	gaagagtagg	ttcagagtgc	60
attccggaac	ccggggcgcg	gcgactcgcg	caggcgccgc	gactccgctc	agtttccggt	120
cgcgcgaaaca	ccaaagtccg	ggaacttaag	catlttccgt	ttctagggtt	gttacgaagc	180
tgcaggagcg	agatggaggt	ggacgcacgc	gggtgtgatg	gtcgagatgt	gttccgggag	240
cgggcaggct	ttagcgaagg	agggaggcag	aacttcgatg	tgaggcctca	gtctcggggc	300
aatgggcttc	ccaaacacgc	ctactggttg	gacctctggc	ttttcattct	tttcgatgtg	360
gtgggtgttc	tcctttgtga	ttttttgcc	tgacttgttc	gctgatatct	aaattaagaa	420
gtgtgttctt	gagtgaattc	tgaaaatggc	tacaaacttc	ttgaataaag	aagacaggac	480
ttccaataga	agaatttcac	atctccaagg	gaccttctct	ttcattttac	actttgttac	540
taattttcag	aactctatta	attgggtagg	atttcaccca	ttcctagatt	agttcttaaa	600
atataaacct	ttgggtcgtg	tttaaaaaat	ttcaaacatc	tgatggcttt	acagggggct	660
aatataaagc	catlttgtact	taaaggctct	gtgtattcat	taagaaatat	agtaattgtc	720
tttaattgtt	taagagttga	tcagggggtt	actatggatt	cgaagtaata	gggatgatta	780
ataaggggaa	gggtttttatg	gaattttcaa	agtcatttta	tttcaaaagc	gggggaaagg	840
gttttgagag	gagggggggc	caagggtgtc	ctgggggttg	ccgaggaggag	c	891

<210> 126  
 <211> 482  
 <212> DNA  
 <213> homo sapiens

<400> 126

tctctaataa	gtaccttttc	agtcctggcc	cagaagttcc	ctcaatttca	gcagcaccga	60
cgggtttata	attcattcag	ttttccaggc	caggcagccc	gctatccttg	gatggccttt	120
ccacgcgaat	gcattcatga	cttgaaccac	acagcaaac	ccacctcaaa	tagtaatttc	180
ttggacttga	atctcccgcc	acagcacaac	acagggtctg	gagggatccc	tgtagcaggg	240
gaagaagagg	tgaagggttc	gaccattgca	ctgtcaacct	cttcccaatc	attacaacaa	300
ggagcagcag	ctacaagtct	ccacctact	gtggcctgac	aacagaaact	agagggagag	360
attagactct	gggggtcctg	catggggcac	tggtattttg	catgatctct	tatgatgttt	420
gcttttaaat	tatacaccca	gaagagccaa	tataaacgtt	cctcatgcct	aaaaaaaaaa	480
aa						482

<210> 127  
 <211> 610  
 <212> DNA  
 <213> homo sapiens

<400> 127

ctcgagccgt	ggggcagtcg	cgcgaatgag	cggagacact	gaccttcagc	gcctcggctc	60
------------	------------	------------	------------	------------	------------	----

cagcgccatg	gcgcccctcca	ggaagtctctt	cgttggggga	aactggaaga	tgaacggggcg120
gaagcagagt	ctggggggagc	tcacgcggac	tcctgaacgcg	gcacaggtgc	cgggccgacac180
cgaggtgggt	tggtgctcccc	ctactgccta	tatcgacttc	gcccggcaga	agctagatccc240
caagatgtct	gtggctgcgc	agaactgccta	caaagtgcct	aatggggctt	ttactggggga300
gatcagcct	ggcatgatca	aagactgcgg	agccacgtgg	gtggctcctg	ggcactcaga360
gagaagcgt	gtctttgggg	agtcagatga	gctgattggg	cagaaaagtg	cccatgctct420
ggcagaggga	ctcggagtaa	tcgcctgcct	tggggagaa	cttagatgaa	agggagagctg480
gcctcactga	gaaggttggt	ttcgagcaga	cagaggggtca	tcgcagataa	cgtgaaggac540
tggtgcaagg	tcgtcctggc	ctatgagcct	ttttttgggc	cattttggtgc	ctggcaaggc600
cttcaaacag					610

<210> 128  
 <211> 2072  
 <212> DNA  
 <213> homo sapiens

<400> 128

gggtcatgta	ggtacaacag	caaccaagaa	gatcgatgct	tacgtccctt	ctgcactcga 60
gccaggacag	actgctgcga	atgaccgtgg	tgacaatggc	cagcgccagg	gtgcaggacc 120
tgatcgggct	catctgctgg	cagtatacaa	gcgaaggagc	ggagccgaag	ctcaatgaca 180
atgcagctgc	ctactgcctg	catattgctg	aggatgatgg	ggaggtggac	accgatctcc 240
ccccgtggga	ttccaatgag	cccatctata	agtttggctt	cagtactttg	gccccgtggt 300
aaaaagtact	catctcctgg	tctgacatcc	aaagagtcac	tctttgttgc	aataaatgct 360
gctatggagt	tctcccttat	tcaggtggac	aacacaaaag	ttaccatgaa	ggaaatctta 420
ctgaagcag	tgaagcgaag	aaaaggatcc	cagaaaagttt	caggccctca	gtaccgcctg 480
gagagcgaga	gcgaagccaa	tgctgcgctt	gacctggaca	gcactttgga	gagccagagc 540
gcattggaggt	tctgcctggt	ccgcgagaac	agttcaaggg	cagacggggt	ttttgaggag 600
gattccgaaa	ttgacatagc	cacagtcacg	gatattgctta	gcagccacca	ttacaagtca 660
ttcaaatgtca	gcattgatcca	cagactgcga	ttcacaacgc	acgtacagct	aggtatctct 720
ggagacaaag	tagagataga	ccctgttacg	aatcagaaag	ccagcactaa	gttttggatt 780
aagcagaaaac	ccatctcaat	cgattccgac	ctgctctgtg	cctgtgacct	tgctgaagag 840
aaaaagcccca	gtcacgcaat	atttaaacctc	acgtatctaa	gcaatcacga	ctataaacac 900
ctctactttg	aatccgagcg	tgctacogtc	aatgaaattg	tgctcaaggt	taactacatc 960
ctggaatcgc	gagctagcac	tgccccgggt	gactactttg	ctcaaaaaac	aagaaaactg1020
aacagacgta	cgagcttcag	cttcacgaag	gagaagaaat	ccgggcagca	gtgacactgg1080
cctccagcct	caatctgttc	cgtagctcag	agcctgcctg	ccagggccaa	gtgccctaga1140
gcaccaaccg	tgctcgtgaa	tctcggggg	gagggccagc	cttggtctac	tgggcagggt1200
caggtgggct	ctcgggggaag	gtgtcggggg	ccccatagga	gggagcgctg	gggacattgc1260
catgggacgg	aagctctgctt	ggcagtggtg	ttgataaagg	atgtctgggg	gtcagaccac1320
ccccatagagg	agccacgtgc	gcgccagcca	ccttcaatgc	ctgcaccact	gcccgaggat1380
gtacagagcc	gtgccacac	atttctctgc	aacttgatca	aatttcttaa	agcaaacacac1440
aaaaatgtac	atttctgttt	ttctctttaa	taaacagggt	cttggtttgat	ctaggttggt1500
atgatggacc	attctttggg	gcggagaggt	gattatgtta	ctctctttaa	aatctgttcc1560
catattgaa	agggcagattg	gaaaagctat	ggttcgattt	ctcagaagaa	atgttttaggt1620
cttagtcaat	agtttttaact	atgccatttg	tttaaatgag	tgcaatttgc	tcgagggatga1680
tgctctacta	aaagttagga	acagagacct	agtggtgtgt	ccaaaggcgt	gtcaacttcc1740
ccttcagcac	acccagcctt	ctgacctcag	agcccaggag	ctgcgtggac	agtgtggggt1800
gccaggagga	ggggcggttg	ctggctccta	ggcacgctgc	actcccagcg	agacatggtc1860
tttccgtttc	ttaaagtacga	agtgtagggt	tcagctggga	gttcccaact	gatgttctct1920
gcttcgctgc	cttggaaagg	gccacattcc	ccattctctc	ttctcttaca	gcgcctgctc1980
cctttttaag	caggcggaag	gtgctgtgtt	ctcacgtttc	agggagaggg	gtgacaggac2040
gactgtgtcg	tgctcgtgtc	ctgggtggac	ag		2072

<210> 129  
 <211> 980  
 <212> DNA  
 <213> homo sapiens

<400> 129

tttatggagt	tagagcagg	gaacttaaaa	acaaaagtg	atttaataac	ttcatgagac 60
tgtgataacc	agtttatatt	tgaaatatat	acagacattt	gggagacgtga	tttgtagacc120

tgatagtcct	ttgcacagtg	atcttcagat	cttaaaagaa	aaagaaggca	tagaataat180
ttgtcttaac	ttctctttta	aggataaact	tcattttgat	ctccatttgg	ctcgagtggt240
gttacctgtt	ctctcaggag	ggatgtgatt	gggtggagga	gcattatgta	tggaaactct300
cacaaaacag	ggctggagca	gtgcctactc	aatagaatcg	gtcatcatcg	aaataaatgc360
caccttagtc	aaagggcaag	ccagagtgcg	gtttggagca	aaataagaatc	aatataatct420
agcaagagcc	caacaatcct	ataattccat	tgtacagata	catgagaaaa	atggctggta480
caccctccca	aaaggaagtg	gctaaatagt	ttgactgttg	tatgttttgc	ctaatgttgc540
tttaaagaaa	atctttccaa	catgcagaca	aaagctttga	gtgccccctat	tacagcagta600
ccgaagatgt	tagtttaatag	atattttagt	ggataaactg	tcacttgaca	ccagatataa660
gttacagcct	tcgcattttg	ctcatttttag	atatcttgga	ctgagcagtg	gggcctttac720
tgtatttttc	ctgataaata	cacatactgg	ccactcctta	tctctttttc	ttgaaaagt780
aaactttttaa	aggcagccaa	gtcaacatca	gggctactga	agttggaggg	ctttgagggt840
aaactttccta	tattgagccc	atgggggttac	aaaggttttg	caatatattg	ttccctttta900
cagccaatac	aggttttta	cggatgtttc	aatattgggt	ttaggggatt	ttaagggccc960
cttaagtca	taatagcctt				980

<210> 130

<211> 792

<212> DNA

<213> homo sapiens

<400> 130

ctgtttggca	gggcgggggc	cctcgcgaag	atggtggcgc	gcgcggcgctg	tggctcccgt 60
cgcttggcca	agctctcagc	cacgcaacgc	gcgcggcgtct	cgctggccctg	gagcccaac120
ccaccgggctc	ccctgacccc	cgccccccgc	gccccggttcc	cggctagcctc	cgcgcccgta180
agggaacacg	gctccggaaag	gggtggtcagc	gcgctggagg	aggtgcccggg	agcagtgccc240
aaagctgactc	gggttccagt	gacgatgagg	cagccagtgga	ggccccgagc	accgcccagtg300
aatgccccag	cctctctcagc	accactgcag	aggacagcct	tgggggggat	gtcgtggat360
agcaaggggc	agcaggaaga	ccttgaggaa	aaagtgaagg	agtatgttga	ctgtctcaca420
gacaagagtg	ccagagcccg	gcaggtgcct	cttgagagcg	tggccctggc	cctagcgctcc480
cgctactccc	cgaactttct	gctggagcgc	cgccctcagc	tagccgatgc	cttggaagaa540
tgcctcaaga	aaaggaaggg	cgaggaacaa	gccccgtgctg	ctgctgtgct	aggcctgtct600
tgcgtgcagc	tggggccctgg	acctaagggt	gaggagctgt	ttcacagcct	cgagcctctg660
ctggtctctg	tgcctagtg	cagcacagct	agccctgctg	cccggtccca	cgtaggttgc720
ctgtgcccca	tgaaccctt	cctgcgaact	atccctcagc	agagtgggtg	gttcccccta780
tcttcagcct	cc				792

<210> 131

<211> 1092

<212> DNA

<213> homo sapiens

<400> 131

gtgggtcccc	ccggttccgg	cgcggttgag	gccttcggtg	gtgaacagtg	ctccagcacc 60
atgtctgggt	tgtctaggcc	accagcccg	cgccgcccct	ctcgtctagc	gttctgtgctt 120
ttgttctctg	tcggcccccag	attgtgctct	gccattctct	tcactctgcc	cattaaactct 180
cgcaagtgtc	tcctgtgagg	gattcacaag	gacctgtctg	tgaactggcg	gtacgagatc 240
tcgagcagct	ctggggggcg	tggcgccctg	cgcagcacct	caagatcacg	gattctgtctg 300
gccattattct	ctaactccaa	gaggatgcaa	ccaaggggaa	atttgccttt	accaactgaag 360
attatgacat	gtttgaagtg	tgtttttaga	gcaaggggaa	agggcgagta	cctgaccaaac 420
tgcgtatctc	agacatcga	catggagtg	agggcgaaaa	ttacgaagag	attgcaaaaag 480
ttgagaagct	caaacattta	gaggtagagc	tgcagccctt	agaagacctt	tcagaatcta 540
ttgttaatga	ttgttccctac	atgaagaaga	gagaagagga	gatgcgtgat	accaacagtg 600
caacaaacac	cctggctccta	tacttcagca	tcttttcaat	gttctgtctc	attggactag 660
ctacctggca	ggtctctctac	ctgcgacgct	tcttcaaggc	caagaaattg	attgagtaat 720
caatgagcca	tattctctct	ccactttgta	cctcagccag	gaaacacatg	ctgggacgtg 780
cctggcctaa	ggcactctac	caacagcacc	atcaaggcac	gttggagcct	tcttgccaga 840
actgactctc	tttgggtgtg	gaggacatgg	ggtagccact	acacccaaca	agtcataatg 900
ggagctctct	tttaatttgg	aggatatttg	ctgggttttg	aacaataggt	ctattattag 960
agtcacctat	gacaaaaaat	aggggggttac	ctagataatg	ccaaagtccg	catttgtccc1020
gggtccctct	gtgggagctg	tgggacgatg	ttttctcttt	tgcccccttt	ccggagcgtg1080

<210> 132  
 <211> 1523  
 <212> DNA  
 <213> homo sapiens

<400> 132

```

ctcatgtcta aagaatttcc tttttgtgtg aaaaagacta agagcatctt caacagtgcc 60
atgcaagaga tggagggtta cgtgggagaac atccgcagaa gttttggggtt ttttaattact 120
ctccatttag gacacctac acacccaaca gccagtatca aatgctgctc gatccccca 180
accccagcgc cggcactgcc aagatagaca agcaggagaa ggtaacgctc aactttgaca 240
tgacggcatc ccccaagatc ctgatgagca agcctgtgct gagtgggggc acaggcgccc 300
ggatttccct gtccgatgat cgcgcgtccc ccattgagcac aaactctctt gtgcacacgg 360
gctccgacgt ggagcaggat gctgagaaga aggccacgtc gagccactct agtgcgacgg 420
aggagtcatt ggacttccag ggataagagc acagcttcac cagccactca ccaagacggg 480
acaagcaggg agtttatccg gcagcccaaa gcccttctct cctcaactgt cagctcctat 540
cacgacgaaa acggacaaaa cctccaccac cggcagcatc ctgaattctta acctggatcg 600
aagcaaaagt gagatggatt tgaaggagct gagcgagtcg gtccagcaac agtccacccc 660
tgctctcttc atctctccca agcgcagatc tctgtagcagg ttccagctga atcttgacaa 720
gaccatagag agtttgcaaa cacaattagg cataaatgaa atctcggaag atgtctatc 780
ggccgtagag cacagcgatt cggaggattc tgagaagtca gatagtgcg atagtgaat 840
tatcagtgat gatgagcaga agtctaagaa cgagccagaa gacacagagg acaagaagg 900
tgttcagatg gacaagagc catctgctgt taaaaaaaag cccaagccta caaacccagt 960
ggagatctaa gaggagcaga aaagcagctc accagccagc gagaaggcag acctggagc 1020
agtcaaggag aaggccagct ctgagcctga gaagagcttt tccgaaaagg caaaaacctt 1080
acctcacccc ataaaggata aactgaaggg aaagatgag acggattccc caacagtc 1140
tttgggcctg gactctgatt cagagagcga acttgtcata gatttaggag aagaccattc 1200
tgggcgggag ggtcgaaaaa atagaagga acccaagaaa ccatctccca atctctccca 1260
tgtaggttaa actccacatt ccaagcaggt gggcagccat tctctccggc aaacacgggt 1320
gctcacccgc tctctccgcc aaactctccg cgtggcgccc acagccacca cagcagctc 1380
ctccacgggt accgtcacgg ccccgccccc cgcgcgccca ggaagcccg tgaaaaagca 1440
gaggcgcttt ttacgaagg aggaactgcc cggcgtgca cggggtccgt gtggaactca 1500
tcaagtaaa tttcaaacgt cct

```

1523

<210> 133  
 <211> 2241  
 <212> DNA  
 <213> homo sapiens

<400> 133

```

cgccgcccaa ggcgcagaag ccgagctggg aaaagggagg cagaggaggc ggaggcagag 60
cgagaggcag agcccggtgc cgagaccca gcgagacgcc gggggggagg gccctcgaaa 120
gcccggctcg cgagctctcc cgacacccga gccggggagg aaaagcagcg acctctcgct 180
cgcatcccc ggagcgcac tcagactggt cccggtagtc aggggctcag gacgagatcc 240
cgaggcaggc tttgctcagc ctccgacgag ggctggccct ttggaaggcg ccttcaacag 300
cggacacaga caggccacca tgaccgagaa ttccacgtcc gccctcgagg ccaagcccaa 360
gggggccaag gccctcaaga agtccacaga ccaccccaag tattcagaca tgatcgtggc 420
tgccattcag gccgagaaga accgcgctgg ctctcgcgc cagtcattc agaagatat 480
caaagccca tacaaagtgg gtgagaacgc tgaactcgag atcaagtgtt cactcaagcg 540
cctggtcacc accgggtgtc tcaagcagac caaaggggtg ggggcctcgt ggctcctccg 600
gctagccaag agcgacgaac ccaagaagtc agtggccttc aagaagacca agaaggaat 660
caagaaggtt gccacgcca agaaggatc caagcccaag aaggctgcct ccaagcccc 720
aaaccaagaa cccaagacca cccgggtcaa gaagggccaa aagaagctgg ctgccacggc 780
caagaagcgc aaaaaaccca agactgtcaa agcgaagccg gtcaaggcgt ccaagcccaa 840
aaaggccaaa ccagtgaaaa ccaagcaaac gtccagtgcc aagagggcgg gcaagaagaa 900
gtgacaatga agtcttttct tgcggacact cccctcattt tcttaataat tgtaataat 960
ttctctcttt ttctctctct gatgctcacc accacctttt gccccctctt gtcttgactt 1020
tataagagac aggatattga ttcttcagaa attacagaa taactatttt tcttaacca 1080
gttgtcgaag gacagcaaca accaatctaa tgatgagaat gtacttatat tttgttttgc 1140
tattaacctt cttacggggt tagggatttg cgggggggct tgtgtgtttt gttggctgt 1200

```



ttgccatgaa	ggtagatgtg	ggtggggaga	agacacaaag	cagtttggtc	tggttagatg1260
agaggaaccc	caggaattgt	gaggttagca	ggaatatctt	tagggtagt	gagttttcct1320
tgagttgggc	acccgttgtg	agagtttcag	aaaccttggc	cagcaggaga	gaggttgtag1380
ggagcagcca	gcgggcaaa	gaaggaggtg	gaaaaaaacc	gccaccgggc	tgactttccac1440
ctccagtggt	tgagcagttg	gggcccacaa	ccagtttctt	tctcattttt	gttagttttgc1500
ctctttcgccg	tccctattttt	cttagggaa	gggagtgggg	tccaagtgtac	agctggatgg1560
gagaagccat	agttttctccc	agtcagctag	gtgttagcca	ttggggggtc	tttgtgctt1620
cagcaaaatt	tctgtgttaa	ccggagtgaa	aaacttcagg	gaagggtggg	gagtcagcca1680
agtgccctcag	tgtgcccctgt	tgaaacttag	gtttttccac	gcaatcgatg	gattgtgtcc1740
taggaagact	ttctttttcc	tctggatttt	tggttctcct	gtacaagagg	tgcttttgc1800
tggtttgggt	gggctgcggc	cacttaaaac	ctcccgatct	cttttttagt	ccttttattat1860
aagttagttg	agctgcggga	gggggggggg	gagtgggcgg	gcagtggaata	tgaaagactta1920
ctgcagtcga	tttgggattt	gctaagtagt	tttacagagc	tagatctgtg	tgcatgtgtg1980
tgttttgtga	tatatacata	tctagggtcta	gtacttagtt	tcacaccggg	gagctgggag2040
aaaaaacctg	tacagttgtc	tttctcttat	ttttaataaa	atagaaaaat	cgccgacctg2100
cgcgctcccc	ccccaccccc	ttttttaaac	aagtgttact	tggtccggga	aaattttgct2160
gtctttgtga	ttttaaaact	ttaaaaataa	ttggaaaaag	gagaaactga	aaaaaaaaaa2220
aaaaaaaaaa	aaaaaaaaaa	a			2241

<210> 134  
 <211> 631  
 <212> DNA  
 <213> homo sapiens

<400> 134

tgacaatggc	ttcttttaaaa	tactcagagg	acaggatcac	ggtggaatcg	aatcagaagt 60
ggtggctgga	attccacgca	ccgatcagta	ctgggaaaag	atctaatctg	ccgtgggacct120
gtcgtgcacg	tctctggggc	gagatggggg	tagaaatgca	tgtgatcgct	taagttccacg180
taagatacaa	gtttccagaca	gggttcggaag	gactgggattg	gcgaacacatc	agacctgtct240
tccaaggaga	caaagtctctg	gctacatccc	agcctgtggt	tacagtgcag	acaggcccatg300
tgagccagcg	ctgcccagcac	agagcgctct	ctcccctccg	tactccaatcc	atctccagggg360
agcaagacag	agacgcaggga	atggaaaagcg	gagtttcttaa	caggatgaaa	gttcccccat420
cagttcccc	agtaacctcca	agcaagtagc	tttccacatt	atccagaggag	gttcccccat480
agatgtgtgt	gggagccctt	tggagaacgc	cagttctcca	ggccccctgc	atctatcgag540
tttgcaatgt	caaaccctctc	tgatctctgt	tcagatgatt	cttaaatagga	gtttattttt600
cgggcagctg	cgaatcaggg	gggtaaccag	g		631

<210> 135  
 <211> 980  
 <212> DNA  
 <213> homo sapiens

<400> 135

ggggccggga	gggtacttgc	ggccgggggt	ggcccaggct	acggcgcgctg	cagggtccg 60
gcaaccgctc	cggaacacag	aaocgctcgc	ctgcgcgcag	ctgaggctgc	aggctctcgg120
ctgcagcgct	gggttgatct	aggatccggc	ttccaacatg	tggcagctct	gggctctcct180
ctgctgctgt	ctggtgttgg	ccaatgccc	gagcaggccc	tctttccatc	ccctgtcgga240
tgagctggct	aaactatgtc	acaaaacggaa	taccacgtgg	caggccgggc	acaaactcta300
caacgtggac	atagcttact	tgaagaggct	atgtggtacc	tctctgggtg	ggcccaagcc360
acccagagga	gttatgttta	ccgaggacct	gaagctgcct	atgacaggga	gttccagcca420
acaattggcca	cagtgctcca	ccatcaaaga	gatcagagac	cagggtctct	gtggctcctg480
ctgggctctc	ggggctgtgg	aagccatctc	tgaccgggac	gcatccaca	ccaatgcgca540
cgctcagctg	gaggtgtcgg	cgaggagcct	gctcacctgc	tggtggcagca	tggtgtggga600
cggtgttaat	gggtgctatc	ctgctgaagc	ttggaaactc	tggaacaagaa	aaggcctggt660
ttctggtggc	ctctatgaat	cccatgtagg	gtgcagacgc	tactccatcc	ctccctgtga720
gcaccacgct	aaaggctccc	ggcccccatg	cacggggggg	ggagataacc	ccaagtgtag780
caagatctgt	gagcctgggt	acagccccgc	ctacaaaacag	gacaagcact	acgggatacaa840
ttctacagcg	tcttccaatg	cgagaaggag	atcatggcgc	agatctacaa	aaacggcccc900
tgaggggggg	gttctctgtg	tattcggact	ctctgcctaga	gtcagggggtg	acaaaagctgc960
cgggaatttg	ggggggccgc				980

<210> 136  
 <211> 2238  
 <212> DNA  
 <213> homo sapiens

<400> 136

```

cacatgtttcg gggaccgagtg ggggtcaatc ttctgggtgct gccctctccag gtctctttcca 60
ggcggtgctat agacgtactc cctctgaggc gaccgatgg ttagaagagg ttgtctaagag 120
ggctccgggct cagcagcccc aggcctcagc tgctcctctg cagccaggttc tccagcctcc 180
tcacaccatc gccatctccc agccagcatc accctttccaa gggaaatgcag tcctcacctc 240
tcagcgtgtg ccagtgggtg tgggtccagc cctgcaacca cgtctttgtcc ctgccacctc 300
ctatctctgtg gccaatggaa tgccctatcc agcccctaag gtgcctgtgg tgggcatcac 360
tcctctccag atgggtggcca acgtatttgg cactgcaggc caccctcagg ctgcccatcc 420
ccatcagta cccagcctgg tcaggcagca gacattccct cactacgagg caagcagtcg 480
taccaccagt cctcttctta agcctcctgc tcagcacctc aacggttctg cagctttcaa 540
tgggtgtatg gatggccagg tggcctcagc agacaggcat acagagggtc ctacaggcac 600
ctgcccagtg gatccttttg aagcccagtg ggctgcatta gaaaataagt ccaagcagcg 660
tactaatccc tcccctacca accctttctc cagtgcatta cagaagacgt ttgaaattga 720
actttaagca atcattattg ctatgtatct tgtccatacc agacaggagg cagggggtag 780
cgggtcaaaagg agtcaaaacag actttgtctc ctgattagta ctcttttcc taatcccaaa 840
gggtcccaagg aacaagtcca ggcccagagt actgtgaggg gtgattttga aagacatggg 900
aaaaagcatt cctagagaaa agctgccttg caattaggct aaagaagtca aggaatggtt 960
gctttctgta ctccctcttc ccttaccctc ttacaaatct ctggcaacag agaggcaaa1020
tatctgaaca agaattata ttccaaagca atttactgaa atgtcaaaaca caacaggaa1080
caaagcaatc tcctcttgtt ttccaggcca ttacactgcc tctgtcagtg agtggcctgt1140
attagatagc aagaagagtg gtttgtgtct aggcctgggga acagagaggg cgcctatgct1200
gccagaattc ccaggagggc atatcagcaa ctgccacgca gagctatatt ttgggggaga1260
agttgagctt ccaattttgag taacagaata aatattatat atatcaaaa ccaaaatctt1320
tatttttatg catttagaat attttaaata gttctcagat attaagaagt ttgttagatt1380
gtaagttaac ttgccaaaagg taaaggggct agttgtaaga aattgtacat aagattgatt1440
tatcatctgat gctactgaa ataaaaagag gaaggctggg aagctgcaga caggatccct1500
agcttgtttt ctgtcagcca ttcatgttaa gtacacatt gcaacaacaa tcatgttat1560
gccaataca gtcactaggt tgtagttttt tttaataaaa ggaaaaagca tatgtctc1620
gttttaaaac tatgatggaa ttctaattgc attattttta tggaaatcaa cgaatatgc1680
tctatagaga atatatcttt tatataattg tgcagtttcc ttatgttaat ctgttaacac1740
taaggttaaca tgacataatc ataccataga agggaacaca ggttaaccata ttggtttgta1800
atatgggtct tgggtgggtt tgttttatcc tttaattttt gttcccaaga cttctgtggg1860
gatggggatt ctggttttat tagctttgtg tgtgtctctc tcccccaaac gcccttttgg1920
tgagacaatc ccccttgacag ttgcagcctc ttgacctcgg atacaataaa gagagctcat1980
ctcattttta cttttgaacg ttggccttac aatcaaatgt aagtttatata tatttgtact2040
gatgaaaaat tataattctg tttaacaaaa atcaaatgttc atggttagaaa atttggcca2100
gttttgctgt cctgtgtttt ttctctttat tttaaatgta atttattttt cgtctcttgg2160
gtcttactct ccattctact gctgctgtaa atccctagtt tagtgactag aaaaaatccc2220
ttaagattca tattttca

```

2238

<210> 137  
 <211> 398  
 <212> DNA  
 <213> homo sapiens

<400> 137

```

tgcagatttg ttggggcagc ccggggaggc tggctccgac acacgactga gtgtgcctac 60
actgtgtcca caggttttta gctgtggagt ttgggagctc agctttggagc ccaattgttt120
ctggcatttc cgtctaatct ttccacttga agacatcgcc tccgttccct ccaagctggg180
agaccagaag tcaacaacag gaggggtggag aggcggggtc tcacaactcg cttggctggg240
gagtcacatg aggttcttgc atoctgaagc aaaccatgga gagctgggtg ggaactccct300
gttttgctgt cctgtgtttt ctaattgcacg cccgaggtca aagagacttt gattttggca360
gatgcccctg atgacccctga aaccaccacaa gaagccaa

```

398

<210> 138  
 <211> 1084

<212> DNA  
<213> homo sapiens

<400> 138

```

ggcggtggcg ggaagtggag cgggcctgga gtcttggcca taaagcctga ggcggcggca 60
cggcggtggt ggcggcttgg agagctcggg agagttccct ggaaccagaa cttggacctt 120
ctcgcttctg tctctcgctt agtctctccc tcggcgggag cctcgcgacg gcccgcccg 180
gagcccccaa cgcaggcccg cgtttgaagg atgacctcta ggaagaaagt gttgctgaag 240
gttatcatcc tggagagattc tggagtcggg aagacatcac tcatgaacca gtatgtgaat 300
aagaattatca gcaatcagta caaagccaca ataggagctg actttcttcg caaggagggtg 360
atggtggatg acaggtctagt cacaatgcag atatgggaca cagcaggaca ggaacgggttc 420
cagtcctctg gtgtggcctt ctacagaggt gcagactgct gogtctctgt atttgatgtg 480
actgccccca acacattcaa aacctagat agctggagag atgagtttct catccaggcc 540
agtccccgag atcctgaaaa ctctccattt gttgtgttgg gaaacaagat tgacctcgaa 600
aacagacaag tggccacaaa cggggcacag cctctggtgct acagcaaaaa caacattccc 660
tacttttgaga ccagtgccaa gaggccatc aacgtggagc aggcgtttcca gacgatttga 720
cggaaatgcac ttaagcagga aacggaggtg gagctgtaca acgaatttcc tgaacctatc 780
aaactgggaca agaattgacc ggccaaggcc tcggcagaaa gctgcagttg ctgagggggc 840
agtgagagtt gagcacagag tcttccacaa accaagaaca cacttagcgg tccaacacaa 900
ttccccctct ctcttccaaa caaaacatc attgatctct cacatccagg tcgcaacaga 960
aaacccccatc aaacacagtt acaccccaca tattctctca cacacacaca cacacggcac 1020
acacacacac acaggttttg acgttatcca gattgcgggc ttgcccgtgt tgggttcgtg 1080
ggggg 1084

```

<210> 139  
<211> 1259  
<212> DNA  
<213> homo sapiens

<400> 139

```

taaaatcacg aagaagagtc cacacactgt ttcacagaaa ggagtgatc atgatttcta 60
gtaactcgaag aacatgttta tgggaacagg gtgactcagc tctcctgggg aggatggatg 120
aggagtttag aggaagagag ggtaccaaagt gaggggaaaag cagcagggtg ggtctggggc 180
atggacagga agcagaggtc gggaaaaagt acatctttta ttcacaggag ttcacaggag 240
ctgaagtggg aatcagtcaca tcgagaatcc acggccgggg accagtagga cttgagggag 300
tgcttactac taagtggctg ctgcgagggg aggaaccaagt ggtctcagat ttctcagagc 360
atgggaagttt aaaaatctct catgagaacc tccctattcc cagagaaaac accaactgaa 420
aagagccagg aaaaaccggg aattttccaa aaggtcttca cgtaaaactt gtcttatctc 480
aggagagagc ccgctcttct ctccagttc ctgctagggt ctgctgtgtg gaaagtgtac 540
ctggtatgct ctgggctccg tttggcaata gcaatcttgg ctgagtgtga cagcttggtc 600
cccagctcac cctttttttt taaaagtaag aaaaatagtt ctaccagat ggactttgcc 660
aagtccaaat atcttctagg attgaaaggt gcattttccc cataaaaaag gcgagggaaa 720
cccagtgctg ctttgtgtca cctcagtgac ttacagtcct ccttgccatt tagttggtag 780
tcagagccagt catccttaac aaatcttttc acattttatt tctttccatc gtagtcatct 840
tgaaaaaaga aagaatttga attttagaaa aggggcaact ctcttttata gcattctcat 900
cagaaaagtc aaaaaatcga tggaaatcatt tccactggga agattgacct tttgtattta 960
tttgtggggt aaattaataa gcatccaga tgcttgagc tctctgcac caggagatgc 1020
ttgtgtcccc gtgtagcagc tggaaaccaa gctgcagcag gagatgcaag ttcaggatg 1080
tttccccatg agctggagga atatctacag cagtgatgct tgaaattttt gtagtaatt 1140
ttttgtctgc ctaccctttt cctccaaaac aaaaattaga ggattattt gattatttgg 1200
attcttcccc ctttttttag aaataaagtt tttttgaaa agccaaaaaa aaaaaaaa 1259

```

<210> 140  
<211> 1938  
<212> DNA  
<213> homo sapiens

<400> 140

```

ccaagatggc ggcacgatgc ctgcccggct gttgggggtg cggtagcagc aggcagcaaa 60
agaccagctg gtcccagatt cgctgctgga gtgctggatg gagctttctc ctgccctctg 120

```

tgacatttcc	aatttttagat	aatgectcac	atctctgtcc	ccccggggacc	ccttggagcc	180
cccatgatcc	ctaagaagacc	agcttgaacc	tagatctcac	ccccaggatg	ttcgggagcc	240
tcgtgagatc	gccttgcacg	ctggccctcc	ttgtgggctc	ccagctggct	gtcatgatgt	300
acctgtcact	gggggggcttc	cgaagtctca	gtgccctatt	tggccgagat	cagggaccga	360
catttgacta	ttctcaccct	cgtgatgtct	acagtaacct	cagtcacctg	cctggggccc	420
cagggggctc	tcocagctct	caaggtctgc	cctactgtcc	agaacgatct	cctctcttag	480
tgggtcctgt	tgcggtgtcc	tttagccacg	tgccatcact	ggcagagatt	gtggagccga	540
atccccgggt	agaaccaggg	ggccgggtacc	gccctgcagg	ttgtgagccc	cgctcccgaa	600
cagccatcat	tgtgctctcat	cgtgccccgg	agcacaccct	gcgctgtctg	ctctaccacc	660
tgcaccctct	tgcgcagcgc	cagcagcttg	cttatggcat	ctatgtctat	caccaggctg	720
gaaatggaa	tttaaacagg	gcataaacgt	tgaacgttgg	ggtgcgagag	gccttgcgtg	780
atgaagatgt	ggactctcgt	ttcttgcacg	atgtggacct	attgcacaaa	aatgaccaca	840
atctgtatgt	gtgtgacccc	cggggacccc	gccatgttgc	cgttgtctatg	aacaagtttg	900
gatacagct	ccctgacccc	cagtactctg	gaggagtctc	agcacttact	cctgaccagt	960
acctgaagat	gaatggcttc	cccaatgaat	actggggctg	gggtgggtgag	gatgacgaca	1020
ttgctaccag	gggtgcgcctg	gctgggatga	agatctctcg	gccccccaca	ttctgtaggac	1080
actataagat	ggtgaagcac	cagaggagata	aggccaatga	ggaaaatccc	cacagatttgg	1140
acctctcgtg	ccgtaccagg	aattcctgga	gcgaagatgg	gatgaactca	ctcacatacc	1200
agttgctggc	tcgagagctg	gggcctctct	ataccaacct	cacagcagac	attgggaactg	1260
acctctgggg	tcctctgggt	ccttctgggc	cacgttacc	acctgggtcc	tcccaagcct	1320
tcctgtcaaga	gatgtgcgaa	cgccggccccc	cagccaggcc	tgggcctcta	tctactgccal	1380
accacacagc	cctcccgagg	tcacactgac	tcctccttcc	tgctcactct	aatcatgaaa	1440
cgaaattcat	gggggttgtat	ttctccccc	ctcagctcct	cactgttctc	agagggatgt	1500
gagggaaactg	aaactctggtg	ccgtgctagg	gggtaggggc	ctctccctca	ctgctggactg	1560
ggagctgggc	tcctgttagac	ctgaggggtc	ctctctctca	tgaggtctctg	tagggcttat	1620
gactgtgaat	ccttgatgtc	atgattttat	gtgacgattc	caggaggtcc	ctgccctgag	1680
agtaggagca	gggctggacc	ccaaagccct	ccctcttcca	tggagagaag	agtgatctgg	1740
cttctcctcg	gacctctgtg	aatattttat	ctatttatgg	ttcccgggaa	gttggttgg	1800
gaaggaagcc	cctccctggg	cattttctgc	ctatgtctga	atagctccct	cttctggctc	1860
tggctcaggg	ggctgggatt	ttgatataat	ttctaataaa	ggactttgtc	tcgcaaaaaa	1920
aaaaaaaaaa	aaaaaaaaaa					1938

&lt;210&gt; 141

&lt;211&gt; 1874

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 141

caaaaaaaaa	ttctaatatt	ctggagtcac	cattcccttc	gacagcattt	tcctctgctt	60
atgaagcccc	agaaatcagt	gttggccatg	atgacaaacta	cagaaaaaac	agagggcagct	120
ttcttggccaa	gacctttcaa	agccatttta	ggctgttagg	ggcagtgagg	tgaaagtacg	180
tccttgggcta	ttagaggttct	aacocatgaag	ttctcaacaa	gtatttttct	tcacctctgc	240
tactcaagta	gcatttactg	tgtctttggg	ttgtgctagg	cccccggggt	tgaagcacag	300
acctcttcca	gggggtttaca	gtctatttga	gactcctcag	ttcttggcac	tttttttttt	360
aatctccacc	agtcattttt	cagacctttt	aaactcctcaa	ttccaaacact	gatttccccct	420
tttgcattct	ccctcctctc	cttcccttga	gccttttgac	tttcattgatg	aattaggatg	480
taaatctgct	caggagacct	ggaggagcag	aggataaata	gcactctcagg	taaagtgtga	540
gtaatcttgag	aaacacatgt	taattcttgc	atattttgta	gcttccatgt	gaggggtttc	600
agcatttgata	tttgtgcatt	ttctaaccag	agatgaggtg	gatatctcac	gtagaacatt	660
ggatattcgt	tgagaaaaaa	agaatagtgt	aaactatttc	ttctttttta	caagatgggt	720
ccaggatttc	ttttttctct	gccataaatg	attataattaa	ttagcttttgt	gtcttacatt	780
ggtagccagc	cagccaaagg	ttgttttatg	cttttggggg	gcataatatt	gggttccattc	840
tcacctatcc	acacacacata	tcctgtatata	tcacctctac	ttctactctc	cccaaattta	900
aaagaagtatg	ggaaatgaga	ggcatttccc	ccaccccaatt	ttctctctca	cacacagact	960
catattacta	gtagggaactt	gagaacttta	tttccaaagt	gtctcaaacat	ttaccaactca	1020
tattaataca	atgtagtctat	tggcaattcc	tgctcctagg	ggagggggaga	taagaaaccc	1080
tcacctctcta	cagggtttggg	tacaagtggc	aaactgtgct	catggccgtg	tagaagcatgt	1140
gtgcctctggc	ttctctgagg	aagctggggg	tcagtacaact	ggcagatgta	aagttattctt	1200
tgaagtacaga	ttgaggctgg	gagacagccg	tagtagatgt	ttctactttg	ttctgctgttc	1260
ttctgaaaga	atattttgggt	ttcctgtata	ggaatgagat	taattctctt	ccaggattatt	1320
tataattctg	ggagacaaaa	cccatgcctc	cccttagcca	tttttactgt	tatcctatttt	1380
agatggccat	gaagaggatg	ctgtgaaatt	cccaacaaac	attgatgctg	acagtcacgc	1440

agtctctgggag tggggaagtg atctttttgtt cccatctctt tcttttagca gtaaaatagc1500  
 tgaggggaaaa gggaggggaaa aggaagttat ggggaatacct gtgggtgggtg tgatccctag1560  
 gtcttggggag ctcttggagg tgtctgtatc agtggatttc ccacccctg tgggaaattal620  
 gtagggtcat ttactgtttt aggtctagcc tatgtggatt ttttccctaac atacctaaagc1680  
 aaacccagtg tcaggatggg aattcttatt ctttcgttca gtttaagtttt tcccttcac1740  
 tgggcaactga agggatagt gaaacaatgt taacattttt ggtagtcttc aaccagggat1800  
 tgtttctgtt taacttctta taggaaagct tgagtaaaat aaatattgtc tttttgtatg1860  
 tcaaaaaaaa aaat 1874

<210> 142  
 <211> 198  
 <212> PRT  
 <213> homo sapiens

<400> 142

Arg 1	Asp	Ile	Trp	Thr 5	Met	Asn	Leu	Gln	Arg 10	Tyr	Trp	Gly	Glu	Ile 15	Pro
Ile	Ser	Ser	Ser 20	Gln	Thr	Asn	Arg	Ser 25	Ser	Phe	Asp	Leu	Leu 30	Pro	Arg
Glu	Phe	Arg 35	Leu	Val	Glu	Val	His 40	Asp	Pro	Pro	Leu	His 45	Gln	Pro	Ser
Ala	Asn 50	Lys	Pro	Lys	Pro	Pro 55	Thr	Met	Leu	Asp	Ile 60	Pro	Ser	Glu	Pro
Cys 65	Ser	Leu	Thr	Ile	His 70	Thr	Ile	Gln	Leu	Ile 75	Gln	His	Asn	Arg	Arg 80
Leu	Arg	Asn	Leu	Ile 85	Ala	Thr	Ala	Gln	Ala 90	Gln	Asn	Gln	Gln	Gln 95	Thr
Glu	Gly	Val	Lys 100	Thr	Glu	Glu	Ser	Glu 105	Pro	Leu	Pro	Ser	Cys 110	Pro	Gly
Ser	Pro	Pro 115	Leu	Pro	Asp	Asp	Leu 120	Leu	Pro	Leu	Asp	Cys 125	Lys	Asn	Pro
Asn	Ala 130	Pro	Phe	Gln	Ile	Arg 135	His	Ser	Asp	Pro	Glu 140	Ser	Asp	Phe	Tyr
Arg 145	Gly	Lys	Gly	Glu	Pro 150	Val	Thr	Glu	Leu	Ser 155	Trp	His	Ser	Cys	Arg 160
Gln	Leu	Leu	Tyr	Gln 165	Gly	Ser	Gly	Thr	Asn 170	Pro	Gly	Gln	Arg	Arg 175	Ala
Phe	Asp	Cys	Ala 180	Asn	Glu	Ser	Val	Leu 185	Glu	Asp	Pro	Asn	Leu 190	Met	Leu
Ala	His	Glu 195	Tyr	Trp	Pro										

<210> 143  
 <211> 92  
 <212> PRT  
 <213> homo sapiens

<400> 143

Ile Val Trp Met Val Arg Leu His Gly Ser Glu Gly Met Ser Ser Ile

1	5							10					15				
Val	Gly	Gly	Phe 20	Gly	Leu	Leu	Ala	Glu 25	Gly	Trp	Cys	Arg	Gly 30	Gly	Ser		
Trp	Thr	Ser 35	Thr	Arg	Arg	Asn	Ser 40	Arg	Gly	Ser	Lys	Ser 45	Lys	Glu	Leu		
Leu	Leu 50	Val	Trp	Leu	Asp	Asp 55	Ile	Gly	Ile	Ser	Pro 60	Gln	Tyr	Leu	Cys		
Arg 65	Phe	Ile	Val	His	Met 70	Ser	Leu	Gln	Val	Gln 75	Gln	Thr	Phe	Ile	Lys 80		
Cys	Gln	Ala	Phe	Cys 85	Val	Gly	Gln	Arg	Leu 90	Ile	Met						

<210> 144  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 144

Asp 1	Pro	Cys	Pro	Glu 5	Arg	Ser	Thr	Lys	Asn 10	Arg	His	Gly	Ala	Gln 15	Gly	
Met	Pro	Lys	Ser 20	Leu	Gln	Gly	Phe	Pro 25	Arg	Ser	Arg	Ser	Ala 30	Gly	Ala	
Gly	Ala	Asn 35	His	Arg	Val	Leu	Arg 40	Ser	Pro	Asp	Val	Gln 45	Gly	Ser	Arg	
Lys	Thr 50	Gly	Arg	Ser	Gly	Pro 55	Glu	Pro	Arg	Gln	Gly 60	Gly	Thr	Thr	Leu	
Phe 65	Thr	Ala	Ala	Ser	Gln 70	Ser	Gly	Leu	Gly	Gly 75	Cys	Leu	Asp	Leu	Glu 80	
Arg	Pro	Glu	Ala	Arg 85	Ile	Ala	Ser	Asp	Pro 90	Glu	Ser	Trp	Phe	Val 95	Asp	

<210> 145  
 <211> 52  
 <212> PRT  
 <213> homo sapiens

<400> 145

Glu 1	Gly	Arg	Val	Gln 5	Gln	Gly	Ser	Phe	Val 10	Asn	Val	Gln	Gln	Gly 15	Pro	
Gln	Glu	Pro	Phe 20	Ile	Glu	Phe	Ile	His 25	Gln	Leu	Thr	Gln	Ala 30	Ile	Lys	
Ser	Thr	His 35	Gly	Thr	Ser	Thr	Ile 40	Pro	Arg	Val	Ser	Arg 45	Ile	Thr	Leu	
Lys	Asp 50	Lys	Pro													

<210> 146  
 <211> 47

09573395.122700

<212> PRT  
<213> homo sapiens

<400> 146

Pro	Ser	Arg	Thr	Ser	His	Ser	Gly	Thr	Leu	Pro	Ile	Pro	Arg	Leu	Lys
1				5					10					15	
Ile	Cys	Phe	Lys	Lys	Arg	Gly	Asn	Met	Asn	Lys	Asp	Pro	Thr	Thr	Leu
			20					25					30		
Leu	Ala	Gln	Val	Leu	Phe	Thr	Leu	Asn	Phe	Leu	Asn	Leu	Asp	Asn	
		35					40					45			

<210> 147  
<211> 66  
<212> PRT  
<213> homo sapiens

<400> 147

Leu	Ser	Lys	Phe	Lys	Lys	Leu	Arg	Val	Asn	Asn	Thr	Cys	Ala	Ser	Ser
1				5					10					15	
Val	Val	Gly	Ser	Leu	Phe	Ile	Phe	Pro	Leu	Phe	Leu	Lys	His	Ile	Phe
			20					25					30		
Lys	Arg	Gly	Met	Gly	Asn	Val	Pro	Leu	Trp	Leu	Val	Leu	Glu	Gly	Tyr
		35					40					45			
Thr	Arg	Tyr	Pro	Trp	Asn	Gly	Arg	Cys	Ser	Met	Cys	Ala	Leu	Asn	Cys
	50					55					60				
Leu	Gly														
65															

<210> 148  
<211> 187  
<212> PRT  
<213> homo sapiens

<400> 148

Arg	Glu	Gly	Glu	Gly	Arg	Pro	Glu	Gly	Asn	Gly	Asp	Ile	Arg	Gly	Gly
1				5					10					15	
Leu	Arg	Ser	Gly	Cys	Asp	Leu	Ser	Leu	Leu	Ala	Pro	Leu	Leu	Pro	Pro
			20					25					30		
Ser	Ser	Ser	Glu	Ser	Trp	Glu	Cys	Cys	Tyr	Pro	Trp	Lys	Ile	Lys	Leu
		35					40					45			
Gly	Leu	Gln	Glu	Leu	Ser	Val	Trp	Glu	Glu	Ser	Met	Ala	Gln	His	Ser
	50					55					60				
Ala	Cys	Val	Pro	Phe	Cys	Ser	Gly	Ser	Leu	Ser	Pro	Pro	Pro	Ser	Gln
65					70					75					80
Pro	Gln	Arg	Leu	Ser	Pro	Ser	Pro	Ser	Ser	Ser	Pro	Glu	Asp	Ser	Ser
				85					90					95	
Asp	Gly	Arg	Ala	Gly	Pro	Pro	Glu	Pro	Thr	Gly	Ser	Ser	Gly	Cys	Thr
			100					105					110		

00673385-122700

Gly	Ser	Trp	Cys	Ser	Leu	Ser	Pro	Val	His	Phe	Ser	His	Trp	Gly	Met
		115					120					125			
Glu	Cys	Pro	Cys	Ile	Leu	Cys	Cys	Arg	Ser	Pro	His	Leu	His	Leu	Arg
	130					135					140				
Gly	Leu	Gly	Ser	Pro	Ser	Ser	Pro	Gln	Cys	Pro	Gln	Ser	Leu	Ser	Gln
145					150					155					160
Thr	Val	Gly	Trp	Asn	Met	Arg	Leu	Glu	Ala	Glu	Arg	Gly	Ser	Glu	His
				165					170					175	
His	Ser	Pro	Cys	Thr	Trp	Val	Ala	Ser	Cys	Pro					
			180					185							

<210> 149

<211> 147

<212> PRT

<213> homo sapiens

<400> 149

Arg	Glu	Asp	Trp	Asn	Arg	Gly	Lys	Gly	Glu	Val	Ala	Pro	Cys	Phe	Val
1				5					10					15	
Gln	Pro	Gly	Ser	Trp	Gln	Pro	Trp	Cys	Trp	Gly	Leu	Asp	Pro	Thr	Thr
			20					25					30		
Pro	Ala	His	Leu	Ala	Glu	His	Leu	Val	Pro	Ile	Glu	Asp	Cys	Leu	Pro
		35					40					45			
Leu	Leu	Leu	His	Leu	Gln	Leu	Pro	Pro	Leu	Leu	Gly	Thr	Phe	His	Thr
	50					55					60				
Leu	Gln	Asp	Cys	Val	Cys	Ser	Gly	Ser	Pro	Glu	Gly	Cys	Ser	Ser	Cys
65					70					75					80
Cys	His	Arg	Ala	Ser	Ile	Leu	Ile	Leu	Leu	Leu	Ile	Val	Gln	Leu	Leu
				85					90					95	
Ser	Val	Cys	Ile	Arg	Leu	Ser	Asp	Gln	Arg	Val	His	Gln	His	Gln	Glu
			100					105					110		
Gly	His	Val	Glu	Gln	Gln	Gly	Thr	His	His	Gly	Gln	Val	Asp	Asp	Asn
		115					120					125			
Asp	Asp	Leu	Asp	Gly	Gly	Gly	Leu	Arg	Ser	Ser	Tyr	Leu	His	Ser	His
	130					135					140				
Ser	Arg	Gln													
145															

<210> 150

<211> 142

<212> PRT

<213> homo sapiens

<400> 150

Phe	Phe	Phe	Phe	Phe	Trp	Arg	Glu	Ile	Lys	Gln	Phe	Asn	Asp	Gly	Phe
1				5					10					15	

00673395-162700



Leu	Asp	Leu	His 20	Thr	Thr	Leu	Arg	Gln 25	Glu	Asp	Lys	Ile	Phe 30	Ser	Pro	
Cys	Thr	Gly 35	Thr	Thr	Lys	Phe	Arg 40	Asp	Lys	Arg	Gln	Pro 45	Lys	Tyr	Arg	
Gly	Cys 50	Gly	Val	Gln	Ile	His 55	Ala	Gln	Pro	Arg	Val 60	Ser	Cys	Ser	Asn	
Arg 65	Pro	Ser	Gly	Ser	Val 70	Thr	Val	Asp	Thr	Gly 75	Glu	Arg	Arg	Asp	Cys 80	
Pro	Asp	Pro	Ser	Ser 85	Ala	Gly	Glu	Gly	Thr 90	Gly	Ser	Arg	Val	Cys 95	Met	
Gly	Thr	Pro	Cys 100	Pro	Ser	Ala	Arg	Ser 105	Ala	Gln	Gly	Thr	Ala 110	Asn	Thr	
Ser	Phe	Gln 115	Cys	Thr	Leu	Lys	Thr 120	Gln	Trp	Ala	Gln	Gly 125	Ala	Gln	Leu	
Ser	His 130	Gln	Ser	Cys	Pro	Gln 135	Gly	Trp	Ser	Trp	Gly 140	Trp	Gly			

<210> 151  
 <211> 464  
 <212> PRT  
 <213> homo sapiens

<400> 151

Arg 1	Gln	Gln	Thr	Val 5	Leu	Gly	Ser	Cys	Ser 10	Ser	Ser	Ile	Leu	Pro 15	Cys	
Gln	Leu	Leu	Lys 20	His	Gln	Gly	Ser	Ser 25	Lys	Thr	Glu	Met	Thr 30	Lys	Asn	
Trp	Leu	Ile 35	Gln	Thr	Lys	Arg	Arg 40	Tyr	Phe	Ser	Ser	Pro 45	Lys	Gln	Met	
Ser	Met 50	Thr	His	Trp	Pro	Arg 55	Thr	Ala	Trp	Leu	Thr 60	Gly	Cys	Ser	Val	
Thr 65	Leu	Phe	Leu	Phe	Pro 70	Ser	Gln	Tyr	Val	Asp 75	Val	Ala	Ser	Leu	Gly 80	
Leu	Val	Pro	Gln	Leu 85	Thr	Gly	Gly	Thr	Leu 90	Tyr	Lys	Tyr	Asn	Asn 95	Phe	
Gln	Met	His	Leu 100	Asp	Arg	Gln	Gln	Phe 105	Leu	Asn	Asp	Leu	Arg 110	Asn	Asp	
Ile	Glu	Lys 115	Lys	Ile	Gly	Phe	Asp 120	Ala	Ile	Met	Arg	Val 125	Arg	Thr	Ser	
Thr	Gly 130	Phe	Arg	Ala	Thr	Asp 135	Phe	Phe	Gly	Gly	Ile 140	Leu	Met	Asn	Asn	
Thr 145	Thr	Asp	Val	Glu	Met 150	Ala	Ala	Ile	Asp	Cys 155	Asp	Lys	Ala	Val	Thr 160	
Val	Glu	Phe	Lys	His 165	Asp	Asp	Lys	Leu	Ser 170	Glu	Asp	Ser	Gly	Ala 175	Leu	

00673395-122700

Ile	Gln	Cys	Ala 180	Val	Leu	Tyr	Thr	Thr 185	Ile	Ser	Gly	Gln	Arg 190	Arg	Leu	
Arg	Ile	His 195	Asn	Leu	Gly	Leu	Asn 200	Cys	Ser	Ser	Gln	Leu 205	Ala	Asp	Leu	
Tyr	Lys 210	Ser	Cys	Glu	Thr	Asp 215	Ala	Leu	Ile	Asn	Phe 220	Phe	Ala	Lys	Ser	
Ala 225	Phe	Lys	Ala	Val	Leu 230	His	Gln	Pro	Leu	Lys 235	Val	Ile	Arg	Glu	Ile 240	
Leu	Val	Asn	Gln	Thr 245	Ala	His	Met	Leu	Ala 250	Cys	Tyr	Arg	Lys	Asn 255	Cys	
Ala	Ser	Pro	Ser 260	Ala	Ala	Ser	Gln	Leu 265	Ile	Leu	Pro	Asp	Ser 270	Met	Lys	
Val	Leu	Pro 275	Val	Tyr	Met	Asn	Cys 280	Leu	Leu	Lys	Asn	Cys 285	Val	Leu	Leu	
Ser	Arg 290	Pro	Glu	Ile	Ser	Thr 295	Asp	Glu	Arg	Ala	Tyr 300	Gln	Arg	Gln	Leu	
Val 305	Met	Thr	Met	Gly	Val 310	Ala	Asp	Ser	Gln	Leu 315	Phe	Phe	Tyr	Pro	Gln 320	
Leu	Leu	Pro	Ile	His 325	Thr	Leu	Asp	Val	Lys 330	Ser	Thr	Met	Leu	Pro 335	Ala	
Ala	Val	Arg	Cys 340	Ser	Glu	Ser	Arg	Leu 345	Ser	Glu	Glu	Gly	Ile 350	Phe	Leu	
Leu	Ala	Asn 355	Gly	Leu	His	Met	Phe 360	Leu	Trp	Leu	Gly	Val 365	Ser	Ser	Pro	
Pro	Glu 370	Leu	Ile	Gln	Gly	Ile 375	Phe	Asn	Val	Pro	Ser 380	Phe	Ala	His	Ile	
Asn 385	Thr	Asp	Met	Thr	Leu 390	Leu	Pro	Glu	Val	Gly 395	Asn	Pro	Tyr	Ser	Gln 400	
Gln	Leu	Arg	Met	Ile 405	Met	Gly	Ile	Ile	Gln 410	Gln	Lys	Arg	Pro	Tyr 415	Ser	
Met	Lys	Leu	Thr 420	Ile	Val	Lys	Gln	Arg 425	Glu	Gln	Pro	Glu	Met 430	Val	Phe	
Arg	Gln	Phe 435	Leu	Val	Glu	Asp	Lys 440	Gly	Leu	Tyr	Gly	Gly 445	Ser	Ser	Tyr	
Val	Asp 450	Phe	Leu	Cys	Cys	Val 455	His	Lys	Glu	Ile	Cys 460	Gln	Leu	Leu	Asn	

<210> 152

<211> 172

<212> PRT

<213> homo sapiens

<400> 152

Thr Met Leu Glu Lys Ile Pro Lys Glu Glu Gln Glu Glu Thr Ser Ala

09673305-122700

1			5				10				15				
Ile	Arg	Val	Gly 20	Phe	Ile	Thr	Tyr	Asn 25	Lys	Val	Leu	His	Phe 30	Phe	Asn
Val	Lys	Ser 35	Asn	Leu	Ala	Gln	Pro 40	Gln	Met	Met	Gly	Val 45	Thr	Asp	Val
Gly	Glu 50	Val	Phe	Val	Pro	Leu 55	Leu	Asp	Gly	Phe	Leu 60	Val	Asn	Tyr	Gln
Glu 65	Ser	Gln	Ser	Val	Ile 70	His	Asn	Leu	Leu	Asp 75	Gln	Ile	Pro	Asp	Met 80
Phe	Ala	Asp	Ser	Asn 85	Glu	Asn	Glu	Thr	Val 90	Phe	Ala	Pro	Val	Ile 95	Gln
Ala	Gly	Met	Glu 100	Ala	Leu	Lys	Ala	Ala 105	Asp	Cys	Pro	Gly	Lys 110	Leu	Phe
Ile	Phe	His 115	Ser	Ser	Leu	Pro	Thr 120	Ala	Glu	Ala	Pro	Gly 125	Lys	Leu	Lys
Asn	Arg 130	Asp	Asp	Lys	Lys	Leu 135	Val	Asn	Thr	Asp	Lys 140	Glu	Lys	Ile	Leu
Phe 145	Gln	Pro	Gln	Thr	Asn 150	Val	Tyr	Asp	Ser	Leu 155	Ala	Lys	Asp	Cys	Val 160
Ala	His	Arg	Leu	Leu 165	Cys	Asp	Thr	Leu	Pro 170	Leu	Ser				
<210> 153															
<211> 141															
<212> PRT															
<213> homo sapiens															
<400> 153															
Gly 1	Ser	Thr	Val	Phe 5	Thr	Glu	Phe	Val	Ile 10	Val	Leu	Glu	Leu	His 15	Gly
His	Cys	Leu	Val 20	Thr	Ile	Asp	Gly	Ser 25	His	Phe	Tyr	Ile	Gly 30	Gly	Val
Val	His	Gln 35	Asp	Ser	Thr	Lys	Glu 40	Ile	Ser	Gly	Ser	Glu 45	Thr	Cys	Ala
Gly	Thr 50	Asn	Pro	His	Asn	Ser 55	Ile	Lys	Ala	Tyr	Phe 60	Leu	Phe	Asn	Ile
Ile 65	Ser	Glu	Val	Val	Gln 70	Lys	Leu	Leu	Ser	Ile 75	Gln	Val	His	Leu	Glu 80
Ile	Val	Val	Phe	Val 85	Lys	Gly	Ser	Ser	Ser 90	Glu	Leu	Arg	Asn	Gln 95	Pro
Gln	Arg	Gly	His 100	Val	His	Ile	Leu	Thr 105	Arg	Lys	Glu	Glu	Glu 110	Cys	His
Arg	Ala	Ala 115	Gly	Glu	Pro	Arg	Ser 120	Pro	Trp	Pro	Met	Ser 125	His	Arg	His

Leu Phe Gly Ala Gly Lys Val Ser Ser Leu Cys Leu Tyr  
130 135 140

<210> 154

<211> 504

<212> PRT

<213> homo sapiens

<400> 154

Leu 1	Asp	Arg	Cys	Gly 5	Leu	Tyr	Pro	Val	Ser 10	Ser	Leu	Leu	Gln	Val 15	Glu
Gly	Ser	Leu	Trp 20	Arg	Ala	Ala	Gly	Val 25	Phe	Gln	Pro	Pro	Pro 30	Gly	Leu
Ala	His	Ala 35	Asn	Asp	Trp	Arg	Phe 40	Thr	Ala	Arg	Val	His 45	Gly	Gly	Ala
Leu	Gly 50	Glu	His	Asp	Lys	Met 55	Val	Ala	Ala	Ala	Thr 60	Gly	Ser	Glu	Ile
Leu 65	Leu	Trp	Ala	Leu	Gln 70	Ala	Glu	Gly	Gly	Gly 75	Ser	Glu	Ile	Gly	Val 80
Phe	His	Leu	Gly	Val 85	Pro	Val	Glu	Ala	Leu 90	Phe	Phe	Val	Gly	Asn 95	Gln
Leu	Ile	Ala	Thr 100	Ser	His	Thr	Gly	Arg 105	Ile	Gly	Val	Trp	Asn 110	Ala	Val
Thr	Lys	His 115	Trp	Gln	Val	Gln	Glu 120	Val	Gln	Pro	Ile	Thr 125	Ser	Tyr	Asp
Ala	Ala 130	Gly	Ser	Phe	Leu	Leu 135	Leu	Gly	Cys	Asn	Asn 140	Gly	Ser	Ile	Tyr
Tyr 145	Val	Asp	Val	Gln	Lys 150	Phe	Pro	Leu	Arg	Met 155	Lys	Asp	Asn	Asp	Leu 160
Leu	Val	Ser	Glu	Leu 165	Tyr	Arg	Asp	Pro	Ala 170	Glu	Asp	Gly	Val	Thr 175	Ala
Leu	Ser	Val	Tyr 180	Leu	Thr	Pro	Lys	Thr 185	Ser	Asp	Ser	Gly	Asn 190	Trp	Ile
Glu	Ile	Ala 195	Tyr	Gly	Thr	Ser	Ser 200	Gly	Gly	Val	Arg	Val 205	Ile	Val	Gln
His	Pro 210	Glu	Thr	Val	Gly	Ser 215	Gly	Pro	Gln	Leu	Phe 220	Gln	Thr	Phe	Thr
Val 225	His	Arg	Ser	Pro	Val 230	Thr	Lys	Ile	Met	Leu 235	Ser	Glu	Lys	His	Leu 240
Ile	Ser	Val	Cys	Ala 245	Asp	Asn	Asn	His	Val 250	Arg	Thr	Trp	Ser	Val 255	Thr
Arg	Phe	Arg	Gly 260	Met	Ile	Ser	Thr	Gln 265	Pro	Gly	Ser	Thr	Pro 270	Leu	Ala
Ser	Phe	Lys 275	Ile	Leu	Ala	Leu	Glu 280	Ser	Ala	Asp	Gly	His 285	Gly	Gly	Cys

00673305.122700

Ser	Ala	Gly	Asn	Asp	Ile	Gly	Pro	Tyr	Gly	Glu	Arg	Asp	Asp	Gln	Gln	
	290					295					300					
Val	Phe	Ile	Gln	Lys	Val	Val	Pro	Ser	Ala	Ser	Gln	Leu	Phe	Val	Arg	
305					310					315					320	
Leu	Ser	Ser	Thr	Gly	Gln	Arg	Val	Cys	Ser	Val	Arg	Ser	Val	Asp	Gly	
				325					330					335		
Ser	Pro	Thr	Thr	Ala	Phe	Thr	Val	Leu	Glu	Cys	Glu	Gly	Ser	Arg	Arg	
			340					345					350			
Leu	Gly	Ser	Arg	Pro	Arg	Arg	Tyr	Leu	Leu	Thr	Gly	Gln	Ala	Asn	Gly	
		355					360					365				
Ser	Leu	Ala	Met	Trp	Asp	Leu	Thr	Thr	Ala	Met	Asp	Gly	Leu	Gly	Gln	
	370					375					380					
Ala	Pro	Ala	Gly	Gly	Leu	Thr	Glu	Gln	Glu	Leu	Met	Glu	Gln	Leu	Glu	
385					390					395					400	
His	Cys	Glu	Leu	Ala	Pro	Pro	Ala	Pro	Ser	Ala	Pro	Ser	Trp	Gly	Cys	
				405					410					415		
Leu	Pro	Ser	Pro	Ser	Pro	Arg	Ile	Ser	Leu	Thr	Ser	Leu	His	Ser	Ala	
			420					425					430			
Ser	Ser	Asn	Thr	Ser	Leu	Ser	Gly	His	Arg	Gly	Ser	Pro	Ser	Pro	Pro	
		435					440					445				
Gln	Ala	Glu	Ala	Arg	Arg	Arg	Gly	Gly	Gly	Ser	Phe	Val	Glu	Arg	Cys	
	450					455					460					
Gln	Glu	Leu	Val	Arg	Ser	Gly	Pro	Asp	Leu	Arg	Arg	Pro	Pro	Thr	Pro	
465					470					475					480	
Ala	Pro	Trp	Pro	Ser	Ser	Gly	Leu	Gly	Thr	Pro	Leu	Thr	Pro	Pro	Lys	
				485					490					495		
Met	Lys	Leu	Asn	Glu	Thr	Ser	Phe									
			500													

<210> 155

<211> 289

<212> PRT

<213> homo sapiens

<400> 155

Gly	Gln	Pro	Ala	Arg	Pro	Gly	Ala	Met	Ala	Ala	Ala	Ala	Thr	Ala	Ala	
1				5					10					15		
Glu	Gly	Val	Pro	Ser	Arg	Gly	Pro	Pro	Gly	Glu	Val	Ile	His	Leu	Asn	
			20					25					30			
Val	Gly	Gly	Lys	Arg	Phe	Ser	Thr	Ser	Arg	Gln	Thr	Leu	Thr	Trp	Ile	
		35					40					45				
Pro	Asp	Ser	Phe	Phe	Ser	Ser	Leu	Leu	Ser	Gly	Arg	Ile	Ser	Thr	Leu	
	50					55					60					
Lys	Asp	Glu	Thr	Gly	Ala	Ile	Phe	Ile	Asp	Arg	Asp	Pro	Thr	Val	Phe	

00673305.122700

65				70				75				80			
Ala	Pro	Ile	Leu	Asn 85	Phe	Leu	Arg	Thr	Lys 90	Glu	Leu	Asp	Pro	Arg 95	Gly
Val	His	Gly	Ser 100	Ser	Leu	Leu	His	Glu 105	Ala	Gln	Phe	Tyr	Gly 110	Leu	Thr
Pro	Leu	Val 115	Arg	Arg	Leu	Gln	Leu 120	Arg	Glu	Glu	Leu	Asp 125	Arg	Ser	Ser
Cys	Gly 130	Asn	Val	Leu	Phe	Asn 135	Gly	Tyr	Leu	Pro	Pro 140	Pro	Val	Phe	Pro
Val	Lys	Arg	Arg	Asn	Arg 150	His	Ser	Leu	Val	Gly 155	Pro	Gln	Gln	Leu	Gly 160
Gly	Arg	Pro	Ala	Pro 165	Val	Arg	Arg	Ser	Asn 170	Thr	Met	Pro	Pro	Asn 175	Leu
Gly	Asn	Ala	Gly 180	Leu	Leu	Gly	Arg	Met 185	Leu	Asp	Glu	Lys	Thr 190	Pro	Pro
Ser	Pro	Ser 195	Gly	Gln	Pro	Glu	Glu 200	Pro	Gly	Met	Val	Arg 205	Leu	Val	Cys
Gly	His 210	His	Asn	Trp	Ile	Ala 215	Val	Ala	Tyr	Thr	Gln 220	Phe	Leu	Val	Cys
Tyr	Arg	Leu	Lys	Glu	Ala 230	Ser	Gly	Gly	Gln	Leu 235	Val	Phe	Ser	Ser	Pro 240
Arg	Leu	Asp	Trp	Pro 245	Met	Arg	Thr	Thr	Gly 250	Ala	Ser	Gln	Pro	Gly 255	Cys
Met	Val	Gly	Leu 260	Trp	Val	Asn	Met	Thr 265	Arg	Trp	Trp	Gln	Gln 270	Pro	Pro
Ala	Ala	Arg 275	Ser	Cys	Tyr	Gly	Leu 280	Cys	Arg	Arg	Lys	Ala 285	Val	Ala	Pro

Arg

&lt;210&gt; 156

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 156

Val 1	Pro	Gln	Asp	Gln 5	Gly	Ile	Pro	Arg	His 10	His	Gly	Ser	Cys	Val 15	Val
Gln	Lys	Glu	Val 20	Ser	Leu	Ser	Phe	Ile 25	Leu	Gly	Gly	Val	Arg 30	Gly	Val
Pro	Arg	Pro 35	Leu	Glu	Gly	His	Gly 40	Ala	Gly	Val	Gly	Gly 45	Arg	Arg	Arg
Ser	Gly 50	Pro	Leu	Arg	Thr	Ser 55	Ser	Trp	Gln	Arg	Ser 60	Thr	Lys	Leu	Pro
Pro	Pro	Arg	Arg	Arg	Ala	Ser	Ala	Cys	Gly	Gly	Leu	Gly	Leu	Pro	Arg

65					70					75					80
Trp	Pro	Asp	Lys	Glu 85	Val	Leu	Leu	Glu	Ala 90	Glu	Trp	Arg	Leu	Val 95	Arg
Glu	Met	Arg	Gly 100	Glu	Gly	Leu	Gly	Arg 105	Gln	Pro	His	Glu	Gly 110	Ala	Glu
Gly	Ala	Gly 115	Gly	Ala	Ser	Ser	Gln 120	Cys	Ser	Ser	Cys	Ser 125	Ile	Ser	Ser
Cys	Ser 130	Val	Arg	Pro	Pro	Ala 135	Gly	Ala	Trp	Pro	Arg 140	Pro	Ser	Met	Ala
Val 145	Val	Arg	Ser	His	Met 150	Ala	Lys	Leu	Pro	Leu 155	Ala	Trp	Pro	Val	Ser 160

Arg

<210> 157

<211> 262

<212> PRT

<213> homo sapiens

<400> 157

Gln 1	Leu	Trp	Gly	Phe 5	Ala	Ala	Gly	Ser	Asp 10	Ser	Arg	Pro	Ala	Met 15	Gly
Cys	Asp	Gly	Gly 20	Thr	Ile	Pro	Lys	Arg 25	His	Glu	Leu	Val	Lys 30	Gly	Pro
Lys	Lys	Val 35	Glu	Lys	Val	Asp	Lys 40	Asp	Ala	Glu	Leu	Val 45	Ala	Gln	Trp
Asn	Tyr 50	Cys	Thr	Leu	Ser	Gln 55	Glu	Ile	Leu	Arg	Arg 60	Pro	Ile	Val	Ala
Cys 65	Glu	Leu	Gly	Arg	Leu 70	Tyr	Asn	Lys	Asp	Ala 75	Val	Ile	Glu	Phe	Leu 80
Leu	Asp	Lys	Ser	Ala 85	Glu	Lys	Ala	Leu	Gly 90	Lys	Ala	Ala	Ser	His 95	Ile
Lys	Ser	Ile	Lys 100	Asn	Val	Thr	Glu	Leu 105	Lys	Leu	Ser	Asp	Asn 110	Pro	Ala
Trp	Glu	Gly 115	Asp	Lys	Gly	Asn	Thr 120	Lys	Gly	Asp	Lys	His 125	Asp	Asp	Leu
Gln	Arg 130	Ala	Arg	Phe	Ile	Cys 135	Pro	Val	Val	Gly	Leu 140	Glu	Met	Asn	Gly
Arg 145	His	Arg	Phe	Cys	Phe 150	Leu	Arg	Cys	Cys	Gly 155	Cys	Val	Phe	Ser	Glu 160
Arg	Ala	Leu	Lys	Glu 165	Ile	Lys	Ala	Glu	Val 170	Cys	His	Thr	Cys	Gly 175	Ala
Ala	Phe	Gln	Glu 180	Asp	Asp	Val	Ile	Val 185	Leu	Asn	Gly	Thr	Lys 190	Glu	Asp
Val	Asp	Val	Leu	Lys	Thr	Arg	Met	Glu	Glu	Arg	Arg	Leu	Arg	Ala	Asn

002221-202220





Glu	Gly 50	Ser	Pro	Thr	Arg	Val 55	Ala	Asn	Phe	Arg	Phe 60	Tyr	Leu	Phe	Gln	
Gly 65	Ser	Leu	Arg	Lys	His 70	Thr	Ala	Ala	Ala	Pro 75	Lys	Glu	Ala	Glu	Pro 80	
Val	Ser	Ala	Val	His 85	Leu	Gln	Ala	His	Asn 90	Gly	Ala	Asp	Glu	Thr 95	Arg	
Pro	Leu	Glu	Val 100	Ile	Val	Leu	Val	Thr 105	Phe	Ser	Val	Ser	Phe 110	Ile	Pro	
Phe	Pro	Gly 115	Arg	Ile	Ile	Arg	Lys 120	Leu	Gln	Leu	Cys	His 125	Ile	Leu	Asn	
Ala	Phe 130	Asn	Val	Arg	Cys	Cys 135	Leu	Pro	Lys	Ser	Leu 140	Phe	Cys	Arg	Phe	
Val 145	Gln	Glu	Lys	Phe	Asn 150	Asp	Gly	Ile	Phe	Val 155	Ile	Lys	Ser	Ala	Lys 160	
Phe	Thr	Gly	Asn	Tyr 165	Trp	Ser	Ser									

<210> 160  
 <211> 238  
 <212> PRT  
 <213> homo sapiens

<400> 160

His 1	Gln	Trp	His	Ile 5	Thr	Ala	Met	Gly	Ser 10	Gln	His	Ser	Ala 15	Ala		
Arg	Pro	Ser	Ser 20	Cys	Arg	Arg	Lys	Gln 25	Glu	Asp	Asp	Arg	Asp 30	Gly	Leu	
Leu	Ala	Glu 35	Arg	Glu	Gln	Glu	Glu 40	Ala	Ile	Ala	Gln	Phe 45	Pro	Tyr	Val	
Glu	Phe 50	Thr	Gly	Arg	Asp	Ser 55	Ile	Thr	Cys	Leu	Thr 60	Cys	Gln	Gly	Thr	
Gly 65	Tyr	Ile	Pro	Thr	Glu 70	Gln	Val	Asn	Glu	Leu 75	Val	Ala	Leu	Ile	Pro 80	
His	Ser	Asp	Gln	Arg 85	Leu	Arg	Pro	Gln	Arg 90	Thr	Lys	Gln	Tyr 95	Val	Leu	
Leu	Ser	Ile	Leu 100	Leu	Cys	Leu	Leu	Ala 105	Ser	Gly	Leu	Val	Val 110	Phe	Phe	
Leu	Phe	Pro 115	His	Ser	Val	Leu	Val 120	Asp	Asp	Asp	Gly	Ile 125	Lys	Val	Val	
Lys	Val 130	Thr	Phe	Asn	Lys	Gln 135	Asp	Ser	Leu	Val	Ile 140	Leu	Thr	Ile	Met	
Ala 145	Thr	Leu	Lys	Ile	Arg 150	Asn	Ser	Asn	Phe	Tyr 155	Thr	Val	Ala	Val	Thr 160	
Ser	Leu	Ser	Ser	Gln	Ile	Gln	Tyr	Met	Asn	Thr	Val	Val	Asn	Phe	Thr	

00673395.122700

165

170

175

Gly	Lys	Ala	Glu	Met	Gly	Gly	Pro	Phe	Ser	Tyr	Val	Tyr	Phe	Phe	Cys
			180					185					190		
Thr	Val	Pro	Glu	Ile	Leu	Val	His	Asn	Ile	Val	Ile	Phe	Met	Arg	Thr
		195					200					205			
Ser	Val	Lys	Ile	Ser	Tyr	Ile	Gly	Leu	Met	Thr	Gln	Ser	Ser	Leu	Glu
	210					215					220				
Thr	His	His	Tyr	Val	Asp	Cys	Gly	Gly	Asn	Ser	Thr	Ala	Ile		
	225				230					235					

&lt;210&gt; 161

&lt;211&gt; 91

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 161

Ser	Ser	His	Glu	Asp	His	Tyr	Val	Val	His	Gln	Asp	Leu	Arg	Tyr	Arg
1				5					10					15	
Ala	Glu	Glu	Val	His	Ile	Gly	Lys	Arg	Ser	Ser	His	Leu	Gly	Leu	Pro
			20					25					30		
Gly	Lys	Ile	His	His	Cys	Val	His	Val	Leu	Asn	Leu	Ala	Gly	Gln	Ala
		35					40					45			
Gly	His	Cys	His	Arg	Val	Glu	Val	Gly	Val	Pro	Asp	Phe	Gln	Gly	Gly
	50					55					60				
His	Asp	Gly	Glu	Asn	Tyr	Lys	Gly	Val	Leu	Leu	Ile	Lys	Cys	Asp	Phe
	65				70					75					80
His	His	Phe	Asp	Ala	Val	Ile	Ile	His	Lys	Asp					
				85					90						

&lt;210&gt; 162

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 162

Met	Arg	Lys	Gln	Glu	Glu	Asn	His	Gln	Thr	Arg	Cys	Gln	Glu	Thr	Lys
1				5					10					15	
Gln	Asp	Gly	Gln	Glu	Asp	Ile	Leu	Leu	Ser	Ser	Leu	Arg	Ala	Gln	Ser
			20					25					30		
Leu	Ile	Thr	Val	Trp	Asp	Gln	Ser	His	Gln	Leu	Ile	Tyr	Leu	Leu	Cys
		35					40					45			
Trp	Asn	Val	Ala	Cys	Pro	Leu	Ala	Arg	Glu	Thr	Gly	Asp	Ala	Ile	Ser
	50					55					60				
Pro	Gly	Glu	Phe	His	Ile	Trp	Glu	Leu	Ser	Asn	Gly	Phe	Phe	Leu	Leu
					70					75					80
Ser	Phe	Ser	Gln	Gln	Thr	Val	Pro	Val	Ile	Phe	Leu	Leu	Ser	Pro	Ala
				85					90					95	

00673306-1-22700

Gly	Gly	Gly	Ala 100	Ser	Ser	Ser	Gly	Met 105	Leu	Arg	Pro	His	Gly 110	Arg	Asp
Met	Pro	Leu 115	Val	Ser	Cys	Pro	Ala 120	Ser	Ser	Val	Gly	Gly 125	Ala	Ala	Arg
Thr	Gln 130	Arg	Ala	Gly											

<210> 163

<211> 91

<212> PRT

<213> homo sapiens

<400> 163

Ala 1	Ala	Gly	Ala	Ala 5	Gly	Pro	His	Arg	Arg 10	Arg	His	Pro	Leu	His 15	Pro
Ser	Leu	Leu	Arg 20	Glu	His	His	Ser	Gln 25	Ala	Gln	Ala	Pro	Glu 30	Gly	Val
Arg	Pro	Gly 35	Gln	Ser	Thr	Leu	Ser 40	Arg	Ile	Glu	Ala	Val 45	Gln	Pro	Gln
Leu	Pro 50	Arg	Pro	Ser	Gly	Leu 55	Pro	Ser	Leu	Trp	Gly 60	Trp	Leu	Pro	Trp
Leu 65	Leu	Gly	Thr	Arg	Pro 70	Gln	Arg	His	Pro	Glu 75	Ile	Pro	Pro	Glu	Thr 80
Gln	Cys	Ala	Ser	Thr 85	Ala	Val	Arg	Arg	Ser 90	Ala					

<210> 164

<211> 174

<212> PRT

<213> homo sapiens

<400> 164

Leu 1	Asp	Asn	Pro	Thr 5	Gln	Arg	Asn	Lys	Asp 10	Gln	Leu	Ile	Arg	Ala 15	Ala
Val	Lys	Phe	Leu 20	Asp	Thr	Asp	Thr	Ile 25	Cys	Tyr	Arg	Val	Glu 30	Glu	Pro
Glu	Thr	Leu 35	Val	Glu	Leu	Gln	Arg 40	Asn	Glu	Trp	Asp 45	Ile	Ile	Glu	
Trp	Ala 50	Glu	Lys	Arg	Tyr	Gly 55	Val	Glu	Ile	Ser	Ser 60	Ser	Thr	Ser	Ile
Met 65	Gly	Pro	Ser	Ile	Pro 70	Ala	Lys	Thr	Arg	Glu 75	Val	Leu	Val	Ser	His 80
Leu	Ala	Ser	Tyr	Asn 85	Thr	Trp	Ala	Leu	Gln 90	Gly	Ile	Glu	Phe	Val 95	Ala
Ala	Gln	Leu	Lys 100	Ser	Met	Val	Leu	Thr 105	Leu	Gly	Leu	Ile	Asp 110	Leu	Arg

00673305.122700

Leu	Thr	Val	Glu	Gln	Ala	Val	Leu	Leu	Ser	Arg	Leu	Glu	Glu	Glu	Tyr
		115					120					125			
Gln	Ile	Gln	Lys	Trp	Gly	Asn	Ile	Glu	Trp	Ala	His	Asp	Tyr	Glu	Leu
	130					135					140				
Gln	Glu	Leu	Arg	Ala	Arg	Thr	Ala	Ala	Gly	Thr	Leu	Phe	Ile	His	Leu
	145				150					155					160
Cys	Ser	Glu	Ser	Thr	Thr	Val	Lys	His	Lys	Leu	Leu	Lys	Glu		
				165					170						

<210> 165  
 <211> 66  
 <212> PRT  
 <213> homo sapiens

<400> 165

Cys	Leu	Gly	Leu	Leu	His	Pro	Val	Ala	Asp	Gly	Val	Gly	Val	Gln	Lys
1				5					10					15	
Leu	His	Gly	Cys	Pro	Asp	Gln	Leu	Ile	Leu	Val	Ser	Leu	Gly	Trp	Val
			20					25					30		
Val	Gln	Ser	Arg	Val	Ala	Gln	Cys	Gly	Gln	Val	His	Gly	Val	Val	Leu
		35					40					45			
Asp	Gly	Ile	Leu	Leu	Gly	Ile	Pro	Leu	Ser	Thr	Leu	Cys	Thr	Cys	Gln
	50					55					60				
Gly	Leu														
	65														

<210> 166  
 <211> 132  
 <212> PRT  
 <213> homo sapiens

<400> 166

Ser	Trp	Arg	Glu	Thr	Glu	Ile	Lys	Glu	Gln	Leu	Thr	Glu	His	Leu	Cys
1				5					10					15	
Thr	Ile	Ile	Gln	Gln	Asn	Glu	Leu	Arg	Lys	Ala	Lys	Lys	Leu	Glu	Glu
			20					25					30		
Leu	Met	Gln	Gln	Leu	Asp	Val	Glu	Ala	Asp	Glu	Glu	Thr	Leu	Glu	Leu
		35					40					45			
Glu	Val	Glu	Val	Glu	Arg	Leu	Leu	His	Glu	Gln	Glu	Val	Glu	Ser	Arg
	50					55					60				
Arg	Pro	Val	Val	Arg	Leu	Glu	Arg	Pro	Phe	Gln	Pro	Ala	Glu	Glu	Ser
	65				70				75						80
Val	Thr	Leu	Glu	Phe	Ala	Lys	Glu	Asn	Arg	Lys	Cys	Gln	Glu	Gln	Ala
				85					90					95	
Val	Ser	Pro	Lys	Val	Asp	Asp	Gln	Cys	Gly	Asn	Ser	Ser	Ser	Ile	Pro
			100					105					110		
Phe	Leu	Ser	Pro	Asn	Cys	Pro	Asn	Gln	Glu	Gly	Asn	Asp	Ile	Ser	Ala

00673395-122700

115

120

125

Ala Leu Ala Thr  
130

&lt;210&gt; 167

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 167

Gln Ile Leu Met Ser His Ser Pro Pro Gln Ala Glu Met Ala Ser Leu  
1 5 10 15  
Asn Glu Pro Leu Val Ser Leu Ile Leu Leu Val Arg Val Ala Ile  
20 25 30  
Ser Arg Pro Pro Pro Gln Ala Pro Lys Ser Leu His Arg Leu Leu His  
35 40 45  
Leu Val Val Ala Ser Thr Pro Pro Thr Ser Trp Pro Phe Gly Ala His  
50 55 60  
Phe Ala Val  
65

&lt;210&gt; 168

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 168

Asn Gly Leu Ser Lys Arg Thr Thr Gly Leu Leu Asp Ser Thr Ser Cys  
1 5 10 15  
Ser Cys Ser Asn Leu Ser Thr Ser Thr Ser Ser Ser Lys Val Ser Ser  
20 25 30  
Ser Ala Ser Thr Ser Ser Cys Cys Ile Asn Ser Ser Asn Phe Leu Ala  
35 40 45  
Phe Arg Ser Ser Phe Cys Cys Met Ile Val Gln Arg Cys Ser Val Ser  
50 55 60  
Cys Ser Phe Ile Ser Val Ser Arg His Glu  
65 70

&lt;210&gt; 169

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 169

Gly Arg Gly Gly Leu Gly Cys Arg Ser Trp Arg Cys Ala Gly Ser Ser  
1 5 10 15  
Arg Pro Tyr Ser Glu Val Phe Ser Val Ala Leu Leu Glu Arg Gly Ser  
20 25 30  
Ser Cys Ile Leu Arg Ile Phe Cys Ile Ser Ala Pro Phe Ser Ser Arg

00673395-122700

			35					40					45				
Cys	His	Arg	Met	Pro	Gln	Ile	Gly	Pro	Val	Pro	Ser	Val	Asn	Gln	Thr		
	50					55					60						
Ser	Glu	Thr	Ala	Ser	Leu	Gln	Gly	Gln	Ser	Pro	Ser	Thr	Asp	Glu	Leu		
65					70					75					80		
Glu	Arg	Asp	Ser	Glu	Met	Gln	Arg	Pro									
				85													

<210> 170  
 <211> 74  
 <212> PRT  
 <213> homo sapiens

<400> 170

Gly	Pro	Leu	His	Phe	Arg	Ile	Pro	Leu	Lys	Leu	Ile	Cys	Thr	Trp	Thr		
1				5					10					15			
Leu	Thr	Leu	Lys	Arg	Gly	Gly	Phe	Arg	Ser	Leu	Ile	His	Arg	Gly	Asp		
			20					25					30				
Arg	Thr	Tyr	Leu	Gly	His	Pro	Met	Ala	Ala	Arg	Arg	Glu	Gly	Ser	Arg		
		35					40					45					
Asn	Ala	Lys	Tyr	Ser	Gln	Asp	Ala	Gly	Gly	Thr	Pro	Leu	Lys	Glu	Arg		
	50					55					60						
His	Gly	Glu	Asn	Phe	Arg	Val	Arg	Ala	Arg								
65					70												

<210> 171  
 <211> 89  
 <212> PRT  
 <213> homo sapiens

<400> 171

Ala	Val	Ala	Phe	Gln	Asn	Pro	Ser	Gln	Ala	His	Leu	Tyr	Leu	Asp	Ser		
1				5					10					15			
Asp	Pro	Glu	Ala	Arg	Arg	Phe	Pro	Lys	Ser	Asp	Ser	Pro	Arg	Gly	Gln		
			20					25					30				
Asp	Leu	Phe	Gly	Ala	Ser	Asp	Gly	Ser	Glu	Lys	Arg	Arg	Glu	Pro	Lys		
		35					40					45					
Cys	Lys	Ile	Phe	Ser	Arg	Cys	Arg	Arg	Asn	Pro	Ser	Gln	Gly	Ala	Pro		
	50					55					60						
Arg	Arg	Lys	Leu	Gln	Ser	Thr	Gly	Ala	Met	Ile	Gln	His	Asn	Ala	Arg		
65					70					75					80		
Thr	Cys	Ser	Pro	Ala	His	Leu	Ser	Pro									
				85													

<210> 172  
 <211> 100  
 <212> PRT  
 <213> homo sapiens

00673395.122700

<400> 172

Pro 1	Ser	Pro	Ala	Val 5	Leu	Gly	Asp	Gln	Pro 10	Pro	Ser	Ala	Ser	Gly 15	Ala
Val	His	Arg	Lys 20	Leu	Ser	Leu	Glu	Val 25	Cys	Cys	Cys	Gln	Glu 30	Arg	Ala
Gln	Met	Gly 35	Pro	Val	Met	Ala	Ala 40	Thr	Ser	Thr	Ser	Cys 45	Gly	Arg	Ala
Arg	Leu 50	Leu	Ala	Arg	Ser	Ala 55	Gln	Trp	Leu	Thr	Thr 60	Met	Leu	Ser	Ser
Ala 65	Ala	Val	Trp	Leu	Gly 70	Ser	Arg	Arg	Leu	Leu 75	Thr	Cys	Gly	Glu	Asn 80
Pro	Ser	Tyr	Ala	Leu 85	Val	Ala	Phe	Leu	Cys 90	Leu	Ser	Arg	Glu	Ser 95	Pro
Ser	Ala	Lys	Pro 100												

<210> 173

<211> 495

<212> PRT

<213> homo sapiens

<400> 173

Ser 1	Arg	Thr	Asn	Thr 5	Pro	Val	Glu	Thr	Trp 10	Lys	Gly	Ser	Lys	Gly 15	Lys
Gln	Ser	Tyr	Thr 20	Tyr	Ile	Ile	Glu	Glu 25	Asn	Thr	Thr	Thr	Ser 30	Phe	Thr
Trp	Ala	Phe 35	Gln	Arg	Thr	Thr	Phe 40	His	Glu	Ala	Ser	Arg 45	Lys	Tyr	Thr
Asn	Asp 50	Val	Ala	Lys	Ile	Tyr 55	Ser	Ile	Asn	Val	Thr 60	Asn	Val	Met	Asn
Gly 65	Val	Ala	Ser	Tyr	Cys 70	Arg	Pro	Cys	Ala	Leu 75	Glu	Ala	Ser	Asp	Val 80
Gly	Ser	Ser	Cys	Thr 85	Ser	Cys	Pro	Ala	Gly 90	Tyr	Tyr	Ile	Asp	Arg 95	Asp
Ser	Gly	Thr	Cys 100	His	Ser	Cys	Pro	Pro 105	Asn	Thr	Ile	Leu	Lys 110	Ala	His
Gln	Pro	Tyr 115	Gly	Val	Gln	Ala	Cys 120	Val	Pro	Cys	Gly	Pro 125	Gly	Thr	Lys
Asn	Asn 130	Lys	Ile	His	Ser	Leu 135	Cys	Tyr	Asn	Asp	Cys 140	Thr	Phe	Ser	Arg
Asn 145	Thr	Pro	Thr	Arg	Thr 150	Phe	Asn	Tyr	Asn	Phe 155	Ser	Ala	Leu	Ala	Asn 160
Thr	Val	Thr	Leu	Ala 165	Gly	Gly	Pro	Ser	Phe 170	Thr	Ser	Lys	Gly	Leu 175	Lys

09573305.122700

Tyr	Phe	His	His	Phe	Thr	Leu	Ser	Leu	Cys	Gly	Asn	Gln	Gly	Arg	Lys
			180					185					190		
Met	Ser	Val	Cys	Thr	Asp	Asn	Val	Thr	Asp	Leu	Arg	Ile	Pro	Glu	Gly
		195					200					205			
Glu	Ser	Gly	Phe	Ser	Lys	Ser	Ile	Thr	Ala	Tyr	Val	Cys	Gln	Ala	Val
	210					215					220				
Ile	Ile	Pro	Pro	Glu	Val	Thr	Gly	Tyr	Lys	Ala	Gly	Val	Ser	Ser	Gln
	225				230					235					240
Pro	Val	Ser	Leu	Ala	Asp	Arg	Leu	Ile	Gly	Val	Thr	Thr	Asp	Met	Thr
				245					250					255	
Leu	Asp	Gly	Ile	Thr	Ser	Pro	Ala	Glu	Leu	Phe	His	Leu	Glu	Ser	Leu
			260					265					270		
Gly	Ile	Pro	Asp	Val	Ile	Phe	Phe	Tyr	Arg	Ser	Asn	Asp	Val	Thr	Gln
		275					280					285			
Ser	Cys	Ser	Ser	Gly	Arg	Ser	Thr	Thr	Ile	Arg	Val	Arg	Cys	Ser	Pro
		290				295					300				
Gln	Lys	Thr	Val	Pro	Gly	Ser	Leu	Leu	Leu	Pro	Gly	Thr	Cys	Ser	Asp
					310					315					320
Gly	Thr	Cys	Asp	Gly	Cys	Asn	Phe	His	Phe	Leu	Trp	Glu	Ser	Ala	Ala
				325					330					335	
Ala	Cys	Pro	Leu	Cys	Ser	Val	Ala	Asp	Tyr	His	Ala	Ile	Val	Ser	Ser
			340					345					350		
Cys	Val	Ala	Gly	Ile	Gln	Lys	Thr	Thr	Tyr	Val	Trp	Arg	Glu	Pro	Lys
		355					360					365			
Leu	Cys	Ser	Gly	Gly	Ile	Ser	Leu	Pro	Glu	Gln	Arg	Val	Thr	Ile	Cys
		370				375					380				
Lys	Thr	Ile	Asp	Phe	Trp	Leu	Lys	Val	Gly	Ile	Ser	Ala	Gly	Thr	Cys
					390					395					400
Thr	Ala	Ile	Leu	Leu	Thr	Val	Leu	Thr	Cys	Tyr	Phe	Trp	Lys	Lys	Asn
				405					410					415	
Gln	Lys	Leu	Glu	Tyr	Lys	Tyr	Ser	Lys	Leu	Val	Met	Asn	Ala	Thr	Leu
			420					425					430		
Lys	Asp	Cys	Asp	Leu	Pro	Ala	Ala	Asp	Ser	Cys	Ala	Ile	Met	Glu	Gly
			435				440					445			
Glu	Asp	Val	Glu	Asp	Asp	Leu	Ile	Phe	Thr	Ser	Lys	Lys	Ser	Leu	Phe
		450				455					460				
Gly	Lys	Ile	Lys	Ser	Phe	Thr	Ser	Lys	Arg	Thr	Pro	Asp	Gly	Phe	Asp
					470					475					480
Ser	Val	Pro	Leu	Lys	Thr	Ser	Ser	Gly	Gly	Pro	Asp	Met	Asp	Leu	
				485					490					495	

<210> 174  
 <211> 118  
 <212> PRT

00573305-122700



<213> homo sapiens

<400> 174

Gly 1	His	Asn	Glu	Glu 5	Ile	Ser	Ser	Ser	Gly 10	Cys	Cys	Arg	Met	Leu 15	Ala
Pro	Lys	Ser	Pro 20	Gln	Ala	Cys	Lys	Gly 25	Ala	Met	Gln	Gly	Glu 30	Glu	Ala
Gly	Glu	Ala 35	Gly	Ser	Ala	Ser	His 40	Arg	Ser	Met	Ser	Gly 45	Pro	Pro	Glu
Asp	Val 50	Phe	Ser	Gly	Thr	Glu 55	Ser	Asn	Pro	Ser	Gly 60	Val	Leu	Leu	Glu
Val 65	Asn	Asp	Leu	Ile	Phe 70	Pro	Lys	Ser	Asp	Phe 75	Leu	Leu	Val	Lys	Met 80
Arg	Ser	Ser	Ser	Thr 85	Ser	Ser	Pro	Ser	Met 90	Met	Ala	Gln	Leu	Ser 95	Ala
Ala	Gly	Arg	Ser 100	Gln	Ser	Leu	Arg	Val 105	Ala	Phe	Ile	Thr	Ser 110	Leu	Glu
Tyr	Leu	Tyr 115	Ser	Ser	Phe										

<210> 175

<211> 172

<212> PRT

<213> homo sapiens

<400> 175

Arg 1	Asn	Thr	Arg	Gly 5	His	Phe	Arg	Ala	Cys 10	Gln	Arg	Lys	Leu 15	Lys	Pro
Cys	Ser	Val	Ser 20	Thr	Val	Tyr	Lys	Phe 25	Asn	Arg	Asn	Ala	Cys 30	Gln	Arg
Gly	Leu	Phe 35	Glu	Lys	Arg	Val	Pro 40	Ser	Glu	Pro	Val	Leu 45	Ser	Val	Gln
Glu	Lys 50	Gly	Val	Leu	Leu	Lys 55	Arg	Lys	Leu	Ser	Leu 60	Leu	Glu	Gln	Asp
Val 65	Ile	Val	Asn	Glu	Asp 70	Gly	Arg	Asn	Lys	Leu 75	Lys	Lys	Gln	Gly	Glu 80
Thr	Pro	Asn	Glu 85	Val	Cys	Met	Phe	Ser	Leu 90	Ala	Tyr	Gly	Asp	Ile 95	Pro
Glu	Glu	Leu	Ile 100	Asp	Val	Ser	Asp	Phe 105	Glu	Cys	Ser	Leu	Cys 110	Met	Arg
Leu	Phe	Phe 115	Glu	Pro	Val	Thr	Thr 120	Pro	Cys	Gly	His	Ser 125	Phe	Cys	Lys
Asn	Cys 130	Leu	Glu	Arg	Cys	Leu 135	Asp	His	Ala	Pro	Tyr 140	Cys	Pro	Leu	Cys
Lys	Glu	Ser	Leu	Lys	Glu	Tyr	Leu	Ala	Asp	Arg	Arg	Tyr	Cys	Val	Thr

00673305-122700

145

150

155

160

Gln Leu Leu Glu Gly Ile Asn Ser Glu Val Ser Ala  
165 170

&lt;210&gt; 176

&lt;211&gt; 248

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 176

Gln 1	Ile	Gly	Gly	Thr 5	Val	Ser	His	Ser	Cys 10	Trp	Lys	Glu	Leu	Ile 15	Val
Lys	Tyr	Leu	Pro 20	Asp	Glu	Leu	Ser	Glu 25	Arg	Lys	Lys	Ile	Tyr 30	Asp	Glu
Glu	Thr	Ala 35	Glu	Leu	Ser	His	Leu 40	Thr	Lys	Asn	Val	Pro 45	Ile	Phe	Val
Cys 50	Thr	Met	Ala	Tyr	Pro	Thr 55	Val	Pro	Cys	Pro	Leu 60	His	Val	Phe	Glu
Pro 65	Arg	Tyr	Arg	Leu	Met 70	Ile	Arg	Arg	Ser	Ile 75	Gln	Thr	Gly	Thr	Lys 80
Gln	Phe	Gly	Met	Cys 85	Val	Ser	Asp	Thr	Gln 90	Asn	Ser	Phe	Ala	Asp 95	Tyr
Gly	Cys	Met	Leu 100	Gln	Ile	Arg	Asn	Val 105	His	Phe	Leu	Pro	Asp 110	Gly	Arg
Ser	Val	Val 115	Asp	Thr	Val	Gly	Gly 120	Lys	Arg	Phe	Arg	Val 125	Leu	Lys	Arg
Gly	Met 130	Lys	Asp	Gly	Tyr	Cys 135	Thr	Ala	Asp	Ile	Glu 140	Tyr	Leu	Glu	Asp
Val 145	Lys	Val	Glu	Asn	Glu 150	Asp	Glu	Ile	Lys	Asn 155	Leu	Arg	Glu	Leu	His 160
Asp	Leu	Val	Tyr	Ser 165	Gln	Ala	Cys	Ser	Trp 170	Phe	Gln	Asn	Leu	Arg 175	Asp
Arg	Phe	Arg	Ser 180	Gln	Ile	Leu	Gln	His 185	Phe	Gly	Ser	Met	Pro 190	Glu	Arg
Arg	Glu	Asn 195	Leu	Gln	Ala	Ala	Pro 200	Asn	Gly	Pro	Ala	Trp 205	Cys	Trp	Trp
Leu 210	Leu	Ala	Val	Leu	Pro	Val 215	Asp	Pro	Arg	Tyr	Gln 220	Leu	Ser	Val	Leu
Ser 225	Met	Lys	Ser	Leu	Lys 230	Glu	Arg	Leu	Thr	Lys 235	Ile	Gln	His	Ile	Leu 240
Thr	Tyr	Phe	Ser	Arg 245	Asp	Gln	Phe								

&lt;210&gt; 177

&lt;211&gt; 133

&lt;212&gt; PRT

00573306-122700

<213> homo sapiens

<400> 177

His 1	Ser	Thr	Ser	Tyr 5	Leu	Leu	Asp	Thr	Leu 10	Leu	Ser	Phe	Leu	Cys 15	Lys	
Glu	Asp	Asn	Met 20	Val	His	Asp	Leu	Asn 25	Asn	Ala	Gln	Asp	Asn 30	Ser	Tyr	
Arg	Thr	Asn 35	Val	Arg	Lys	Gly	Leu 40	Leu	Leu	Ala	Gln	Lys 45	Thr	Thr	Ser	
Cys	Arg 50	Glu	Asn	Thr	Arg	Asn 55	Leu	Arg	His	Arg	Leu 60	Ile	Leu	Leu	Glu	
Tyr 65	His	His	Lys	Leu	Arg 70	Lys	Thr	Tyr	Arg	Leu 75	His	Trp	Glu	Phe	Leu 80	
Leu	Val	Phe	Ser	Ala 85	Tyr	Phe	Phe	His	Leu 90	His	Leu	Gln	Ser	His 95	Pro	
Val	Leu	Lys	Glu 100	Thr	Thr	Phe	Phe	Ser 105	Ala	Glu	His	Leu	Phe 110	Leu	Glu	
Leu	Thr	Glu 115	Gln	Val	Leu	Arg	Ala 120	Leu	Phe	Phe	Gln	Thr 125	Val	Leu	Ser	
Gly	Arg 130	His	Phe	Cys												

<210> 178

<211> 152

<212> PRT

<213> homo sapiens

<400> 178

Ser 1	Ala	Val	Lys	Arg 5	Gly	Trp	Asp	Leu	Asn 10	Met	Ala	Ala	Val	Val 15	Ala	
Ala	Thr	Ala	Leu 20	Lys	Gly	Arg	Gly	Ala 25	Arg	Asn	Ala	Arg	Val 30	Leu	Arg	
Gly	Ile	Leu 35	Ala	Gly	Ala	Thr	Ala 40	Asn	Lys	Ala	Ser	His 45	Asn	Arg	Thr	
Arg	Ala 50	Leu	Gln	Ser	His	Ser 55	Ser	Pro	Glu	Gly	Lys 60	Glu	Glu	Pro	Glu	
Pro 65	Leu	Ser	Pro	Glu	Leu 70	Glu	Tyr	Ile	Pro	Arg 75	Lys	Arg	Gly	Lys	Asn 80	
Pro	Met	Lys	Ala	Val 85	Gly	Leu	Ala	Trp	Ala 90	Ile	Gly	Phe	Pro	Cys 95	Gly	
Ile	Leu	Leu	Phe 100	Ile	Leu	Thr	Lys	Arg 105	Glu	Val	Asp	Lys	Asp 110	Arg	Val	
Lys	Gln	Met 115	Lys	Ala	Arg	Gln	Asn 120	Met	Arg	Leu	Ser	Asn 125	Thr	Gly	Glu	
Tyr	Glu	Ser	Gln	Arg	Phe	Arg	Ala	Ser	Ser	Gln	Ser	Ala	Pro	Ser	Pro	

00673305-122700

130

135

140

Asp Val Gly Ser Gly Val Gln Thr  
145 150

&lt;210&gt; 179

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 179

Glu	Gly	Arg	Ser	Ala	Pro	Gln	Val	Cys	Thr	Pro	Asp	Pro	Thr	Ser	Gly
1				5					10					15	
Asp	Gly	Ala	Leu	Trp	Glu	Glu	Ala	Leu	Asn	Leu	Trp	Leu	Ser	Tyr	Ser
			20					25					30		
Pro	Val	Leu	Asp	Asn	Arg	Met	Phe	Cys	Arg	Ala	Phe	Ile	Cys	Phe	Thr
		35					40					45			
Arg	Ser	Leu	Ser	Thr	Ser	Arg	Leu	Val	Arg	Met	Lys	Arg	Arg	Ile	Pro
	50					55					60				
Gln	Gly	Lys	Pro	Met	Ala	Gln	Ala	Ser	Pro	Thr	Ala	Phe	Met	Gly	Phe
	65				70					75					80
Leu	Pro	Leu	Phe	Leu	Gly	Met	Tyr	Ser	Ser	Ser	Gly	Asp	Arg	Gly	Ser
				85					90					95	
Gly	Ser	Ser	Leu	Pro	Ser	Gly	Glu	Leu	Trp	Leu	Cys	Arg	Ala	Arg	Val
			100					105					110		
Leu	Leu														

&lt;210&gt; 180

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 180

Gly	Leu	Ala	Thr	Ala	Trp	Ala	Ser	Cys	Ala	Leu	Trp	Trp	Thr	Ser	Glu
1				5					10					15	
Ala	Arg	Thr	Gly	Ile	Trp	Ala	Lys	Pro	Glu	Asp	Leu	Thr	Val	Asn	Ser
			20					25					30		
Leu	Gly	Gly	Ser	Gln	Arg	Ser	Ser	Gly	Leu	His	Pro	Arg	Pro	Asn	Ile
		35					40					45			
Arg	Gly	Arg	Gly	Thr	Leu	Gly	Gly	Ser	Pro	Glu	Pro	Leu	Ala	Leu	Ile
	50					55					60				
Leu	Ala	Arg	Val	Gly	Gln	Pro	His	Val	Leu	Pro	Ser	Leu	His	Leu	Leu
	65				70					75					80
His	Thr	Val	Leu	Val	His	Phe	Pro	Leu	Gly	Glu	Asp	Glu	Glu	Glu	Asp
				85					90					95	
Thr	Thr	Arg	Glu	Ala	Asp	Gly	Pro	Gly	Gln	Ser	His	Ser	Phe	His	Gly
			100					105					110		

00673305.122700

Val Leu Ala Pro Leu Ser Gly Asn Val Phe Gln Leu Arg Gly  
115 120 125

<210> 181  
<211> 74  
<212> PRT  
<213> homo sapiens

<400> 181

Leu Val Lys Cys Pro Lys Gly Glu Phe Ser Phe His Ser Asn Lys Asp  
1 5 15  
Arg Phe Ala His Ser Leu Lys Gln Asn Val Ala Met Asn Ile Gln Pro  
20 30  
Leu His Thr Tyr Lys Asp Val Arg Met Ile Pro Pro Thr Lys His Thr  
35 40 45  
His Ser His Thr Arg Thr His Thr His Met His Thr Arg Ala Cys Thr  
50 55 60  
His Gly His Met His Thr His Thr His Thr  
65 70

<210> 182  
<211> 84  
<212> PRT  
<213> homo sapiens

<400> 182

Ile Leu Ile Ser Phe Lys Gln Arg Gln Ile Cys Ala Phe Thr Gln Ala  
1 5 15  
Glu Cys Gly His Glu Tyr Ser Ala Pro Ala Tyr Ile Gln Arg Cys Thr  
20 25 30  
His Asp Ser Pro His Gln Ala His Thr Gln Ser His Thr His Thr His  
35 40 45  
Thr His Ala His Thr Arg Val His Thr Arg Thr His Ala His Thr His  
50 55 60  
Ala His Val Asn Thr Cys Thr His Ala His Thr Cys Thr His Ala His  
65 70 75 80  
Thr Asp Thr Leu

<210> 183  
<211> 70  
<212> PRT  
<213> homo sapiens

<400> 183

Val Cys Pro Cys Val His Val Cys Thr Cys Val His Val Cys Met Cys  
1 5 15  
Leu Arg Val Arg Val Cys Val His Val Ser Val Cys Ala Arg Ala Cys  
20 25 30  
Val His Val Cys Val Cys Ala Cys Val Thr Val Cys Val Leu Gly Gly

006733005.122700



<210> 187  
 <211> 37  
 <212> PRT  
 <213> homo sapiens

<400> 187

Ser	Pro	Leu	Leu	Trp	Phe	Pro	Ala	Leu	Ser	Ala	Phe	Ser	Gly	Ile	Ser
1				5					10					15	
Leu	Phe	Ile	Ile	Tyr	Phe	His	Asp	Leu	Ser	Ala	Lys	Leu	Leu	Ile	Phe
			20					25					30		
Cys	Arg	Lys	Lys	Val											
		35													

<210> 188  
 <211> 100  
 <212> PRT  
 <213> homo sapiens

<400> 188

Met	Pro	Asp	Phe	Lys	Ile	Ala	Arg	Arg	Lys	Gln	Thr	Leu	Arg	Ile	Lys
1				5					10					15	
Lys	Ala	Gly	His	Leu	Leu	Asn	Pro	Trp	Leu	His	His	Lys	Ala	Leu	Gly
			20					25					30		
Leu	Gly	Phe	Leu	Tyr	Leu	Ile	Glu	Val	Phe	Ser	Val	Ala	Leu	Gly	Ala
		35					40					45			
Val	Cys	Leu	Ser	Pro	Thr	Pro	Lys	Asp	Ala	Arg	Lys	Thr	Ser	Thr	Ile
	50					55					60				
Ser	His	Val	Ala	Thr	Phe	Thr	Ser	Met	Pro	His	Lys	Cys	Leu	Ser	Glu
65					70					75					80
Ser	Pro	Asn	Ser	Ala	Phe	Pro	Gln	Asn	Lys	Pro	Asn	Ala	Ile	Arg	Gln
				85					90					95	
Lys	Lys	Lys	Lys												
				100											

<210> 189  
 <211> 256  
 <212> PRT  
 <213> homo sapiens

<400> 189

Arg	Ser	Gln	Ala	Gly	Pro	Glu	Ala	Gly	Gln	Pro	Leu	Pro	Gly	Ser	Gly
1				5					10					15	
Lys	Arg	Ser	Ser	Cys	Cys	His	Cys	Ser	Ser	Gly	Ala	Cys	Ser	Met	Gly
			20					25					30		
Pro	Leu	Pro	Arg	Thr	Val	Glu	Leu	Phe	Tyr	Asp	Val	Leu	Ser	Pro	Tyr
		35					40					45			
Ser	Trp	Leu	Gly	Phe	Glu	Ile	Leu	Cys	Arg	Tyr	Gln	Asn	Ile	Trp	Asn

09673395.122700

50					55					60					
Ile 65	Asn	Leu	Gln	Leu	Arg 70	Pro	Ser	Leu	Ile	Thr 75	Gly	Ile	Met	Lys	Asp 80
Ser	Gly	Asn	Lys	Pro 85	Pro	Gly	Leu	Leu	Pro 90	Arg	Lys	Gly	Leu	Tyr 95	Met
Ala	Asn	Asp	Leu 100	Lys	Leu	Leu	Arg	His 105	His	Leu	Gln	Ile	Pro 110	Ile	His
Phe	Pro	Lys 115	Asp	Phe	Leu	Ser	Val 120	Met	Leu	Glu	Lys	Gly 125	Ser	Leu	Ser
Ala	Met 130	Arg	Phe	Leu	Thr	Ala 135	Val	Asn	Leu	Glu	His 140	Pro	Glu	Met	Leu
Glu 145	Lys	Ala	Ser	Arg	Glu 150	Leu	Trp	Met	Arg	Val 155	Trp	Ser	Arg	Asn	Glu 160
Asp	Ile	Thr	Glu	Pro 165	Gln	Ser	Ile	Leu	Ala 170	Ala	Ala	Glu	Lys	Ala 175	Gly
Met	Ser	Ala	Glu 180	Gln	Ala	Gln	Gly	Leu 185	Leu	Glu	Lys	Ile	Ala 190	Thr	Pro
Lys	Val	Lys 195	Asn	Gln	Leu	Lys	Glu 200	Thr	Thr	Glu	Ala	Ala 205	Cys	Arg	Tyr
Gly	Ala 210	Phe	Gly	Leu	Pro	Ile 215	Thr	Val	Ala	His	Val 220	Asp	Gly	Gln	Thr
His 225	Met	Leu	Phe	Gly	Ser 230	Asp	Arg	Met	Glu	Leu 235	Leu	Ala	His	Leu	Leu 240
Gly	Glu	Lys	Trp	Met 245	Gly	Pro	Ile	Pro	Pro 250	Ala	Val	Asn	Ala	Arg 255	Leu

&lt;210&gt; 190

&lt;211&gt; 196

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 190

Ser 1	Leu	Ala	Phe	Thr 5	Ala	Gly	Gly	Ile	Gly 10	Pro	Ile	His	Phe	Ser 15	Pro
Ser	Arg	Cys	Ala 20	Ser	Ser	Ser	Ile	Arg 25	Ser	Glu	Pro	Asn	Asn 30	Met	Trp
Val	Trp	Pro 35	Ser	Thr	Trp	Ala	Thr 40	Val	Met	Gly	Ser	Pro 45	Lys	Ala	Pro
Tyr 50	Leu	Gln	Ala	Ala	Ser	Val 55	Val	Ser	Leu	Ser	Trp 60	Phe	Phe	Thr	Phe
Gly 65	Val	Ala	Ile	Phe	Ser 70	Arg	Ser	Pro	Trp	Ala 75	Cys	Ser	Ala	Asp	Ile 80
Pro	Ala	Phe	Ser	Ala 85	Ala	Ala	Arg	Met	Leu 90	Cys	Gly	Ser	Val	Met 95	Ser



Ser	Phe	Leu	Asp 100	Gln	Thr	Arg	Ile	His 105	Ser	Ser	Arg	Asp	Ala 110	Phe	Ser
Ser	Ile	Ser 115	Gly	Cys	Ser	Lys	Phe 120	Thr	Ala	Val	Arg	Lys 125	Arg	Met	Ala
Asp	Lys 130	Leu	Pro	Phe	Ser	Ser 135	Ile	Thr	Asp	Lys	Lys 140	Ser	Leu	Gly	Lys
Trp 145	Met	Gly	Ile	Trp	Arg 150	Trp	Cys	Leu	Arg	Ser 155	Phe	Lys	Ser	Phe	Ala 160
Met	Tyr	Ser	Pro	Leu 165	Arg	Gly	Ser	Arg	Pro 170	Gly	Gly	Leu	Phe	Pro 175	Leu
Ser	Phe	Met	Ile 180	Pro	Val	Met	Arg	Leu 185	Gly	Arg	Asn	Cys	Arg 190	Leu	Met
Phe	Gln	Ile 195	Phe												

<210> 191  
 <211> 116  
 <212> PRT  
 <213> homo sapiens

<400> 191

Glu 1	Gln	Arg	Ala	Ser 5	Ala	Met	Arg	Ser	Ser 10	Arg	Ala	Phe	Arg	Thr 15	Val
Cys	Ser	Ser	Trp 20	Ala	Thr	His	Gly	Gln 25	Leu	Pro	Ala	Gly	Leu 30	Asp	Asp
Lys	Thr	Asn 35	Ile	Lys	Thr	Val	Cys 40	Thr	Tyr	Trp	Glu	Asp 45	Phe	His	Ser
Cys	Thr 50	Val	Thr	Ala	Leu	Thr 55	Asp	Cys	Gln	Glu	Gly 60	Ala	Lys	Asp	Met
Trp 65	Asp	Lys	Leu	Arg	Lys 70	Glu	Ser	Lys	Asn	Leu 75	Asn	Ile	Gln	Gly	Ser 80
Leu	Phe	Glu	Leu	Cys 85	Gly	Ser	Gly	Asn	Gly 90	Ala	Ala	Gly	Ser	Leu 95	Leu
Pro	Ala	Phe	Pro 100	Val	Leu	Leu	Val	Ser 105	Leu	Ser	Ala	Ala	Leu 110	Ala	Thr
Trp	Leu	Ser 115	Phe												

<210> 192  
 <211> 182  
 <212> PRT  
 <213> homo sapiens

<400> 192

Lys 1	Arg	Glu	Ser	Gly 5	Phe	Pro	Thr	Ile	Leu 10	Tyr	Glu	Cys	Phe	Gln 15	His
His	Arg	Glu	Ser	Gln	Arg	Pro	Gln	Arg	Thr	Asn	Gly	Ser	Ser	Ser	Arg

00673395.122700

20										25					30															
Phe	Pro	Gly	Ala	Trp	Ser	Glu	Cys	Gly	Trp	Ala	Arg	Gly	Gly	Ser	Trp															
		35					40					45																		
Pro	His	Ala	Gln	Lys	Glu	Ser	Gln	Val	Ala	Lys	Ala	Ala	Glu	Arg	Asp															
	50					55					60																			
Thr	Arg	Ser	Thr	Gly	Asn	Ala	Gly	Ser	Arg	Asp	Pro	Ala	Ala	Pro	Leu															
	65				70					75					80															
Pro	Leu	Pro	Gln	Ser	Ser	Asn	Lys	Leu	Pro	Trp	Met	Leu	Arg	Phe	Leu															
				85					90					95																
Asp	Ser	Phe	Leu	Ser	Leu	Ser	His	Ile	Ser	Phe	Ala	Pro	Ser	Trp	Gln															
			100					105					110																	
Ser	Val	Arg	Ala	Val	Thr	Val	Gln	Leu	Trp	Lys	Ser	Ser	Gln	Tyr	Val															
		115					120					125																		
His	Thr	Val	Leu	Met	Phe	Val	Leu	Ser	Ser	Arg	Pro	Ala	Gly	Ser	Trp															
		130				135					140																			
Pro	Cys	Val	Ala	Gln	Leu	Glu	Gln	Thr	Val	Arg	Lys	Ala	Leu	Glu	Asp															
	145				150					155				160																
Arg	Ile	Ala	Leu	Ala	Arg	Cys	Ser	His	Gly	Leu	His	Gln	Ile	Arg	Tyr															
				165					170					175																
Leu	His	Arg	Glu	Asp	Gln																									
			180																											

<210> 193  
 <211> 105  
 <212> PRT  
 <213> homo sapiens  
 <400> 193

His	Leu	Ala	Asn	Lys	Thr	Gln	Glu	Ile	Lys	Arg	Asn	Lys	Lys	Glu	Asn
1				5					10					15	
Gln	Asp	Phe	Pro	Gln	Ser	Tyr	Met	Ser	Val	Phe	Ser	Ile	Thr	Glu	Asn
			20					25					30		
His	Asn	Val	Pro	Lys	Glu	Leu	Met	Asp	Leu	Pro	Leu	Asp	Phe	Arg	Glu
		35					40					45			
His	Gly	Val	Ser	Val	Gly	Gly	Arg	Ala	Gly	Gly	Ala	Gly	Pro	Thr	Leu
	50					55					60				
Arg	Arg	Lys	Ala	Arg	Ser	Leu	Lys	Leu	Pro	Arg	Glu	Thr	Pro	Gly	Ala
	65				70					75					80
Pro	Gly	Thr	Pro	Gly	Ala	Gly	Thr	Pro	Pro	Pro	Arg	Cys	Arg	Cys	Arg
				85					90					95	
Arg	Val	Arg	Ile	Ser	Cys	Leu	Gly	Cys							
			100					105							

<210> 194  
 <211> 426  
 <212> PRT

<213> homo sapiens

<400> 194

Glu 1	Ile	Tyr	Ser	Leu 5	Ser	Arg	Phe	Ile	Glu 10	Val	Lys	Met	Ser	Lys 15	Lys
Ile	Ser	Gly	Gly 20	Ser	Val	Val	Glu	Met 25	Gln	Gly	Asp	Glu	Met 30	Thr	Arg
Ile	Ile	Trp 35	Glu	Leu	Ile	Lys	Glu 40	Lys	Leu	Ile	Phe	Pro 45	Tyr	Val	Glu
Leu	Asp 50	Leu	His	Ser	Tyr	Asp 55	Leu	Gly	Ile	Glu	Asn 60	Arg	Asp	Ala	Thr
Asn 65	Asp	Gln	Val	Thr	Lys 70	Asp	Ala	Ala	Glu	Ala 75	Ile	Lys	Lys	His	Asn 80
Val	Gly	Val	Lys	Cys 85	Ala	Thr	Ile	Thr	Pro 90	Asp	Glu	Lys	Arg	Val 95	Glu
Glu	Phe	Lys	Leu 100	Lys	Gln	Met	Trp	Lys 105	Ser	Pro	Asn	Gly	Thr 110	Ile	Arg
Asn	Ile	Leu 115	Gly	Gly	Thr	Val	Phe 120	Arg	Glu	Ala	Ile	Ile 125	Cys	Lys	Asn
Ile	Pro 130	Arg	Leu	Val	Ser	Gly 135	Trp	Val	Lys	Pro	Ile 140	Ile	Ile	Gly	Arg
His 145	Ala	Tyr	Gly	Asp	Gln 150	Tyr	Arg	Ala	Thr	Asp 155	Phe	Val	Val	Pro	Gly 160
Pro	Gly	Lys	Val	Glu 165	Ile	Thr	Tyr	Thr	Pro 170	Ser	Asp	Gly	Thr	Gln 175	Lys
Val	Thr	Tyr	Leu 180	Val	His	Asn	Phe	Glu 185	Glu	Gly	Gly	Gly	Val 190	Ala	Met
Gly	Met	Tyr 195	Asn	Gln	Asp	Lys	Ser 200	Ile	Glu	Asp	Phe	Ala 205	His	Ser	Ser
Phe	Gln 210	Met	Ala	Leu	Ser	Lys 215	Gly	Trp	Pro	Leu	Tyr 220	Leu	Ser	Thr	Lys
Asn 225	Thr	Ile	Leu	Lys	Lys 230	Tyr	Asp	Gly	Arg	Phe 235	Lys	Asp	Ile	Phe	Gln 240
Glu	Ile	Tyr	Asp	Lys 245	Gln	Tyr	Lys	Ser	Gln 250	Phe	Glu	Ala	Gln	Lys 255	Ile
Trp	Tyr	Glu	His 260	Arg	Leu	Ile	Asp	Asp 265	Met	Val	Ala	Gln	Ala 270	Met	Lys
Ser	Glu	Gly 275	Gly	Phe	Ile	Trp	Ala 280	Cys	Lys	Asn	Tyr	Asp 285	Gly	Asp	Val
Gln	Ser 290	Asp	Ser	Val	Ala	Gln 295	Gly	Tyr	Gly	Ser	Leu 300	Gly	Met	Met	Thr
Ser 305	Val	Leu	Val	Cys	Pro 310	Asp	Gly	Lys	Thr	Val 315	Glu	Ala	Glu	Ala	Ala 320

00573305.122700

His	Gly	Thr	Val	Thr 325	Arg	His	Tyr	Arg	Met 330	Tyr	Gln	Lys	Gly	Gln 335	Glu
Thr	Ser	Thr	Asn 340	Pro	Ile	Ala	Ser	Ile 345	Phe	Ala	Trp	Thr	Arg 350	Gly	Leu
Ala	His	Arg 355	Ala	Lys	Leu	Asp	Asn 360	Asn	Lys	Glu	Leu	Ala 365	Phe	Phe	Ala
Asn	Ala 370	Leu	Glu	Glu	Val	Ser 375	Ile	Glu	Thr	Ile	Glu 380	Ala	Gly	Phe	Met
Thr 385	Lys	Asp	Leu	Ala	Ala 390	Cys	Ile	Lys	Gly	Leu 395	Pro	Asn	Val	Gln	Arg 400
Ser	Asp	Tyr	Leu	Asn 405	Thr	Phe	Glu	Phe	Met 410	Asp	Lys	Leu	Gly	Glu 415	Asn
Leu	Lys	Ile	Lys 420	Leu	Ala	Gln	Ala	Lys 425	Leu						

<210> 195  
 <211> 97  
 <212> PRT  
 <213> homo sapiens

<400> 195

Arg 1	Leu	Leu	Pro	Lys 5	His	Leu	Gln	Arg	Arg 10	Gln	Ala	Leu	Tyr	Cys 15	Tyr
Gln	Ala	Leu	Leu 20	Cys	Gly	Leu	Thr	Leu 25	Trp	Ser	Arg	Gln	Lys 30	Trp	Lys
Gln	Trp	Asp 35	Trp	Trp	Thr	Ser	Pro 40	Val	Leu	Ser	Gly	Thr 45	Cys	Gly	Ser
Asp	Gly 50	Leu	Gln	Ser	Arg	Gly 55	Gln	Pro	Leu	Leu	Leu 60	Leu	Ser	Cys	His
Leu 65	Asp	Lys	Pro	Ala	Arg 70	Trp	Ser	Ser	Cys	Arg 75	Glu	Ser	His	Thr	Leu 80
Gly	Pro	Gln	Ser	Pro 85	Thr	Ala	Arg	His	His 90	His	Ser	Phe	Tyr	Arg 95	Pro

Arg

<210> 196  
 <211> 93  
 <212> PRT  
 <213> homo sapiens

<400> 196

Leu 1	Ile	Leu	Ile	Ile 5	His	Pro	His	Gly	Asn 10	Thr	Thr	Thr	Phe	Phe 15	Lys
Val	Met	Tyr	Gln 20	Val	Cys	His	Leu	Leu 25	Gly	Ser	Val	Thr	Trp 30	Cys	Val
Gly	Tyr	Leu	Tyr	Phe	Ser	Arg	Pro	Arg	Asn	Asn	Lys	Ile	Ser	Cys	Ser

00673305-122700

35						40				45					
Val	Leu 50	Ile	Pro	Ile	Ser	Met 55	Thr	Thr	Tyr	Asp	Asp 60	Arg	Phe	Tyr	Pro
Ser 65	Thr	His	Lys	Pro	Gly 70	Asp	Ile	Phe	Ala	Asp 75	Asn	Gly	Phe	Ser	Glu 80
Asp	Arg	Ala	Thr	Gln 85	Asn	Ile	Ser	Tyr	Gly 90	Ala	Ile	Trp			

```
<210> 197
<211> 410
<212> PRT
<213> homo sapiens
```

&lt;400&gt; 197

Thr 1	Asp	Gln	Pro	Asn 5	Ile	Gln	Ser	Val	Lys 10	Ile	His	Ser	Leu	Pro 15	Leu
Arg	Asn	Pro	Asn 20	Lys	Gly	Cys	Glu	Cys 25	Pro	Pro	Arg	Arg	Asp 30	Gly	Phe
Gly	Phe	Ile 35	Lys	Cys	Val	Asp	Arg 40	Asp	Val	Arg	Met	Phe 45	Phe	His	Phe
Ser	Glu 50	Ile	Leu	Asp	Gly	Asn 55	Gln	Leu	His	Ile	Ala 60	Asp	Glu	Val	Glu
Phe 65	Thr	Val	Val	Pro	Asp 70	Met	Leu	Ser	Ala	Gln 75	Arg	Asn	His	Ala	Ile 80
Arg	Ile	Lys	Lys	Leu 85	Pro	Lys	Gly	Thr	Val 90	Ser	Phe	His	Ser	His 95	Ser
Asp	His	Arg	Phe 100	Leu	Gly	Thr	Val	Glu 105	Lys	Glu	Ala	Thr	Phe 110	Ser	Asn
Pro	Lys	Thr 115	Thr	Ser	Pro	Asn	Lys 120	Gly	Lys	Glu	Lys	Glu 125	Ala	Glu	Asp
Gly	Ile 130	Ile	Ala	Tyr	Asp	Asp 135	Cys	Gly	Val	Lys	Leu 140	Thr	Ile	Ala	Phe
Gln 145	Ala	Lys	Asp	Val	Glu 150	Gly	Ser	Thr	Ser	Pro 155	Gln	Ile	Gly	Asp	Lys 160
Val	Glu	Phe	Ser	Ile 165	Ser	Asp	Lys	Gln	Arg 170	Pro	Gly	Gln	Gln	Val 175	Ala
Thr	Cys	Val	Arg 180	Leu	Leu	Gly	Arg	Asn 185	Ser	Asn	Ser	Lys	Arg 190	Leu	Leu
Gly	Tyr	Val 195	Ala	Thr	Leu	Lys	Asp 200	Asn	Phe	Gly	Phe	Ile 205	Glu	Thr	Ala
Asn	His 210	Asp	Lys	Glu	Ile	Phe 215	Phe	His	Tyr	Ser	Glu 220	Phe	Ser	Gly	Asp
Val 225	Asp	Ser	Leu	Glu	Leu 230	Gly	Asp	Met	Val	Glu 235	Tyr	Ser	Leu	Ser	Lys 240

0367395-1300

Gly	Lys	Gly	Asn	Lys	Val	Ser	Ala	Glu	Lys	Val	Asn	Lys	Thr	His	Ser	
				245					250					255		
Val	Asn	Gly	Ile	Thr	Glu	Glu	Ala	Asp	Pro	Thr	Ile	Tyr	Ser	Gly	Lys	
			260					265					270			
Val	Ile	Arg	Pro	Leu	Arg	Ser	Val	Asp	Pro	Thr	Gln	Thr	Glu	Tyr	Gln	
		275					280					285				
Gly	Met	Ile	Glu	Ile	Val	Glu	Glu	Gly	Asp	Met	Lys	Gly	Glu	Val	Tyr	
	290					295					300					
Pro	Phe	Gly	Ile	Val	Gly	Met	Ala	Asn	Lys	Gly	Asp	Cys	Leu	Gln	Lys	
305					310					315					320	
Gly	Glu	Ser	Val	Lys	Phe	Gln	Leu	Cys	Val	Leu	Gly	Gln	Asn	Ala	Gln	
				325					330					335		
Thr	Met	Ala	Tyr	Asn	Ile	Thr	Pro	Leu	Arg	Arg	Ala	Thr	Val	Glu	Cys	
			340					345					350			
Val	Lys	Asp	Gln	Phe	Gly	Phe	Ile	Asn	Tyr	Glu	Val	Gly	Asp	Ser	Lys	
		355					360					365				
Lys	Leu	Phe	Phe	His	Val	Lys	Glu	Val	Gln	Asp	Gly	Ile	Glu	Leu	Gln	
	370					375					380					
Ala	Gly	Asp	Glu	Val	Glu	Phe	Ser	Val	Ile	Pro	Lys	Ser	Ser	Gly	Gly	
385					390					395					400	
Leu	Ala	Gly	Ser	Gly	Ala	Cys	Arg	Cys	Phe							
				405					410							

<210> 198  
 <211> 126  
 <212> PRT  
 <213> homo sapiens

<400> 198

Leu	Asn	Ala	Ile	Leu	Asn	Phe	Phe	His	Met	Glu	Lys	Glu	Leu	Leu	Ala	
1				5					10					15		
Ile	Ser	Tyr	Phe	Ile	Val	Asn	Glu	Ala	Lys	Leu	Ile	Phe	His	Thr	Phe	
			20					25					30			
His	Cys	Gly	Pro	Ala	Gln	Gly	Cys	Asp	Val	Val	Ser	His	Ser	Leu	Cys	
		35					40					45				
Ile	Leu	Ala	Gln	Asp	Thr	Gln	Leu	Glu	Leu	Asp	Ala	Leu	Pro	Phe	Leu	
	50					55					60					
Gln	Ala	Ile	Pro	Phe	Val	Gly	His	Pro	Asn	Asp	Ala	Lys	Trp	Ile	Asp	
65					70					75					80	
Leu	Thr	Phe	His	Ile	Ala	Leu	Leu	His	Asn	Leu	Asn	His	Ser	Leu	Val	
				85					90					95		
Leu	Ser	Leu	Cys	Trp	Ile	Asn	Thr	Pro	Gln	Gly	Ala	Asn	Tyr	Phe	Ala	
			100					105					110			
Arg	Val	Asn	Gly	Gly	Ile	Ser	Phe	Leu	Ser	Asn	Ala	Ile	His			
		115					120					125				

09573395.122700

<210> 199  
 <211> 85  
 <212> PRT  
 <213> homo sapiens

<400> 199

Lys	Ser	His	Thr	Ser	Cys	Asn	Leu	Leu	Ser	Arg	Pro	Leu	Phe	Val	Thr
1				5					10					15	
Asn	Thr	Lys	Phe	Asn	Leu	Ile	Ser	Tyr	Leu	Arg	Arg	Ser	Arg	Ser	Phe
			20					25					30		
His	Ile	Leu	Gly	Leu	Lys	Ser	Asn	Ser	Gln	Phe	His	Pro	Thr	Val	Ile
		35					40					45			
Ile	Ser	Asn	Asn	Ala	Ile	Leu	Ser	Leu	Leu	Leu	Phe	Ala	Phe	Ile	Trp
	50					55					60				
Ala	Ser	Gly	Phe	Arg	Ile	Gly	Lys	Ser	Gly	Phe	Phe	Phe	Tyr	Arg	Ala
65					70					75					80
Gln	Lys	Thr	Val	Ile											
				85											

<210> 200  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 200

Ala	Thr	Met	Arg	Leu	Ser	Val	Cys	Leu	Leu	Met	Val	Ser	Leu	Ala	Leu
1				5					10					15	
Cys	Cys	Tyr	Gln	Ala	His	Ala	Leu	Val	Cys	Pro	Ala	Val	Ala	Ser	Glu
			20					25					30		
Ile	Thr	Val	Phe	Leu	Phe	Leu	Ser	Asp	Ala	Ala	Val	Asn	Leu	Gln	Val
		35					40					45			
Ala	Lys	Leu	Asn	Pro	Pro	Pro	Glu	Ala	Leu	Ala	Ala	Lys	Leu	Glu	Val
	50					55					60				
Lys	His	Cys	Thr	Asp	Gln	Ile	Ser	Phe	Lys	Lys	Arg	Leu	Leu	Ile	
65					70					75					

<210> 201  
 <211> 50  
 <212> PRT  
 <213> homo sapiens

<400> 201

Ser	Val	Gln	Cys	Phe	Thr	Ser	Asn	Leu	Ala	Ala	Arg	Ala	Ser	Gly	Gly
1				5					10					15	
Gly	Leu	Ser	Leu	Ala	Thr	Trp	Arg	Phe	Thr	Ala	Ala	Ser	Leu	Lys	Asn
			20					25					30		
Lys	Lys	Thr	Val	Ile	Ser	Glu	Ala	Thr	Ala	Gly	Gln	Thr	Arg	Ala	Trp
		35					40					45			

00673305.722700

Ala Trp  
50

<210> 202  
<211> 72  
<212> PRT  
<213> homo sapiens

<400> 202

Gln	Val	Ala	Val	Glu	Lys	Thr	Leu	Glu	Thr	Gln	Val	Glu	His	Phe	Tyr
1				5					10					15	
Met	Ser	His	Thr	His	Ile	Phe	Ser	Leu	Phe	Pro	Pro	Arg	Thr	Phe	Ser
			20					25					30		
Asn	Glu	Lys	Pro	Phe	Leu	Lys	Arg	Tyr	Leu	Ile	Gly	Ala	Val	Leu	His
		35					40					45			
Phe	Gln	Leu	Gly	Cys	Lys	Ser	Phe	Trp	Arg	Trp	Ile	Lys	Phe	Gly	Asn
	50					55					60				
Leu	Glu	Val	Tyr	Arg	Ser	Val	Thr								
65					70										

<210> 203  
<211> 53  
<212> PRT  
<213> homo sapiens

<400> 203

Ser	Phe	Ser	Pro	Ser	Leu	Thr	Thr	Arg	Ala	Met	Asn	Ser	Ser	Ala	Ser
1				5					10					15	
Ser	Thr	Ser	Thr	Cys	Ser	Ser	Tyr	Thr	Leu	Gly	Thr	Arg	Leu	Pro	Val
			20					25					30		
Gly	Gly	Arg	Gly	Pro	Thr	Lys	Val	Thr	Cys	Cys	Thr	Ser	Asn	Arg	Leu
		35					40					45			
Thr	Leu	Ser	Leu	Asp											
	50														

<210> 204  
<211> 121  
<212> PRT  
<213> homo sapiens

<400> 204

Ala	Leu	Val	Val	Arg	Phe	Leu	Thr	Lys	Arg	Phe	Ile	Gly	Asp	Tyr	Glu
1				5					10					15	
Arg	Asn	Ala	Gly	Asn	Leu	Tyr	Thr	Arg	Gln	Val	Gln	Ile	Glu	Gly	Glu
			20					25					30		
Thr	Leu	Ala	Leu	Gln	Val	Gln	Asp	Thr	Pro	Gly	Ile	Gln	Val	His	Glu
		35					40					45			
Asn	Ser	Leu	Ser	Cys	Ser	Glu	Gln	Leu	Asn	Arg	Cys	Ile	Arg	Trp	Ala
	50					55					60				

00573305.122700



Asp 65	Ala	Val	Val	Ile	Val 70	Phe	Ser	Ile	Thr	Asp 75	Tyr	Lys	Ser	Tyr	Glu 80
Leu	Ile	Ser	Gln	Leu 85	His	Gln	His	Val	Gln 90	Gln	Leu	His	Leu	Gly 95	His
Pro	Ala	Ala	Cys 100	Gly	Trp	Ser	Trp	Ala 105	Asn	Lys	Ser	Asp	Leu 110	Leu	His
Ile	Lys	Gln 115	Val	Asp	Pro	Gln	Leu 120	Gly							

<210> 205  
 <211> 205  
 <212> PRT  
 <213> homo sapiens

<400> 205

Gly 1	Pro	Leu	Pro	Ala 5	Leu	Ala	Ala	Gly	Ser 10	Thr	Phe	Pro	Val	Leu 15	Ala
Cys	Ser	Ser	Ala 20	Met	Ala	Pro	Lys	Gly 25	Ser	Ser	Lys	Gln	Gln 30	Ser	Glu
Glu	Asp	Leu 35	Leu	Leu	Gln	Asp	Phe 40	Ser	Arg	Asn	Leu	Ser 45	Ala	Lys	Ser
Ser	Ala 50	Leu	Phe	Phe	Gly	Asn 55	Ala	Phe	Ile	Val	Ser 60	Ala	Ile	Pro	Ile
Trp 65	Leu	Tyr	Trp	Arg	Ile 70	Trp	His	Met	Asp	Leu 75	Ile	Gln	Ser	Ala	Val 80
Leu	Tyr	Ser	Val	Met 85	Thr	Leu	Val	Ser	Thr 90	Tyr	Leu	Val	Ala	Phe 95	Ala
Tyr	Lys	Asn 100	Val	Lys	Phe	Val	Leu	Lys 105	His	Lys	Val	Ala	Gln 110	Lys	Arg
Glu	Asp	Ala 115	Val	Ser	Lys	Glu	Val 120	Thr	Arg	Lys	Leu	Ser 125	Glu	Ala	Asp
Asn	Arg 130	Lys	Met	Ser	Arg	Lys 135	Glu	Lys	Asp	Glu	Arg 140	Ile	Leu	Trp	Lys
Lys 145	Asn	Glu	Val	Ala	Asp 150	Tyr	Glu	Ala	Thr	Thr 155	Phe	Ser	Ile	Phe	Tyr 160
Asn	Asn	Thr	Leu	Phe 165	Leu	Val	Val	Val	Ile 170	Val	Ala	Ser	Phe	Phe 175	Ile
Leu	Lys	Asn	Phe 180	Asn	Pro	Thr	Val	Asn 185	Tyr	Ile	Leu	Ser	Ile 190	Ser	Ala
Ser	Ser	Gly 195	Leu	Ile	Ala	Leu	Leu 200	Ser	Thr	Gly	Ser	Lys 205			

<210> 206  
 <211> 106  
 <212> PRT  
 <213> homo sapiens

00673395.122700

<400> 206

Val 1	Leu	His	Gln	Asp 5	Ser	Ser	Pro	Ser	Cys 10	Leu	Leu	Ala	Pro	Asn 15	Arg	
Pro	Cys	Gln	Leu 20	His	Pro	Leu	Ala	Leu 25	Cys	Leu	Trp	Val	Ala 30	Cys	Gly	
Ile	Trp	Lys 35	Ser	Ser	Arg	Val	Val 40	Arg	Val	Gly	Asp	Thr 45	Arg	Cys	Phe	
Tyr	Ser 50	Leu	Glu	Pro	Leu	Lys 55	Asn	Pro	Ala	Glu	Cys 60	Asn	Ser	Val	Phe	
Val 65	Tyr	Trp	Leu	Phe	Phe 70	Asp	Arg	Leu	Leu	Lys 75	Leu	Asn	Glu	Leu	Lys 80	
Gly	Lys	Leu	Arg	Val 85	Leu	Gly	Arg	Leu	Leu 90	Lys	Gly	Lys	Lys	Cys 95	Leu	
Ala	Met	Cys	Cys 100	Asn	His	Lys	Arg	Arg 105	Lys							

<210> 207

<211> 105

<212> PRT

<213> homo sapiens

<400> 207

Ser 1	Thr	Tyr	Gly	Gln 5	Tyr	Val	Val	His	Cys 10	Gly	Val	Glu	Val	Leu 15	Gln	
Tyr	Glu	Glu	Gly 20	Ser	Asn	Asn	Asp	His 25	Asp	Gln	Glu	Gln	Ser 30	Val	Val	
Ile	Glu	Asp 35	Gly	Lys	Cys	Cys	Ser 40	Phe	Ile	Ile	Ser	Asn 45	Phe	Ile	Leu	
Leu 50	Pro	Gln	Asp	Ser	Phe	Ile 55	Phe	Leu	Leu	Pro	Arg 60	His	Leu	Ser	Ile	
Ile 65	Ser	Phe	Arg	Lys	Phe 70	Ser	Ser	His	Phe	Phe 75	Gly	Asn	Ser	Ile	Leu 80	
Pro	Leu	Leu	Cys 85	Tyr	Phe	Val	Leu	Glu	Asn 90	Lys	Phe	His	Ile	Leu 95	Val	
Cys	Lys	Gly	Tyr 100	Gln	Ile	Cys	Ala	Tyr 105								

<210> 208

<211> 549

<212> PRT

<213> homo sapiens

<400> 208

Leu 1	Tyr	Pro	Asn	Phe 5	Leu	Val	Asn	Glu	Leu 10	Ile	Leu	Lys	Gln	Lys 15	Gln	
Arg	Phe	Glu	Glu	Lys	Arg	Phe	Lys	Leu	Asp	His	Ser	Val	Ser	Ser	Thr	

09673395.122700

20								25					30				
Asn	Gly	His 35	Arg	Trp	Gln	Ile	Phe 40	Gln	Asp	Trp	Leu	Gly 45	Thr	Asp	Gln		
Asp	Asn 50	Leu	Asp	Leu	Ala	Asn 55	Val	Asn	Leu	Met	Leu 60	Glu	Leu	Leu	Val		
Gln 65	Lys	Lys	Lys	Gln	Leu 70	Glu	Ala	Glu	Ser	His 75	Ala	Ala	Gln	Leu	Gln 80		
Ile	Leu	Met	Glu	Phe 85	Leu	Lys	Val	Ala	Arg 90	Arg	Asn	Lys	Arg	Glu 95	Gln		
Leu	Glu	Gln	Ile 100	Gln	Lys	Glu	Leu	Ser 105	Val	Leu	Glu	Glu	Asp 110	Ile	Lys		
Arg	Val	Glu 115	Glu	Met	Ser	Gly	Leu 120	Tyr	Ser	Pro	Val	Ser 125	Glu	Asp	Ser		
Thr	Val 130	Pro	Gln	Phe	Glu	Ala 135	Pro	Ser	Pro	Ser	His 140	Ser	Ser	Ile	Ile		
Asp 145	Ser	Thr	Glu	Tyr	Ser 150	Gln	Pro	Pro	Gly	Phe 155	Ser	Gly	Ser	Ser	Gln 160		
Thr	Lys	Lys	Gln	Pro 165	Trp	Tyr	Asn	Ser	Thr 170	Leu	Ala	Ser	Arg	Arg 175	Lys		
Arg	Leu	Thr	Ala 180	His	Phe	Glu	Asp	Leu 185	Glu	Gln	Cys	Tyr	Phe 190	Ser	Thr		
Arg	Met	Ser 195	Arg	Ile	Ser	Asp	Asp 200	Ser	Arg	Thr	Ala	Ser 205	Gln	Leu	Asp		
Glu	Phe 210	Gln	Glu	Cys	Leu	Ser 215	Lys	Phe	Thr	Arg	Tyr 220	Asn	Ser	Val	Arg		
Pro 225	Leu	Ala	Thr	Leu	Ser 230	Tyr	Ala	Ser	Asp	Leu 235	Tyr	Asn	Gly	Ser	Ser 240		
Ile	Val	Ser	Ser	Ile 245	Glu	Phe	Asp	Arg	Asp 250	Cys	Asp	Tyr	Phe	Ala 255	Ile		
Ala	Gly	Val	Thr 260	Lys	Lys	Ile	Lys	Val 265	Tyr	Glu	Tyr	Asp	Thr 270	Val	Ile		
Gln	Asp	Ala 275	Val	Asp	Ile	His	Tyr 280	Pro	Glu	Asn	Glu	Met 285	Thr	Cys	Asn		
Ser	Lys 290	Ile	Ser	Cys	Ile	Ser 295	Trp	Ser	Ser	Tyr	His 300	Lys	Asn	Leu	Leu		
Ala 305	Ser	Ser	Asp	Tyr	Glu 310	Gly	Thr	Val	Ile	Leu 315	Trp	Asp	Gly	Phe	Thr 320		
Gly	Gln	Arg	Ser	Lys 325	Val	Tyr	Gln	Glu	His 330	Glu	Lys	Arg	Cys	Trp 335	Ser		
Val	Asp	Phe	Asn 340	Leu	Met	Asp	Pro	Lys 345	Leu	Leu	Ala	Ser	Gly 350	Ser	Asp		
Asp	Ala	Lys	Val	Lys	Leu	Trp	Ser	Thr	Asn	Leu	Asp	Asn	Ser	Val	Ala		



<210> 210  
 <211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 210

Phe	Pro	Ser	Ser	Leu	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Cys
1				5				10						15	
Gly	Ser	Ile	Asn	Phe	Tyr	Cys	Phe	Val	Ile	Tyr	Phe	Tyr	Ser	Lys	Glu
			20					25					30		
Phe	Val	Ser	Leu	Ser	Gln	Lys	Leu	Asp	Asn	Thr	Thr	Lys	Ser	Ser	Asn
		35					40					45			
Val	His	Gly	Val	Thr	Leu	Met	Val	Glu	Ser	Trp	Leu	Gly	Ile	Pro	Asn
	50					55					60				
Val	Pro	Lys	Val	Ile	Lys	Glu	Gly	Lys	Glu	Lys	Lys	Lys	Lys	Ile	Phe
65					70					75					80
Lys	Thr	Asn	Pro	Lys	Pro	Met	Met	Thr	Leu	Gly	Arg	Asp	Ile	Thr	
				85					90					95	

<210> 211  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 211

Lys	Lys	Met	Val	Arg	Leu	Gly	Leu	Phe	Ser	Cys	Leu	Leu	Ala	Ile	Tyr
1				5					10					15	
Ser	Leu	Leu	Trp	Ile	Val	Cys	Ile	Pro	Tyr	Leu	Leu	Ser	Ile	Gly	Leu
			20					25					30		
Cys	Val	Asp	Ile	Leu	Phe	Leu	Phe	Val	Gln	His	Leu	Leu	Pro	His	Leu
		35					40					45			
Leu	Val	Thr	Gln	Pro	Leu	Phe	Ile	Cys	Gly	Glu	Pro	Ile	Pro	Cys	Gly
	50					55					60				
Leu	Gly	Glu	His	Val	Thr	Arg	Pro	Gly	Leu	Leu	Ser	Pro	Thr	Ala	Ser
65					70					75					80

<210> 212  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 212

Leu	Lys	Lys	Gly	Lys	Trp	Ala	Lys	Ala	Ile	His	Asn	Arg	Lys	Cys	Lys
1				5					10					15	
Trp	Pro	Arg	Asn	Met	Lys	Arg	Cys	Ser	Ser	Ser	Leu	Ile	Phe	Lys	Glu
			20					25					30		
Lys	Lys	Glu	Ile	Leu	Pro	Thr	Arg	Leu	Ala	Lys	Ile	Phe	Lys	Asp	Ser
		35					40					45			

006733085 122700

Gly Leu Ala Asp Tyr Arg Gln Thr Gly Ile Leu Thr Asn Asp Gly Val  
50 55 60

Val Asn Trp  
65

<210> 213  
<211> 78  
<212> PRT  
<213> homo sapiens

<400> 213

Ser	Pro	Glu	Val	Gly	Gln	Ala	Leu	Gly	Thr	Ala	Gly	Ser	Arg	Ala	Ser
1				5					10					15	
Arg	Lys	Met	Thr	Ser	Glu	Leu	Ser	Ser	Leu	Ser	Ile	Ser	Ala	Ser	Ile
			20					25					30		
Arg	Val	Ser	Pro	Gln	Thr	Asp	Ser	Leu	His	Met	Ala	Gln	Ile	Gln	Ala
		35					40					45			
Tyr	Met	Val	Leu	Gly	Ser	Trp	Asp	Leu	His	Lys	Ala	Phe	Phe	Pro	Val
	50					55					60				
Val	Pro	Ala	Glu	Val	Leu	Leu	Arg	Ala	Phe	Leu	Ser	Leu	Ala		
65					70					75					

<210> 214  
<211> 105  
<212> PRT  
<213> homo sapiens

<400> 214

Gln	Ala	Gly	Lys	Arg	Ala	Leu	Tyr	Lys	His	Thr	Gln	Thr	Asn	Thr	Ser
1				5					10					15	
Gly	Asp	Gly	Cys	Val	Leu	Leu	Glu	Gln	Arg	Leu	Ile	Lys	His	Ser	Val
			20					25					30		
Cys	Trp	Leu	Ser	Val	Pro	Leu	Leu	Glu	Asn	Asn	Glu	Leu	Gly	Lys	Glu
		35					40					45			
Gln	Leu	Ile	Arg	Lys	Cys	Ala	Leu	Leu	Thr	Val	His	Ile	Thr	Thr	Lys
	50					55					60				
Ser	Trp	Gln	Leu	Leu	Lys	Glu	Lys	Gly	Leu	Cys	Arg	Cys	Arg	Ser	Asn
65					70					75				80	
Leu	Ser	Val	Asn	Ser	Cys	Gln	Gln	Pro	Gln	Arg	Leu	Pro	Pro	Gln	His
			85						90					95	
Thr	Leu	Ile	Thr	Cys	Val	Cys	Leu	Ala							
			100					105							

<210> 215  
<211> 216  
<212> PRT  
<213> homo sapiens

<400> 215

00673395.122700

Leu 1	Ser	Leu	Thr	Ser 5	Arg	Met	Glu	Glu	Ala 10	Glu	Leu	Val	Lys	Gly 15	Arg
Leu	Gln	Ala	Ile 20	Thr	Asp	Lys	Arg	Lys 25	Ile	Gln	Glu	Glu	Ile 30	Ser	Gln
Lys	Arg	Leu 35	Lys	Ile	Glu	Glu	Asp 40	Lys	Leu	Lys	His	Gln 45	His	Leu	Lys
Lys	Lys 50	Ala	Leu	Arg	Glu	Lys 55	Trp	Leu	Leu	Asp	Gly 60	Ile	Ser	Ser	Gly
Lys 65	Glu	Gln	Glu	Glu	Met 70	Lys	Lys	Gln	Asn	Gln 75	Gln	Asp	Gln	His	Gln 80
Ile	Gln	Val	Leu	Glu 85	Gln	Ser	Ile	Leu	Arg 90	Leu	Glu	Lys	Glu	Ile 95	Gln
Asp	Leu	Glu	Lys 100	Ala	Glu	Leu	Gln	Ile 105	Ser	Thr	Lys	Glu	Glu 110	Ala	Ile
Leu	Lys	Lys 115	Leu	Lys	Ser	Ile	Glu 120	Arg	Thr	Thr	Glu	Asp 125	Ile	Ile	Arg
Ser	Val 130	Lys	Val	Glu	Arg	Glu 135	Glu	Arg	Ala	Glu	Glu 140	Ser	Ile	Glu	Asp
Ile 145	Tyr	Ala	Asn	Ile	Pro 150	Asp	Leu	Pro	Lys	Ser 155	Tyr	Ile	Pro	Ser	Arg 160
Leu	Arg	Lys	Glu	Ile 165	Asn	Glu	Glu	Lys	Glu 170	Asp	Asp	Glu	Gln	Asn 175	Arg
Lys	Ala	Leu	Tyr 180	Ala	Met	Glu	Ile	Lys 185	Val	Glu	Lys	Asp	Leu 190	Arg	Thr
Gly	Glu	Ser 195	Thr	Val	Leu	Ser	Ser 200	Ile	Pro	Leu	Pro	Ser 205	Asp	Asp	Phe
Lys	Arg 210	Ser	Arg	Ser	Lys	Ser 215	Leu								

<210> 216  
 <211> 112  
 <212> PRT  
 <213> homo sapiens

<400> 216

Phe 1	Cys	Phe	Phe	Ile 5	Ser	Ser	Cys	Ser	Phe 10	Pro	Leu	Leu	Ile	Pro 15	Ser
Arg	Ser	His	Phe 20	Ser	Leu	Lys	Ala	Phe 25	Phe	Phe	Lys	Cys	Trp 30	Cys	Phe
Ser	Leu	Ser 35	Ser	Ser	Ile	Phe	Arg 40	Arg	Phe	Cys	Glu	Ile 45	Ser	Ser	Cys
Ile	Phe 50	Leu	Leu	Ser	Val	Met 55	Ala	Trp	Ser	Leu	Pro 60	Phe	Thr	Ser	Ser
Ala 65	Ser	Ser	Ile	Leu	Glu 70	Val	Lys	Asp	Ser	Gln 75	Thr	Gly	Lys	Gln	Val 80

00673395.122700

Gln	Ser	Tyr	His	Lys 85	Ser	Arg	Ser	Leu	Leu 90	Gly	Glu	Arg	Ser	Gly 95	Gly
Asp	Arg	Arg	Glu 100	Ala	Gly	Arg	Asn	Pro 105	Leu	Phe	Ala	Pro	Val 110	Glu	Lys

<210> 217

<211> 339

<212> PRT

<213> homo sapiens

<400> 217

Ser 1	Ser	Gln	Leu	Arg 5	Arg	Arg	Leu	Val	Pro 10	Ala	Pro	Ala	Ala	Pro 15	Arg
Pro	Arg	Pro	Asn 20	His	Gly	Val	Leu	Arg 25	Gly	Arg	Leu	Arg	Gly 30	Asp	Arg
Trp	Gln	Trp 35	Ser	His	Trp	Ala	Lys 40	Trp	Ala	Met	Leu	Phe 45	Ala	Ser	Gly
Gly	Phe 50	Gln	Val	Lys	Leu	Tyr 55	Asp	Ile	Glu	Gln	Gln 60	Gln	Ile	Arg	Asn
Ala 65	Leu	Glu	Asn	Ile	Arg 70	Lys	Glu	Met	Lys	Leu 75	Leu	Glu	Gln	Ala	Gly 80
Ser	Leu	Lys	Gly	Ser 85	Leu	Ser	Val	Glu	Glu 90	Gln	Leu	Ser	Leu	Ile 95	Ser
Gly	Cys	Pro	Asn 100	Ile	Gln	Glu	Ala	Val 105	Glu	Gly	Ala	Met	His 110	Ile	Gln
Glu	Cys	Val 115	Pro	Glu	Asp	Leu	Glu 120	Leu	Lys	Lys	Lys	Ile 125	Phe	Ala	Gln
Leu	Asp 130	Ser	Ile	Ile	Asp	Asp 135	Arg	Val	Ile	Leu	Ser 140	Ser	Ser	Thr	Ser
Cys 145	Leu	Met	Pro	Ser	Lys 150	Leu	Phe	Ala	Gly	Leu 155	Val	His	Val	Lys	Gln 160
Cys	Ile	Val	Ala	His 165	Pro	Val	Asn	Pro	Pro 170	Tyr	Tyr	Ile	Pro	Leu 175	Val
Glu	Leu	Val	Pro 180	His	Pro	Glu	Thr	Ala 185	Pro	Thr	Thr	Val	Asp 190	Arg	Thr
His	Ala	Leu 195	Met	Lys	Lys	Ile	Gly 200	Gln	Cys	Pro	Met	Arg 205	Val	Gln	Lys
Glu	Val 210	Ala	Gly	Phe	Val	Leu 215	Asn	Arg	Leu	Gln	Tyr 220	Ala	Ile	Ile	Ser
Glu 225	Ala	Trp	Arg	Leu	Val 230	Glu	Glu	Gly	Ile	Val 235	Ser	Pro	Ser	Asp	Leu 240
Asp	Leu	Val	Met	Ser 245	Glu	Gly	Leu	Gly	Met 250	Arg	Tyr	Ala	Phe	Ile 255	Gly
Pro	Leu	Glu	Thr	Met	His	Leu	Asn	Ala	Glu	Gly	Met	Leu	Ser	Tyr	Cys

00673305-122700



			260					265				270					
Asp	Arg	Tyr	Ser	Glu	Gly	Ile	Lys	His	Val	Leu	Gln	Thr	Phe	Gly	Pro		
		275					280					285					
Ile	Pro	Glu	Phe	Ser	Arg	Ala	Thr	Ala	Glu	Lys	Val	Asn	Gln	Asp	Met		
	290					295					300						
Cys	Met	Lys	Val	Pro	Asp	Asp	Pro	Glu	His	Leu	Ala	Ala	Arg	Arg	Gln		
	305				310					315					320		
Trp	Arg	Asp	Glu	Cys	Leu	Met	Arg	Leu	Ala	Lys	Leu	Lys	Ser	Gln	Val		
				325					330					335			
Gln	Pro	Gln															

<210> 218

<211> 109

<212> PRT

<213> homo sapiens

<400> 218

Lys	Asp	Pro	Gln	Ile	Thr	Gln	Lys	Gly	Ile	Thr	Lys	Ile	Ile	Thr	Lys		
1				5					10					15			
Ile	Phe	Cys	Pro	His	Ile	Asn	Met	Lys	Thr	Thr	Ile	Thr	Gly	Cys	Gln		
			20					25					30				
Ile	Ile	Leu	Lys	Cys	Asn	Gln	Ala	Glu	Lys	Glu	Lys	Val	Lys	Ile	Ser		
		35					40					45					
Arg	Leu	Ser	Ala	Gln	Val	Ala	Gly	Asn	Arg	Gln	Pro	Arg	Glu	Arg	Lys		
	50					55					60						
Cys	Cys	Cys	Ala	Ala	Arg	Pro	Arg	Ala	Met	Ile	Gln	Ser	Asp	Gly	Gln		
	65				70					75					80		
Thr	Thr	Gly	Leu	His	His	Pro	Thr	Gln	Ala	Ala	His	Lys	Thr	Ala	Ser		
				85					90					95			
Leu	Gly	Ser	Pro	Trp	Ala	Ala	Thr	Tyr	Val	Thr	Glu	Gly					
			100					105									

<210> 219

<211> 98

<212> PRT

<213> homo sapiens

<400> 219

Leu	Asn	Ile	Pro	Ser	Ala	Leu	Arg	Cys	Met	Val	Ser	Arg	Gly	Pro	Met		
1				5					10					15			
Asn	Ala	Tyr	Arg	Met	Pro	Asn	Pro	Ser	Asp	Met	Thr	Arg	Ser	Arg	Ser		
			20					25					30				
Leu	Gly	Asp	Thr	Ile	Pro	Ser	Ser	Thr	Ser	Arg	Gln	Ala	Ser	Leu	Met		
		35				40					45						
Ile	Ala	Tyr	Cys	Arg	Arg	Phe	Arg	Thr	Lys	Pro	Ala	Thr	Ser	Phe	Trp		
	50					55					60						

00573305-122700

Thr 65	Arg	Met	Gly	His	Cys 70	Pro	Ile	Phe	Phe	Ile 75	Arg	Ala	Trp	Val	Leu 80
Ser	Thr	Val	Val	Gly 85	Ala	Val	Ser	Gly	Trp 90	Gly	Thr	Ser	Ser	Thr 95	Ser

Gly Met

<210> 220  
 <211> 129  
 <212> PRT  
 <213> homo sapiens

<400> 220

Thr 1	Met	Phe	Phe	Thr 5	Cys	Gly	Pro	Asn	Glu 10	Ala	Met	Val	Val	Ser 15	Gly
Phe	Cys	Arg	Ser 20	Pro	Pro	Val	Met	Val 25	Ala	Gly	Gly	Arg	Val 30	Phe	Val
Leu	Pro	Cys 35	Ile	Gln	Gln	Ile	Gln 40	Arg	Ile	Ser	Leu	Asn 45	Thr	Leu	Thr
Leu	Asn 50	Val	Lys	Ser	Glu	Lys 55	Val	Tyr	Thr	Arg	His 60	Gly	Val	Pro	Ile
Ser 65	Val	Thr	Gly	Ile	Ala 70	Gln	Val	Lys	Leu	Ser 75	Glu	Pro	Phe	Pro	His 80
Ser	Pro	Leu	Pro	His 85	His	Pro	Leu	Ser	Gln 90	Thr	Leu	Arg	His	Leu 95	Leu
Ala	Thr	Val	Phe 100	Ser	Thr	Leu	Ala	Cys 105	Arg	Glu	Val	Pro	Leu 110	Leu	Val
Ser	Ser	Phe 115	Pro	Gly	Thr	Pro	Arg 120	His	Leu	Pro	Pro	Pro 125	Pro	Phe	Phe

Pro

<210> 221  
 <211> 118  
 <212> PRT  
 <213> homo sapiens

<400> 221

Asp 1	Gly	Asp	Pro	Met 5	Ala	Ser	Val	Asn	Leu 10	Phe	Thr	Leu	Asp	Ile 15	Glu
Gly	Gln	Cys 20	Val	Glu	Arg	Asp	Pro	Leu 25	Asp	Leu	Leu	Asp	Ala 30	Gly	Gln
Asp	Lys	Asp 35	Thr	Pro	Ser	Ser	His 40	His	Asp	Trp	Gly	Ala 45	Ser	Ala	Glu
Pro	Gly 50	Asp	His	His	Gly	Leu 55	Ile	Trp	Ala	Thr	Ser 60	Glu	Lys	His	Gly
Ser 65	Gly	Trp	Ser	Phe	Arg 70	Asp	Ala	Gly	Gly	Ser 75	Pro	Ala	Gly	Val	Ser 80

00573305-122700

Gly	Arg	Ala	Gly	Ser 85	Arg	Arg	Asp	Leu	Gly 90	Ala	Gly	Gln	Gly	Pro 95	Leu
Ala	Asp	Gln	Leu 100	Ser	Trp	Glu	Leu	Ala 105	Pro	Ser	Arg	Val	Pro 110	His	Pro
Ala	Ala	Pro 115	Arg	Cys	Cys										

<210> 222  
 <211> 119  
 <212> PRT  
 <213> homo sapiens

<400> 222

Trp 1	Pro	Ser	Gly	Gly 5	Pro	Leu	Thr	Ser	Pro 10	Gly	Gln	Cys	Gly	Gln 15	Ser
Gln	Pro	Pro	Ser 20	Ser	Pro	Ala	Thr	Ser 25	Asp	Arg	Arg	Pro	Pro 30	Thr	Ser
Pro	Cys	Ser 35	Ala	Pro	Gly	Phe	Leu 40	Pro	Val	Ala	Arg	Val 45	Gly	Val	Gly
Lys	Val 50	Trp	Trp	Gly	Ser	His 55	Glu	Val	Arg	Gly	Lys 60	Ala	Glu	Arg	Glu
Gly 65	Arg	Ala	Leu	Ser	Glu 70	Met	Leu	Leu	Pro	Phe 75	Gln	Gly	Lys	Lys	Gly 80
Gly	Gly	Gly	Lys	Cys 85	Leu	Gly	Val	Pro	Gly 90	Lys	Asp	Glu	Thr	Ser 95	Arg
Gly	Thr	Ser	Leu 100	Gln	Ala	Arg	Val	Glu 105	Lys	Thr	Val	Ala	Arg 110	Arg	Cys
Leu	Asn	Val 115	Trp	Glu	Arg	Gly									

<210> 223  
 <211> 93  
 <212> PRT  
 <213> homo sapiens

<400> 223

Gly 1	Arg	Arg	Thr	Leu 5	Phe	Leu	Ala	Thr	Phe 10	Gly	Gly	Tyr	Pro	Gly 15	Ser
Leu	Gly	Cys	Ser 20	Leu	Ser	Gly	Glu	Ala 25	Asn	Ile	Ser	Leu	Val 30	Ser	Phe
Phe	His	Pro 35	Leu	Asn	Cys	Lys	Leu 40	Arg	Ile	Thr	Gln	Ala 45	His	His	Tyr
Ser	Arg 50	Leu	Gly	Leu	Ala	Ser 55	Gln	Ser	Thr	Leu	Cys 60	Pro	Ala	Cys	His
Cys 65	Cys	Lys	Glu	Leu	Leu 70	Leu	Cys	Gln	Pro	Lys 75	Gln	Arg	Lys	Tyr	Gly 80
Phe	Ser	Cys	Ile	Ile	Phe	Pro	Phe	Gly	Trp	Phe	Val	Phe			

00673305.1.22700

<210> 224  
 <211> 94  
 <212> PRT  
 <213> homo sapiens

<400> 224

Asn	Leu	Ile	Tyr	Pro	Asn	Ser	Ser	Met	Tyr	Ser	Asp	Thr	Phe	Ser	Glu
1				5					10					15	
Lys	Ala	Arg	Ile	Gly	Ala	Val	Leu	Ser	Ile	Lys	Gly	Lys	Ser	Ser	
			20				25					30			
Asp	His	Leu	His	Tyr	Asn	Phe	Leu	Cys	Leu	Phe	Ser	Ala	Gly	Glu	Glu
		35					40					45			
Ile	His	Ile	Tyr	Ser	Thr	Pro	His	Trp	Thr	Leu	Gln	Asn	Ala	Cys	Ile
	50					55					60				
Phe	Cys	Pro	Ser	Ala	Ile	Cys	Ser	Leu	Pro	Phe	Cys	Leu	Leu	Lys	Glu
65					70					75					80
Leu	Ser	Asn	Ile	Val	Phe	Pro	Lys	Met	Phe	Ser	Thr	Gly	His		
				85					90						

<210> 225  
 <211> 92  
 <212> PRT  
 <213> homo sapiens

<400> 225

Gly	His	His	Met	His	Ile	Leu	Asp	Arg	Phe	Cys	Thr	Ala	Gln	Leu	Glu
1				5					10					15	
Trp	Val	Pro	Val	Thr	Trp	Thr	Gly	Val	Gln	Tyr	Thr	Ile	Cys	Val	Gln
			20					25					30		
Tyr	Arg	Lys	Pro	Ser	Ser	Ala	Val	Ala	Arg	Glu	Leu	Tyr	Ser	Asn	Ser
		35					40				45				
Leu	Ser	Ala	Gln	Ala	Asn	Gln	Val	Arg	Lys	Thr	Ala	Ile	Trp	Leu	Glu
	50					55					60				
Asp	Phe	Gln	Glu	Thr	Ala	Val	Pro	Val	Arg	Gly	Arg	Tyr	Tyr	Leu	Arg
65					70					75					80
Gly	Gly	Arg	Gly	Thr	Asp	Ile	Lys	Gln	Glu	Gly	Phe				
				85					90						

<210> 226  
 <211> 458  
 <212> PRT  
 <213> homo sapiens

<400> 226

Arg	Gly	Lys	Arg	Arg	His	Arg	Leu	Pro	Ala	Leu	Pro	Pro	Arg	Leu	
1				5				10					15		
Leu	Ser	Pro	Ser	Ala	Ala	Thr	Met	Ser	Ala	Ser	Ala	Val	Phe	Ile	Leu

00673395.122700

			20						25						30					
Asp	Val	Lys 35	Gly	Lys	Pro	Leu	Ile 40	Ser	Arg	Asn	Tyr	Lys 45	Gly	Asp	Val					
Ala	Met 50	Ser	Lys	Ile	Glu	His 55	Phe	Met	Pro	Leu	Leu 60	Val	His	Gly	Glu					
Glu 65	Glu	Gly	Ala	Leu	Ala 70	Pro	Leu	Leu	Ser	His 75	Gly	Gln	Val	His	Phe 80					
Leu	Trp	Ile	Lys	His 85	Ser	Asn	Leu	Tyr	Leu 90	Val	Ala	Thr	Thr	Ser 95	Lys					
Asn	Ala	Asn	Ala 100	Ser	Leu	Val	Tyr	Ser 105	Phe	Leu	Tyr	Lys	Thr 110	Ile	Glu					
Val	Phe	Cys 115	Glu	Tyr	Phe	Lys	Glu 120	Leu	Glu	Glu	Glu	Ser 125	Ile	Arg	Asp					
Asn	Phe 130	Val	Ile	Val	Tyr	Glu 135	Leu	Leu	Asp	Glu	Leu 140	Met	Asp	Phe	Gly					
Phe 145	Pro	Gln	Thr	Thr	Asp 150	Ser	Lys	Ile	Leu	Gln 155	Glu	Tyr	Ile	Thr	Gln 160					
Gln	Ser	Asn	Lys	Leu 165	Glu	Thr	Gly	Lys	Ser 170	Arg	Val	Pro	Pro	Thr 175	Val					
Thr	Asn	Ala	Val 180	Ser	Trp	Arg	Ser	Glu 185	Gly	Ile	Lys	Tyr	Lys 190	Lys	Asn					
Glu	Val	Phe 195	Ile	Asp	Val	Ile	Glu 200	Ser	Val	Asn	Leu	Leu 205	Val	Asn	Ala					
Asn	Gly 210	Ser	Val	Leu	Leu	Ser 215	Glu	Ile	Val	Gly	Thr 220	Ile	Lys	Leu	Lys					
Val 225	Phe	Leu	Ser	Gly	Met 230	Pro	Glu	Leu	Arg	Leu 235	Gly	Leu	Asn	Asp	Arg 240					
Val	Leu	Phe	Glu	Leu 245	Thr	Gly	Arg	Ser	Lys 250	Asn	Lys	Ser	Val	Glu 255	Leu					
Glu	Asp	Val	Lys 260	Phe	His	Gln	Cys	Val 265	Arg	Leu	Ser	Arg	Phe 270	Asp	Asn					
Asp	Arg	Thr 275	Ile	Ser	Phe	Ile	Pro 280	Pro	Asp	Gly	Asp	Phe 285	Glu	Leu	Met					
Ser	Tyr 290	Arg	Leu	Ser	Thr	Gln 295	Val	Lys	Pro	Leu	Ile 300	Trp	Ile	Glu	Ser					
Val 305	Ile	Glu	Lys	Phe	Ser 310	His	Ser	Arg	Val	Glu 315	Ile	Met	Val	Lys	Ala 320					
Lys	Gly	Gln	Phe	Lys 325	Lys	Gln	Ser	Val	Ala 330	Asn	Gly	Val	Glu	Ile 335	Ser					
Val	Pro	Val	Pro 340	Ser	Asp	Ala	Asp	Ser 345	Pro	Arg	Phe	Lys	Thr 350	Ser	Val					
Gly	Ser	Ala	Lys	Tyr	Val	Pro	Glu	Arg	Asn	Val	Val	Ile	Trp	Ser	Ile					

355					360					365					
Lys	Ser	Phe	Pro	Gly	Gly	Lys	Glu	Tyr	Leu	Met	Arg	Ala	His	Phe	Gly
	370					375					380				
Leu	Pro	Ser	Val	Glu	Lys	Glu	Glu	Val	Glu	Gly	Arg	Pro	Pro	Ile	Gly
385				390						395					400
Val	Lys	Phe	Glu	Ile	Pro	Tyr	Phe	Thr	Val	Ser	Gly	Ile	Gln	Val	Arg
			405						410					415	
Tyr	Met	Lys	Ile	Ile	Glu	Lys	Ser	Gly	Tyr	Gln	Gly	Pro	Ala	Leu	Gly
			420					425					430		
Phe	Arg	Tyr	Ile	His	Pro	Glu	Trp	Ala	Ile	Thr	Asn	Phe	Arg	Tyr	Gln
		435					440					445			
Leu	Gly	Arg	Gly	Glu	Glu	Met	Gly	Gly	Phe						
	450					455									

<210> 227  
 <211> 120  
 <212> PRT  
 <213> homo sapiens

<400> 227

Leu	Val	Thr	Lys	Val	Gly	Asn	Arg	Pro	Leu	Trp	Val	Asn	Val	Ala	Lys
1				5					10					15	
Pro	Gln	Gly	Arg	Ala	Leu	Val	Thr	Thr	Phe	Leu	Asn	Asp	Leu	His	Val
			20					25					30		
Ser	Asp	Leu	Asp	Pro	Arg	Asp	Gly	Glu	Val	Gly	Asp	Leu	Lys	Leu	Asp
		35					40					45			
Pro	Asp	Gly	Gly	Pro	Ala	Leu	His	Leu	Phe	Leu	Phe	His	Thr	Gly	Glu
	50					55					60				
Ala	Lys	Val	Gly	Ser	His	Gln	Val	Leu	Leu	Ala	Pro	Arg	Glu	Arg	Leu
65					70					75					80
Asn	Thr	Pro	Asn	His	Asp	Val	Ser	Leu	Arg	His	Ile	Leu	Gly	Ala	Ala
				85					90					95	
His	Thr	Gly	Leu	Glu	Ser	Gly	Gly	Val	Gly	Ile	Ala	Gly	Tyr	Arg	His
			100					105					110		
Arg	Tyr	Leu	His	Thr	Val	Gly	His								
		115					120								

<210> 228  
 <211> 246  
 <212> PRT  
 <213> homo sapiens

<400> 228

Gly	Ile	Ser	Asn	Leu	Thr	Pro	Met	Gly	Gly	Arg	Pro	Ser	Thr	Ser	Ser
1				5					10					15	
Phe	Ser	Thr	Leu	Gly	Arg	Pro	Lys	Trp	Ala	Arg	Ile	Lys	Tyr	Ser	Leu
			20					25					30		

00673306.123700

Pro	Pro	Gly 35	Lys	Asp	Leu	Ile	Leu 40	Gln	Ile	Thr	Thr	Phe 45	Leu	Ser	Gly	.
Thr	Tyr 50	Leu	Ala	Leu	Pro	Thr 55	Leu	Val	Leu	Asn	Leu 60	Gly	Glu	Ser	Ala	
Ser 65	Leu	Gly	Thr	Gly	Thr 70	Asp	Ile	Ser	Thr	Pro 75	Leu	Ala	Thr	Asp	Cys 80	
Phe	Leu	Asn	Cys	Pro 85	Leu	Ala	Leu	Thr	Met 90	Ile	Ser	Thr	Arg	Leu 95	Trp	
Glu	Asn	Phe	Ser 100	Met	Thr	Asp	Ser	Ile 105	Gln	Ile	Ser	Gly	Leu 110	Thr	Trp	
Val	Leu	Arg 115	Arg	Tyr	Asp	Met	Ser 120	Ser	Lys	Ser	Pro	Ser 125	Gly	Gly	Met	
Lys	Glu 130	Met	Val	Arg	Ser	Leu 135	Ser	Lys	Arg	Glu	Ser 140	Arg	Thr	His	Trp	
Trp 145	Asn	Phe	Thr	Ser	Ser	Ser 150	Ser	Thr	Asp	Leu 155	Phe	Leu	Leu	Arg	Pro 160	
Val	Ser	Ser	Lys	Ser 165	Thr	Arg	Ser	Leu	Arg 170	Pro	Ser	Arg	Ser	Ser 175	Gly	
Ile	Pro	Asp	Arg 180	Asn	Thr	Leu	Ser	Leu 185	Met	Val	Pro	Thr	Ile 190	Ser	Leu	
Arg	Arg	Thr 195	Leu	Pro	Leu	Ala	Leu 200	Thr	Ser	Arg	Leu	Thr 205	Asp	Ser	Met	
Thr	Ser 210	Met	Lys	Thr	Ser	Phe 215	Phe	Leu	Tyr	Leu	Ile 220	Pro	Ser	Glu	Arg	
Gln 225	Asp	Thr	Ala	Leu	Val 230	Thr	Val	Gly	Gly	Thr 235	Arg	Asp	Leu	Pro	Val 240	
Ser	Ser	Leu	Leu	Leu 245	Cys											

&lt;210&gt; 229

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 229

Met 1	Asn	Thr	Arg	Leu 5	Gln	Val	Glu	His	Pro 10	Val	Thr	Glu	Met	Ile 15	Thr	
Gly	Thr	Asp	Leu 20	Val	Glu	Trp	Gln	Leu 25	Arg	Ile	Ala	Ala	Gly 30	Glu	Lys	
Ile	Pro	Leu 35	Ser	Gln	Glu	Glu	Ile 40	Thr	Leu	Gln	Gly	His 45	Ala	Phe	Glu	
Ala	Arg 50	Ile	Tyr	Ala	Glu	Asp 55	Pro	Ser	Asn	Asn	Phe 60	Met	Pro	Val	Ala	
Gly	Pro	Leu	Val	His	Leu	Ser	Thr	Pro	Arg	Ala	Asp	Pro	Ser	Thr	Arg	

65					70					75					80				
Ile	Glu	Thr	Gly	Val	Arg	Gln	Gly	Asp	Glu	Val	Ser	Val	His	Tyr	Asp				
				85					90					95					
Pro	Met	Ile	Ala	Lys	Trp	Val	Val	Trp	Ala	Ala	Asp	Arg	Gln	Ala	Ala				
			100					105					110						
Leu	Thr	Lys	Leu	Arg	Tyr	Ser	Leu	Arg	Gln	Tyr	Asn	Ile	Val	Gly	Leu				
		115					120					125							
Pro	Thr	Asn	Ile	Asp	Phe	Leu	Leu	Asn	Leu	Ser	Gly	His	Pro	Glu	Phe				
		130				135					140								
Glu	Ala	Gly	Asn	Val	His	Thr	Asp	Phe	Ile	Pro	Gln	His	His	Lys	Gln				
		145			150					155					160				
Leu	Leu	Leu	Ser	Arg	Lys	Ala	Ala	Ala	Lys	Glu	Ser	Leu	Cys	Gln	Ala				
				165					170					175					
Ala	Leu	Gly	Leu	Ile	Leu	Lys	Glu	Lys	Ala	Met	Thr	Asp	Thr	Phe	Thr				
			180					185					190						
Leu	Gln	Ala	His	Asp	Gln	Phe	Ser	Pro	Phe	Ser	Ser	Ser	Ser	Gly	Arg				
		195					200					205							
Arg	Leu	Asn	Ile	Ser	Tyr	Thr	Arg	Asn	Met	Thr	Leu	Lys	Asp	Gly	Lys				
		210				215					220								
Asn	Asn	Val	Ala	Ile	Ala	Val	Thr	Tyr	Asn	His	Asp	Gly	Ser	Tyr	Ser				
		225			230					235					240				
Met	Gln	Ile	Glu	Asp	Lys	Thr	Phe	Gln	Val	Leu	Gly	Asn	Leu	Tyr	Ser				
				245					250					255					
Glu	Gly	Asp	Cys	Thr	Tyr	Leu	Lys	Cys	Ser	Val	Asn	Gly	Val	Ala	Ser				
			260					265					270						
Lys	Ala	Lys																	
		275																	

<210> 230

<211> 117

<212> PRT

<213> homo sapiens

<400> 230

Ser	Glu	Val	Ile	Ile	Leu	Glu	Asn	Thr	Ile	Tyr	Leu	Phe	Ser	Lys	Glu
1				5					10					15	
Gly	Ser	Ile	Glu	Ile	Asp	Ile	Pro	Val	Pro	Lys	Tyr	Leu	Ser	Ser	Val
			20					25					30		
Ser	Ser	Gln	Glu	Thr	Gln	Gly	Gly	Pro	Leu	Ala	Pro	Met	Thr	Gly	Thr
		35					40					45			
Ile	Glu	Lys	Val	Phe	Val	Lys	Ala	Gly	Asp	Lys	Val	Lys	Ala	Gly	Asp
	50					55					60				
Ser	Leu	Met	Val	Met	Ile	Ala	Met	Lys	Met	Glu	His	Thr	Ile	Lys	Ser
65					70					75					80

09672395.122700



Pro	Lys	Asp	Gly	Thr	Val	Lys	Lys	Val	Phe	Tyr	Arg	Glu	Gly	Ala	Gln
				85					90					95	
Ala	Asn	Arg	His	Thr	Pro	Leu	Val	Glu	Phe	Glu	Glu	Glu	Glu	Ser	Asp
			100					105					110		
Lys	Arg	Glu	Ser	Glu											
		115													

<210> 231  
 <211> 103  
 <212> PRT  
 <213> homo sapiens

<400> 231

Ser	Leu	Arg	Phe	Thr	Ser	Asn	Ser	Ile	Asn	Arg	Thr	Phe	Gln	Val	Ser
1				5					10					15	
Ala	Val	Ser	Leu	Ala	Val	Lys	Ile	Thr	Lys	Asp	Leu	Glu	Ser	Phe	Ile
			20					25					30		
Phe	Asn	Leu	His	Ala	Ile	Arg	Pro	Ile	Met	Val	Ile	Arg	Tyr	Ser	Tyr
		35					40					45			
Gly	Tyr	Ile	Val	Phe	Thr	Ile	Phe	Lys	Ser	His	Val	Ser	Gly	Ile	Arg
	50					55					60				
Asp	Ile	Gln	Ser	Ser	Ser	Thr	Ala	Arg	Arg	Lys	Trp	Arg	Glu	Leu	Ile
65					70					75					80
Met	Cys	Leu	Lys	Ser	Glu	Ser	Val	Gly	His	Gly	Phe	Leu	Leu	Glu	Asp
				85					90					95	
Glu	Thr	Gln	Gly	Cys	Leu	Ala									
			100												

<210> 232  
 <211> 234  
 <212> PRT  
 <213> homo sapiens

<400> 232

Ala	Asp	Lys	Met	Phe	Leu	Leu	Pro	Leu	Pro	Ala	Ala	Gly	Arg	Val	Val
1				5					10					15	
Val	Arg	Arg	Leu	Ala	Val	Arg	Arg	Phe	Gly	Ser	Arg	Ser	Leu	Ser	Thr
			20					25					30		
Ala	Asp	Met	Thr	Lys	Gly	Leu	Val	Leu	Gly	Ile	Tyr	Ser	Lys	Glu	Lys
		35					40					45			
Glu	Asp	Asp	Val	Pro	Gln	Phe	Thr	Ser	Ala	Gly	Glu	Asn	Phe	Asp	Lys
	50					55					60				
Leu	Leu	Ala	Gly	Lys	Leu	Arg	Glu	Thr	Leu	Asn	Ile	Ser	Gly	Pro	Pro
65					70					75					80
Leu	Lys	Ala	Gly	Lys	Thr	Arg	Thr	Phe	Tyr	Gly	Leu	His	Gln	Asp	Phe
				85					90					95	
Pro	Ser	Val	Val	Leu	Val	Gly	Leu	Gly	Lys	Lys	Ala	Ala	Gly	Ile	Asp

00673305.122700

100										105					110				
Glu	Gln	Glu	Asn	Trp	His	Glu	Gly	Lys	Glu	Asn	Ile	Arg	Ala	Ala	Val				
		115					120					125							
Ala	Ala	Gly	Cys	Arg	Gln	Ile	Gln	Asp	Leu	Glu	Leu	Ser	Ser	Val	Glu				
	130					135					140								
Val	Asp	Pro	Cys	Gly	Asp	Ala	Gln	Ala	Ala	Ala	Glu	Gly	Ala	Val	Leu				
145					150					155					160				
Gly	Leu	Tyr	Glu	Tyr	Asp	Asp	Leu	Lys	Gln	Lys	Lys	Lys	Met	Ala	Val				
				165					170					175					
Ser	Ala	Lys	Leu	Tyr	Gly	Ser	Gly	Asp	Gln	Glu	Ala	Trp	Gln	Lys	Gly				
			180					185					190						
Val	Leu	Phe	Ala	Ser	Gly	Gln	Glu	Leu	Gly	His	Ala	Asn	Leu	Met	Gly				
		195					200					205							
Asp	Ala	Ser	Gln	Leu	Arg	Leu	Thr	Pro	Thr	Arg	Phe	Cys	Arg	Asn	Tyr				
	210					215					220								
Leu	Arg	Arg	Phe	Ser	Lys	Leu	Val	Val	Ser										
225					230														

&lt;210&gt; 233

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 233

Leu	Pro	Ile	Leu	Lys	Ile	Phe	Ser	Asn	Asn	Phe	Gly	Lys	Ile	Trp	Leu	
1				5					10					15		
Ala	Ser	Ile	Ser	Ile	Gly	Trp	Arg	Leu	Pro	Ser	Asn	Trp	Arg	Ala	Gln	
			20					25					30			
Val	Leu	Ala	Gln	Lys	Gln	Thr	Gly	Leu	Leu	Ser	Ala	Arg	Pro	Pro	Asp	
		35					40					45				
Pro	His	Phe	His	Arg	Ala	Leu	Pro	Thr	Gln	Pro	Ser	Ser	Phe	Phe	Ala	
	50					55					60					
Leu	Gly	His	Arg	Ile	His	Arg	Asp	Gln	Ala	Pro	Leu	Pro	Pro	Gln	Gln	
65					70					75					80	
Pro	Glu	Arg	Leu	His	Arg	Asp	Pro	Pro	Pro	Gln	Thr	Arg	Ala	Pro	Gly	
				85					90					95		
Leu	Glu	Ser	Ala	Cys	Thr	Pro	Leu	Gln	Gln	Gln	Leu					
			100					105								

&lt;210&gt; 234

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 234

Cys	Phe	Leu	Cys	Leu	His	Ala	Ser	Phe	Pro	Val	Arg	Arg	Phe	Gln	Leu	
1				5					10					15		

Pro	Phe	Cys	Arg 20	Gly	Gln	Leu	Ala	Pro 25	Arg	Trp	Gly	Ser	Pro 30	Asp	Ala
Asp	His	Lys 35	Arg	Phe	Glu	Ser	Ser 40	Leu	Pro	Ser	Glu	Val 45	Val	Gln	Ile
Cys	Ser 50	Lys	Ser	Leu	Ser	Ala 55	Phe	Gln	Leu	Thr	Ile 60	Tyr	Gln	Asn	Ser
Leu	Leu	His	Leu												

<210> 235  
 <211> 187  
 <212> PRT  
 <213> homo sapiens

<400> 235

Gln 1	Arg	Val	Arg	Ala 5	Ala	Leu	Leu	Ser	Ser 10	Ala	Met	Glu	Asp	Ser 15	Glu
Ala	Leu	Gly	Phe 20	Glu	His	Met	Gly	Leu 25	Asp	Pro	Arg	Leu	Leu 30	Gln	Ala
Val	Thr	Asp 35	Leu	Gly	Trp	Ser	Arg 40	Pro	Thr	Leu	Ile	Gln 45	Glu	Lys	Ala
Ile	Pro 50	Leu	Ala	Leu	Glu	Gly 55	Lys	Asp	Leu	Leu	Ala 60	Arg	Ala	Arg	Thr
Gly 65	Ser	Gly	Lys	Thr 70	Ala	Tyr	Ala	Ile	Pro 75	Met	Leu	Gln	Leu	Leu 80	
Leu	His	Arg	Lys	Ala 85	Thr	Gly	Pro	Val 90	Glu	Gln	Ala	Val	Arg 95	Gly	
Leu	Val	Leu	Val 100	Pro	Thr	Lys	Glu	Leu 105	Ala	Arg	Gln	Ala	Gln 110	Ser	Met
Ile	Gln	Gln 115	Leu	Ala	Thr	Tyr	Cys 120	Ala	Arg	Asp	Val	Arg 125	Val	Ala	Asn
Val	Ser 130	Ala	Ala	Glu	Asp	Ser 135	Val	Ser	Gln	Arg	Ala 140	Val	Leu	Met	Glu
Lys 145	Pro	Asp	Val	Val 150	Val	Gly	Thr	Pro	Ser	Arg 155	Ile	Leu	Ser	His	Leu 160
Gln	Gln	Asp	Ser	Leu 165	Lys	Leu	Arg	Asp	Ser 170	Leu	Glu	Leu	Leu	Val 175	Val
Asp	Glu	Ala	Asp 180	Leu	Leu	Phe	Ser	Leu 185	Trp	Leu					

<210> 236  
 <211> 76  
 <212> PRT  
 <213> homo sapiens

<400> 236

00673305-122700

Asp 1	Ile	Gly	His	Ser 5	Asp	Ile	Pro	Ser	Thr 10	Val	Gly	Ser	Gln	Leu 15	Leu
Asn	His	Gly	Leu 20	Cys	Leu	Pro	Cys	Gln 25	Leu	Leu	Gly	Arg	Asn 30	Lys	Asn
Lys	Ala	Ser 35	His	Cys	Leu	Phe	Tyr 40	His	Arg	Thr	Cys	Arg 45	Leu	Pro	Met
Glu	Gln 50	Gln	Leu	Gln	His	Arg 55	Asn	Ser	Ile	Ser	Gly 60	Arg	Leu	Pro	Gly
Ala 65	Arg	Ala	Gly	Pro	Ser 70	Gln	Glu	Val	Leu	Pro 75	Phe				

<210> 237  
 <211> 112  
 <212> PRT  
 <213> homo sapiens

<400> 237

Thr 1	Gly	Leu	Cys	Asn 5	Ile	Ser	Ser	Leu	Ser 10	Ala	Cys	Thr	Ser	Ser 15	Leu
Lys	Val	Ala	Asp 20	Met	Arg	Lys	Ala	Leu 25	Leu	Lys	Ser	Gly	Gly 30	Lys	Val
Thr	Arg	Gly 35	Arg	Leu	Leu	Glu	Leu 40	Phe	Phe	Lys	Ala	Lys 45	Gly	Lys	Lys
Glu	Gly 50	Gln	Leu	Arg	Pro	Pro 55	Pro	Lys	Ala	Pro	Gly 60	Ser	His	Glu	Val
Ser 65	Gly	Cys	Leu	Ala	Ala 70	Ser	Gly	Leu	Ile	Cys 75	Glu	Met	Gly	Ser	Leu 80
Leu	Pro	His	Leu	Ala 85	Ser	Pro	Ser	Ala	Gln 90	Leu	Ser	Glu	Arg	Leu 95	Ser
Leu	Gln	Gln	Leu 100	Arg	His	Trp	Pro	Leu 105	Gly	His	Pro	Glu	His 110	Ser	Arg

<210> 238  
 <211> 108  
 <212> PRT  
 <213> homo sapiens

<400> 238

Cys 1	His	Ala	Arg	Leu 5	Asn	Thr	Asp	Ser	Ser 10	Arg	Leu	Ala	Met	Lys 15	Leu
Leu	Met	Val	Leu 20	Met	Leu	Ala	Ala	Leu 25	Leu	Leu	His	Cys	Tyr 30	Ala	Asp
Ser	Gly	Cys 35	Lys	Leu	Leu	Glu	Asp 40	Met	Val	Glu	Lys	Thr 45	Ile	Asn	Ser
Asp	Ile 50	Ser	Ile	Pro	Glu	Tyr 55	Lys	Glu	Leu	Leu	Gln 60	Glu	Phe	Ile	Asp
Ser	Asp	Ala	Ala	Ala	Glu	Ala	Met	Gly	Lys	Phe	Lys	Gln	Cys	Phe	Leu

00673306.1.22700

65					70					75					80
Asn	Gln	Ser	His	Arg 85	Thr	Leu	Lys	Asn	Phe 90	Gly	Leu	Met	Met	His 95	Thr
Val	Tyr	Asp	Ser 100	Ile	Trp	Cys	Asn	Met 105	Lys	Ser	Asn				

<210> 239  
 <211> 82  
 <212> PRT  
 <213> homo sapiens

<400> 239

Leu 1	Val	Glu	Glu	Thr 5	Leu	Leu	Glu	Phe	Pro 10	His	Ser	Leu	Cys	Ser 15	Gly
Ile	Thr	Val	Tyr 20	Glu	Leu	Leu	Lys	Lys 25	Leu	Phe	Val	Phe	Arg 30	Tyr	Arg
Tyr	Val	Gly 35	Ile	Asp	Gly	Leu	Phe 40	Asn	His	Val	Leu	Gln 45	Glu	Phe	Ala
Ala	Arg 50	Ile	Cys	Ile	Ala	Val 55	Gln	Glu	Glu	Gly	Arg 60	Gln	His	Glu	Asp
His 65	Gln	Gln	Leu	His	Gly 70	Glu	Ala	Ala	Ala	Val 75	Cys	Val	Gln	Ser	Cys 80
Val	Ala														

<210> 240  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 240

Leu 1	Leu	Phe	Ile	Leu 5	His	Gln	Met	Leu	Ser 10	Tyr	Thr	Val	Cys	Ile 15	Ile
Ser	Pro	Lys	Phe 20	Phe	Arg	Val	Leu	Cys 25	Asp	Trp	Leu	Arg	Lys 30	His	Cys
Leu	Asn	Phe 35	Pro	Ile	Ala	Ser	Ala 40	Ala	Ala	Ser	Leu	Ser 45	Met	Asn	Ser

<210> 241  
 <211> 56  
 <212> PRT  
 <213> homo sapiens

<400> 241

Gln 1	Ala	Val	Gly	Glu 5	Lys	Leu	Ser	Ser	Arg 10	Asp	Ser	Asp	Leu	Met 15	Glu
Asp	Arg	Cys	Phe 20	Pro	His	Phe	Ser	Phe 25	Ser	Pro	Lys	Lys	Val 30	Leu	Leu
Leu	Ser	Pro 35	Phe	Lys	Gln	Pro	Val 40	Ser	Leu	Asn	Phe	Cys 45	Gly	His	Gly

00673305-122700



<210> 245  
 <211> 74  
 <212> PRT  
 <213> homo sapiens

<400> 245

Ser	Gly	Pro	Leu	Leu	Pro	Ala	Lys	Asn	Arg	Glu	Val	Ala	Gly	Leu	Lys
1				5					10					15	
Thr	Leu	Ser	Val	Thr	Phe	Gln	Phe	Leu	Lys	His	His	Cys	Tyr	Leu	Leu
			20					25					30		
Lys	Val	Val	Gly	Leu	Cys	Ile	Ser	Phe	Ser	Asn	Thr	Ser	Pro	Phe	Ile
		35					40					45			
Ser	Leu	Phe	Pro	Ile	His	Thr	Thr	Val	His	Met	Cys	Ala	Arg	Ala	His
	50					55					60				
Ala	His	Thr	His	Thr	His	Ser	Gln	Leu	Val						
65					70										

<210> 246  
 <211> 69  
 <212> PRT  
 <213> homo sapiens

<400> 246

Ala	Arg	Ile	Gln	Thr	Pro	Glu	Gln	His	Ser	Gln	Val	Thr	Leu	Phe	Asp
1				5					10					15	
Tyr	Asn	Glu	Glu	Met	Lys	Met	Gly	Gly	Tyr	Leu	Lys	Ile	Gly	Ile	Pro
			20					25					30		
Ser	Ala	Leu	Lys	Val	Ser	Lys	Leu	Leu	Thr	Cys	Glu	Gln	His	Arg	Thr
		35					40					45			
Pro	Leu	Leu	Trp	Ser	Ser	Phe	Gln	Leu	Arg	Met	Leu	Gln	Phe	Ser	Lys
	50					55					60				
Ser	Ile	Tyr	Tyr	Ser											
65															

<210> 247  
 <211> 236  
 <212> PRT  
 <213> homo sapiens

<400> 247

Gln	Leu	Arg	Gly	Gly	Val	Gln	Arg	His	Asp	Arg	Arg	Glu	Gly	Glu	Met
1				5					10					15	
Val	Cys	Val	Glu	Leu	Val	Ala	Ser	Asp	Lys	Thr	Asn	Thr	Phe	Gln	Gly
			20					25					30		
Val	Ile	Phe	Gln	Gly	Ser	Ile	Arg	Tyr	Glu	Ala	Leu	Lys	Lys	Val	Tyr
		35					40					45			
Asp	Asn	Arg	Val	Ser	Val	Ala	Ala	Arg	Met	Ala	Gln	Lys	Met	Ser	Phe
	50					55					60				

00673305.122700

Gly 65	Phe	Tyr	Lys	Tyr	Ser 70	Asn	Met	Glu	Phe	Val 75	Arg	Met	Lys	Gly	Pro 80
Gln	Gly	Lys	Gly	His 85	Ala	Glu	Met	Ala	Val 90	Ser	Arg	Val	Ser	Thr 95	Gly
Asp	Thr	Ala	Pro 100	Cys	Gly	Thr	Glu	Glu 105	Asp	Ser	Ser	Pro	Ala 110	Ser	Pro
Met	His	Glu 115	Arg	Val	Thr	Ser	Phe 120	Ser	Arg	Pro	Pro	Thr 125	Pro	Glu	Arg
Asn	Asn 130	Arg	Pro	Ala	Phe	Phe 135	Ser	Pro	Ser	Leu	Lys 140	Arg	Lys	Val	Pro
Arg 145	Asn	Arg	Ile	Ala	Glu 150	Met	Lys	Lys	Ser	His 155	Ser	Ala	Asn	Asp	Ser 160
Glu	Glu	Phe	Phe	Arg 165	Glu	Asp	Asp	Gly	Gly 170	Ala	Asp	Leu	His	Asn 175	Ala
Thr	Asn	Leu	Arg 180	Ser	Arg	Ser	Leu	Ser 185	Gly	Thr	Gly	Arg	Ser 190	Leu	Val
Gly	Ser	Trp 195	Leu	Lys	Leu	Asn	Arg 200	Ala	Asp	Gly	Asn	Phe 205	Leu	Leu	Tyr
Ala	His 210	Leu	Thr	Tyr	Val	Thr 215	Leu	Pro	Leu	His	Arg 220	Ile	Leu	Thr	Asp
Ile 225	Leu	Glu	Val	Arg	Gln 230	Lys	Pro	Ile	Leu	Met 235	Thr				

<210> 248  
 <211> 161  
 <212> PRT  
 <213> homo sapiens

<400> 248

Asp 1	Glu	Glu	Val	Ala 5	Leu	Gly	Gln	Arg	Gln 10	Arg	Gly	Val	Leu 15	Gly
Gly	Arg	Arg	Trp 20	Ser	Arg	Ser	Ala	Gln 25	Cys	Asn	Gln	Pro	Ala 30	Ser
Val	Pro	Val 35	Gly	His	Arg	Thr	Val 40	Pro	Gly	Arg	Val	Leu 45	Ala	Glu Ala
Glu	Gln 50	Ser	Arg	Trp	Lys	Leu 55	Pro	Ser	Leu	Cys	Thr 60	Leu	Asn	Leu Arg
His 65	Val	Ala	Ala	Ala	Ser 70	Asp	Phe	Asn	Arg	His 75	Pro	Gly	Ser	Ser Ala 80
Glu	Ala	His	Pro	Asp 85	Asp	Leu	Ala	Ala	Cys 90	Gly	Ala	Cys	Ala	Glu Pro 95
Arg	Pro	Gly	Pro 100	Ala	Leu	Gly	Val	Leu 105	Pro	Ser	Ala	Tyr	Leu 110	Ser Thr
Ala	Thr	Gly	Val	Cys	Asp	Gly	Thr	Pro	Val	Leu	Glu	Pro	Gln	Pro Gly

00573305.122700



115					120					125					
Glu	Ala	Thr	Arg	Leu	Pro	Gly	Pro	Gly	Pro	Thr	Ala	Arg	Thr	Pro	Ala
	130					135					140				
Gln	Thr	Glu	Val	Pro	Leu	Thr	Gly	Pro	Ala	Gly	Ala	Ala	Ser	Ala	Leu
145					150					155					160

Cys

<210> 249  
 <211> 218  
 <212> PRT  
 <213> homo sapiens

<400> 249

Val	Cys	Ile	Glu	Lys	Glu	Val	Ser	Ile	Cys	Ser	Val	Gln	Leu	Gln	Pro
1				5					10					15	
Gly	Pro	Asp	Gln	Gly	Pro	Ser	Cys	Ala	Arg	Gln	Gly	Pro	Arg	Pro	Gln
			20					25					30		
Val	Gly	Cys	Ile	Val	Gln	Ile	Gly	Ser	Thr	Val	Val	Leu	Pro	Glu	Glu
		35					40					45			
Leu	Leu	Ala	Val	Val	Gly	Arg	Val	Arg	Leu	Leu	His	Leu	Ser	Asp	Pro
	50					55					60				
Val	Pro	Gly	His	Leu	Pro	Leu	Glu	Gly	Trp	Gly	Glu	Glu	Gly	Arg	Pro
	65				70					75					80
Val	Val	Pro	Phe	Trp	Gly	Gly	Gly	Ser	Ala	Glu	Gly	Gly	His	Pro	Leu
				85					90					95	
Val	His	Gly	Arg	Ser	Trp	Ala	Gly	Val	Leu	Phe	Ser	Pro	Thr	Gly	Gly
			100					105					110		
Cys	Val	Thr	Cys	Arg	His	Ser	Ala	Asp	Arg	His	Leu	Gly	Val	Ala	Leu
		115					120					125			
Ala	Leu	Gly	Ala	Leu	His	Ala	His	Lys	Leu	His	Val	Ala	Val	Leu	Val
	130					135					140				
Glu	Ala	Lys	Arg	His	Leu	Leu	Cys	His	Ala	Gly	Gly	His	Ala	His	Pro
145					150					155					160
Val	Val	Ile	His	Leu	Leu	Glu	Arg	Leu	Val	Ala	Asp	Gly	Ala	Leu	Lys
				165					170					175	
Asp	Asp	Pro	Leu	Glu	Arg	Val	Gly	Phe	Val	Thr	Ser	His	Gln	Leu	His
			180					185					190		
Thr	Asp	His	Leu	Ser	Phe	Pro	Thr	Val	Met	Ser	Leu	Asn	Thr	Ser	Ser
		195					200					205			
Lys	Leu	Ser	Ile	Met	Lys	Lys	Met	Leu	Gly						
	210					215									

<210> 250  
 <211> 133  
 <212> PRT  
 <213> homo sapiens

00673305.122700

<400> 250

Tyr 1	Pro	Gln	Asp	Pro 5	Pro	Gly	Gly	Ala	Ser 10	Arg	Arg	Leu	Leu	Asp 15	Asp
Leu	Glu	Leu	Cys 20	Pro	Gly	Glu	Lys	Thr 25	Ala	Pro	Val	Trp	Ala 30	Leu	Ser
Ala	Glu	Glu 35	Glu	Ala	Ala	Met	His 40	Phe	Ser	Leu	Ala	Phe 45	Phe	Leu	His
Gly	Ser 50	Ser	Val	Phe	Leu	Gln 55	Ile	Thr	Cys	Cys	His 60	Glu	Phe	Leu	Cys
Met 65	Arg	His	Ile	Ser	Ser 70	Cys	Leu	Tyr	Ala	Glu 75	Val	Pro	Phe	Ile	Leu 80
Ser	Ile	Gly	Trp	Trp 85	Thr	Gly	Glu	Arg	Gly 90	Pro	Arg	Cys	Pro	Thr 95	Ser
Cys	Ala	Ser	Ala 100	Val	Gly	Gly	Asp	Arg 105	Ala	Pro	Arg	His	Gly 110	Gly	Gly
Gly	His	Leu 115	Pro	His	Val	Trp	Gly 120	Gly	Arg	Arg	His	Pro 125	Gly	Thr	Glu
Gly	Ser 130	Leu	Gln	Arg											

<210> 251

<211> 71

<212> PRT

<213> homo sapiens

<400> 251

Arg 1	Leu	Pro	Ser	Val 5	Pro	Gly	Cys	Leu	Arg 10	Pro	Pro	Gln	Thr	Cys 15	Gly
Arg	Cys	Pro	Pro 20	Pro	Pro	Cys	Leu	Gly 25	Ala	Arg	Ser	Pro	Pro 30	Thr	Ala
Leu	Ala	His 35	Asp	Val	Gly	His	Leu 40	Gly	Pro	Leu	Ser	Pro 45	Val	His	Gln
Pro	Ile 50	Glu	Arg	Met	Lys	Gly 55	Thr	Ser	Ala	Tyr	Arg 60	His	Asp	Glu	Ile
Cys 65	Leu	Met	His	Lys	Asn 70	Ser									

<210> 252

<211> 95

<212> PRT

<213> homo sapiens

<400> 252

Arg 1	Gly	Leu	Gln	His 5	Thr	Asp	Met	Met	Lys 10	Tyr	Ala	Ser	Cys	Ile 15	Lys
Ile	His	Asp	Asn	Met	Leu	Phe	Ala	Lys	Lys	Gln	Thr	Asn	His	Ala	Gly

09673305-122700

20					25					30					
Lys	Met	Pro	Gly	Lys	Ser	Ala	Trp	Gln	Leu	Pro	Pro	Gln	His	Ser	Gly
		35					40					45			
Pro	Thr	Gln	Glu	Arg	Phe	Ser	Pro	Gln	Asp	Thr	Ala	Pro	Ser	Arg	Pro
	50					55					60				
Glu	Ala	Ser	Val	Met	Pro	Leu	Leu	Ala	Gly	Pro	Glu	Gly	Ile	Arg	Ala
	65					70					75				80
Pro	Leu	Leu	Leu	Thr	Val	Asp	Ala	Ala	Thr	His	Ser	Met	Gln	His	
				85					90					95	

<210> 253

<211> 194

<212> PRT

<213> homo sapiens

<400> 253

Gln	Lys	Lys	Lys	Met	Ser	Phe	Arg	Lys	Val	Asn	Ile	Ile	Ile	Leu	Val
1				5					10					15	
Leu	Ala	Val	Ala	Leu	Phe	Leu	Leu	Val	Leu	His	His	Asn	Phe	Leu	Ser
			20					25					30		
Leu	Ser	Ser	Leu	Leu	Arg	Asn	Glu	Val	Thr	Asp	Ser	Gly	Ile	Val	Gly
		35					40					45			
Pro	Gln	Pro	Ile	Asp	Phe	Val	Pro	Asn	Ala	Leu	Arg	His	Ala	Val	Asp
	50					55					60				
Gly	Arg	Gln	Glu	Glu	Ile	Pro	Val	Val	Ile	Ala	Ala	Ser	Glu	Asp	Arg
	65				70					75					80
Leu	Gly	Gly	Ala	Ile	Ala	Ala	Ile	Asn	Ser	Ile	Gln	His	Asn	Thr	Arg
				85					90					95	
Ser	Asn	Val	Ile	Phe	Tyr	Ile	Val	Thr	Leu	Asn	Asn	Thr	Ala	Asp	His
			100					105					110		
Leu	Arg	Ser	Trp	Leu	Asn	Ser	Asp	Ser	Leu	Lys	Ser	Ile	Arg	Tyr	Lys
		115					120					125			
Ile	Val	Asn	Phe	Asp	Pro	Lys	Leu	Leu	Glu	Gly	Lys	Val	Lys	Glu	Asp
	130					135					140				
Pro	Asp	Gln	Gly	Glu	Ser	Met	Lys	Pro	Leu	Thr	Phe	Ala	Arg	Phe	Tyr
	145					150				155					160
Leu	Pro	Ile	Leu	Gly	Ser	Gln	Arg	Gln	Arg	Lys	Ala	Arg	Leu	His	Gly
				165					170					175	
Val	Asp	Asp	Val	Ile	Cys	Gly	Arg	Trp	Asp	Phe	Leu	Pro	Phe	Thr	Leu
			180					185					190		
Gln	Gln														

<210> 254

<211> 109

<212> PRT

<213> homo sapiens

00673395-122700

<400> 254

Arg	Phe	His	Gly	Phe	Pro	Leu	Val	Arg	Ile	Leu	Leu	Tyr	Phe	Ser	Phe
1				5					10					15	
Gln	Lys	Phe	Arg	Val	Lys	Ile	Asp	Asn	Phe	Val	Ser	Asp	Ala	Phe	Gln
			20					25					30		
Gly	Ile	Thr	Val	Glu	Pro	Gly	Pro	Glu	Met	Val	Cys	Cys	Ile	Val	Glu
		35					40					45			
Ser	Asn	Asn	Val	Glu	Asn	His	Ile	Gly	Ala	Ser	Val	Val	Leu	Asn	Ala
	50					55					60				
Val	Tyr	Ser	Cys	Asn	Gly	Pro	Pro	Lys	Pro	Val	Phe	Arg	Cys	Ser	Asp
65					70					75					80
Asp	His	Arg	Asn	Leu	Leu	Leu	Ser	Pro	Ile	Tyr	Cys	Met	Ser	Glu	Ser
				85					90					95	
Ile	Trp	Asp	Lys	Val	Tyr	Arg	Leu	Arg	Pro	Tyr	Asn	Ser			
			100					105							

<210> 255

<211> 57

<212> PRT

<213> homo sapiens

<400> 255

Asn	Leu	Ala	Lys	Val	Lys	Gly	Phe	Met	Asp	Ser	Pro	Trp	Ser	Gly	Ser
1				5					10					15	
Ser	Phe	Thr	Phe	Pro	Ser	Lys	Ser	Leu	Gly	Ser	Lys	Leu	Thr	Ile	Leu
			20					25					30		
Tyr	Leu	Met	Leu	Phe	Arg	Glu	Ser	Leu	Leu	Ser	Gln	Asp	Arg	Arg	Trp
		35					40					45			
Ser	Ala	Val	Leu	Leu	Arg	Val	Thr	Met							
	50					55									

<210> 256

<211> 230

<212> PRT

<213> homo sapiens

<400> 256

Leu	Pro	Ala	Ala	Thr	Asn	Arg	Leu	Lys	Arg	Gly	Lys	Gly	Ser	Ser	Thr
1				5					10					15	
Gly	Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His
			20					25					30		
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly	Lys
		35					40					45			
Ser	Gly	Ile	Gln	Gly	Phe	Arg	Gly	Gln	Gly	Val	Ser	Ser	Asn	Met	Arg
	50					55					60				
Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser	Gly	Asp	Asn

00673395.122700

65					70					75					80				
Tyr	Arg	Gly	Gln	Gly 85	Ser	Ser	Trp	Gly	Ser 90	Gly	Gly	Gly	Asp	Ala 95	Val				
Gly	Gly	Val	Asn 100	Thr	Val	Asn	Ser	Glu 105	Thr	Ser	Pro	Gly	Met 110	Phe	Asn				
Phe	Asp	Thr 115	Phe	Trp	Lys	Asn	Phe 120	Lys	Ser	Lys	Leu	Gly 125	Phe	Ile	Asn				
Trp	Asp 130	Ala	Ile	Asn	Lys	Asn 135	Gln	Val	Pro	Pro	Pro 140	Ser	Thr	Arg	Ala				
Leu 145	Leu	Tyr	Phe	Ser	Arg 150	Leu	Trp	Glu	Asp	Phe 155	Lys	Gln	Asn	Thr	Pro 160				
Phe	Leu	Asn	Trp	Lys 165	Ala	Ile	Ile	Glu	Gly 170	Ala	Asp	Ala	Ser	Ser 175	Leu				
Gln	Lys	Arg	Ala 180	Gly	Arg	Ala	Glu	Ser 185	Glu	Leu	Gln	Leu	Gln 190	Pro	Ala				
Cys	Val	Ser 195	His	Cys	Leu	Trp	Trp 200	Glu	Val	Leu	Ser	Gln 205	Asp	Pro	Cys				
Lys	Gly 210	Gly	Glu	Ser	His	Leu 215	Leu	Pro	Arg	Leu	Pro 220	Gly	Cys	Asn	Leu				
Gly 225	Leu	Leu	Ala	Val	Gly 230														

<210> 257  
 <211> 141  
 <212> PRT  
 <213> homo sapiens  
 <400> 257

Thr 1	Arg	Thr	Arg	Ser 5	Arg	Pro	Pro	Ala	Pro 10	Glu	Pro	Ser	Ser	Thr 15	Ser
Ala	Asp	Ser	Gly 20	Arg	Ile	Ser	Asn	Arg 25	Thr	Leu	Leu	Ser	Ser 30	Thr	Gly
Lys	Gln	Leu 35	Leu	Arg	Val	Arg	Thr 40	Arg	His	His	Cys	Arg 45	Asn	Val	Gln
Ala	Glu 50	Pro	Ser	Gln	Asn	Tyr 55	Asn	Tyr	Asn	Gln	His 60	Ala	Tyr	Pro	Thr
Ala 65	Tyr	Gly	Gly	Lys	Tyr 70	Ser	Val	Lys	Thr	Pro 75	Ala	Lys	Gly	Gly	Ser 80
Leu	Thr	Phe	Phe	Leu 85	Gly	Phe	Pro	Gly	Ala 90	Thr	Trp	Ala	Cys	Leu 95	Gln
Leu	Gly	Glu	Val 100	Leu	Val	Arg	Gln	Phe 105	Leu	Ala	Thr	Asn	His 110	Arg	Arg
Pro	Arg	Lys 115	Lys	His	Trp	Val	Arg 120	Gln	Gly	Lys	Leu	Leu 125	Pro	Pro	Leu

Gly Pro Pro Ala Leu Trp Gln Ala Pro Gly Pro Gly Leu  
130 135 140

<210> 258  
<211> 165  
<212> PRT  
<213> homo sapiens

<400> 258

Arg	Val	Arg	Thr	Leu	Asn	Asn	Cys	Phe	Pro	Val	Glu	Glu	Arg	Ser	Val
1				5					10					15	
Leu	Phe	Glu	Ile	Leu	Pro	Glu	Ser	Ala	Glu	Val	Glu	Glu	Gly	Ser	Gly
			20					25					30		
Ala	Gly	Gly	Arg	Asp	Leu	Val	Leu	Val	Tyr	Gly	Ile	Pro	Val	Asp	Glu
		35					40					45			
Thr	Gln	Leu	Gly	Phe	Lys	Ile	Leu	Pro	Glu	Ser	Val	Lys	Val	Lys	His
	50					55					60				
Pro	Arg	Arg	Arg	Leu	Arg	Val	His	Ser	Ile	Asp	Ser	Thr	Asn	Ser	Val
	65				70					75				80	
Thr	Ser	Ser	Thr	Ala	Pro	Ala	Arg	Pro	Leu	Pro	Pro	Ile	Ile	Val	Ser
				85					90					95	
Arg	Ala	Ser	Lys	Glu	Ala	Ile	Ala	Leu	Phe	Ala	Tyr	Phe	Pro	His	Val
			100					105					110		
Ala	Gly	Asn	Ser	Leu	Ser	Ser	Glu	Ala	Leu	Asn	Pro	Arg	Phe	Pro	Ala
		115					120					125			
Pro	Ala	Gly	Phe	Ile	Pro	Trp	Leu	Phe	Thr	Pro	Gly	Phe	Met	Ser	Ile
	130					135					140				
Ser	Ser	Ala	Ala	Pro	Thr	Val	Val	Ala	Gly	Gly	Gly	Ala	Gly	Ala	Gly
	145				150					155					160
Ser	Leu	Pro	Pro	Leu											
				165											

<210> 259  
<211> 126  
<212> PRT  
<213> homo sapiens

<400> 259

Glu	Arg	Ser	His	Leu	Gln	Pro	Gly	Ala	Val	Gly	Ile	Thr	Glu	Ser	Pro
1				5					10					15	
Ile	Leu	Gly	Leu	Gly	Ser	Ala	Met	Thr	Thr	Glu	Ile	Gly	Trp	Trp	Lys
			20					25					30		
Leu	Thr	Phe	Leu	Arg	Lys	Lys	Lys	Ser	Thr	Pro	Lys	Val	Leu	Tyr	Glu
		35					40					45			
Ile	Pro	Asp	Thr	Tyr	Ala	Gln	Thr	Glu	Gly	Asp	Ala	Glu	Pro	Pro	Arg
	50					55					60				
Pro	Asp	Ala	Gly	Gly	Pro	Asn	Ser	Asp	Phe	Asn	Thr	Arg	Leu	Glu	Lys

00673395-122700

65						70											80
Ile	Val	Asp	Lys	Ser	Thr	Lys	Gly	Lys	His	Val	Lys	Val	Ser	Asn	Ser		
				85					90					95			
Gly	Arg	Phe	Lys	Glu	Lys	Lys	Lys	Val	Arg	Ala	Thr	Leu	Ala	Glu	Asn		
			100					105					110				
Pro	Asn	Leu	Phe	Asp	Asp	His	Glu	Glu	Gly	Arg	Ser	Ser	Lys				
		115					120					125					

<210> 260  
 <211> 121  
 <212> PRT  
 <213> homo sapiens

<400> 260

Tyr	Val	Leu	Asn	Thr	Ile	Ile	Val	Gly	Lys	Gly	Glu	Glu	Lys	Ile	Pro
1				5					10					15	
His	Pro	Leu	Pro	Arg	Phe	Gly	Pro	Cys	Ser	Phe	Pro	Leu	Arg	Val	Cys
			20					25					30		
Asp	Leu	Pro	Ser	Ala	Lys	Val	Met	Ala	Lys	Thr	Gly	Thr	Asn	Arg	Pro
		35					40					45			
Asn	Tyr	His	Gln	Ser	Ser	Leu	Leu	Gln	His	Pro	Asn	Arg	Val	Pro	Gly
	50					55					60				
Ser	Ser	Val	Pro	Ser	Ala	Pro	Glu	Gly	Lys	Val	Pro	Gly	Ser	Leu	Leu
65					70					75				80	
Pro	Val	Leu	Gly	Gly	Glu	Leu	Lys	Phe	Ser	Val	Ser	Ala	Ser	Gly	Ser
				85					90					95	
Thr	Glu	Thr	Ser	Pro	Tyr	His	Val	Ala	Ser	Gly	Lys	Cys	Ala	Leu	Leu
			100					105					110		
Arg	Ile	Gly	Pro	Gly	Ser	Ser	His	Arg							
		115					120								

<210> 261  
 <211> 86  
 <212> PRT  
 <213> homo sapiens

<400> 261

Thr	Arg	Val	Pro	Leu	Tyr	Val	Val	Arg	Gly	Arg	Val	Glu	Asp	Pro	Gly
1				5					10					15	
Ile	Ser	Gln	Ala	Leu	Gln	Lys	Trp	Arg	His	Ile	Asn	Thr	Asn	Leu	Lys
			20					25					30		
Asn	Ser	His	Phe	Leu	Pro	Ala	Gly	Ile	Asn	Trp	Pro	His	Ser	Phe	Ser
		35					40					45			
Tyr	Gly	Gln	Arg	Gly	Gln	Arg	Gly	Lys	Val	Leu	Ser	Gln	Ile	Trp	Leu
	50					55					60				
Met	Ala	Gly	Ser	Gln	Glu	Val	Leu	Ala	Pro	Ser	Ser	Ala	Leu	His	Phe
65					70					75				80	

09673326.122700

Asp Asp Arg Pro Ser Ser  
85

<210> 262  
<211> 73  
<212> PRT  
<213> homo sapiens

<400> 262

Gly	Ser	Gly	Ser	Pro	Ala	Pro	Arg	Lys	Leu	His	Asp	Phe	Ala	Leu	Cys
1				5					10					15	
Ser	Ala	Pro	Leu	Cys	Pro	Leu	Phe	Pro	Arg	Glu	Thr	Ser	Arg	Ser	His
			20					25					30		
Ile	Phe	Leu	Thr	Asp	Phe	Glu	Ala	Val	Cys	Leu	His	Ser	Asp	Trp	Glu
		35					40					45			
His	Trp	Asp	His	Phe	His	His	Ala	Asp	Ser	Gly	Gly	Asn	Gly	Cys	Ile
	50					55					60				
Pro	Phe	His	Asp	Pro	Thr	Cys	Val	Tyr							
65					70										

<210> 263  
<211> 106  
<212> PRT  
<213> homo sapiens

<400> 263

Phe	Val	Ala	Met	Cys	Ser	Lys	Gln	Ala	Ser	Leu	Asn	His	Gly	Leu	Leu
1				5					10					15	
Gly	Leu	Thr	Leu	Val	Phe	Leu	Gly	Pro	Leu	Asn	Arg	His	Arg	Ser	Gly
			20					25					30		
His	Gly	Lys	Gly	Tyr	Ile	His	Tyr	His	His	Cys	Arg	His	Asp	Glu	Asn
		35					40					45			
Asp	Pro	Ser	Val	Pro	Asn	Gln	Asn	Ala	Asn	Arg	Gln	Leu	Gln	Asn	Gln
	50					55					60				
Ser	Arg	Lys	Cys	Gly	Ile	Trp	Lys	Ser	Leu	Leu	Glu	Arg	Gly	Gly	Arg
65					70					75					80
Gly	Glu	Leu	Ser	Arg	Gly	Arg	Asn	Arg	Ala	Val	Tyr	Ala	Glu	Leu	Gly
				85					90					95	
Thr	Pro	Ser	Leu	Arg	Ala	Arg	Gly	Gly	Arg						
			100					105							

<210> 264  
<211> 66  
<212> PRT  
<213> homo sapiens

<400> 264

Val	Leu	Arg	Trp	Tyr	Ser	Ser	Asp	Pro	Ser	Ile	Asp	Thr	Gly	Arg	Val
1				5					10					15	

00673305 122700



Met	Glu	Arg	Asp 20	Thr	Ser	Ile	Thr	Thr 25	Thr	Val	Gly	Met	Met 30	Lys	Met
Ile	Pro	Val 35	Phe	Pro	Ile	Arg	Met 40	Gln	Thr	Asp	Ser	Phe 45	Lys	Ile	Ser
Gln	Glu 50	Asn	Val	Gly	Ser	Gly 55	Ser	Leu	Ser	Trp	Lys 60	Glu	Gly	Ala	Glu
Gly 65	Ser														

<210> 265  
 <211> 108  
 <212> PRT  
 <213> homo sapiens

<400> 265

Gly 1	Cys	Ala	Cys	Phe 5	Arg	Pro	Pro	Ser	Pro 10	Ala	Gly	Gly	Ala	Arg 15	Thr
Ser	Ala	Gly	Arg 20	Ser	Pro	Ser	Ser	Ala 25	Asp	Val	Gly	Ser	Arg 30	Thr	Gln
Ser	Arg	Ser 35	Arg	Arg	Arg	Ala	Ala 40	His	Ser	Arg	Cys	Cys 45	Val	Ala	Phe
Pro	Ser 50	Ser	Phe	Thr	Pro	Arg 55	Ser	Arg	Arg	Arg	Pro 60	Lys	Arg	Arg	Arg
Arg 65	Arg	Arg	Glu	Asn	Asp 70	Pro	Ala	Ala	Ser	Ser 75	Leu	Pro	Pro	Ala	His 80
Leu	Pro	Cys	Ser 85	Val	Ser	Gln	Ser	Ala	Ala 90	Gly	Ala	Arg	Leu	Val 95	Leu
Arg	Pro	Arg	Ala 100	Cys	Gly	Ala	Gln	Ala 105	Gln	Arg	Pro				

<210> 266  
 <211> 109  
 <212> PRT  
 <213> homo sapiens

<400> 266

Gly 1	Ala	Pro	Ala	Phe 5	Ala	Leu	Leu	Leu	Gln 10	Arg	Glu	Gly	Arg	Gly 15	Leu
Pro	Arg	Gly	Gly 20	Val	Arg	Leu	Val	Leu 25	Thr	Leu	Ala	Ala	Glu 30	Pro	Lys
Val	Asp	Arg 35	Gly	Gly	Gly	Leu	His 40	Ile	Pro	Val	Val	Ala 45	Leu	Arg	Phe
Leu	Pro 50	Leu	Ser	Leu	Arg	Ala 55	His	Gly	Gly	Gly	Gln 60	Ser	Gly	Gly	Asp
Gly 65	Gly	Ala	Arg	Thr	Thr 70	Arg	Arg	Pro	Val	Leu 75	Phe	Leu	Leu	Arg	Thr 80

0067305-12200

Cys	Pro	Ala	Arg	Ser 85	Val	Ser	Arg	Arg	Pro 90	Ala	Pro	Gly	Leu	Cys 95	Ser
Asp	Leu	Ala	Leu 100	Ala	Ala	Pro	Arg	Pro 105	Ser	Gly	Arg	Ser			

<210> 267  
 <211> 157  
 <212> PRT  
 <213> homo sapiens

<400> 267

Ile 1	Glu	Ala	Ala	Gly 5	Cys	Thr	Phe	Pro	Leu 10	Leu	Arg	Cys	Val	Ser 15	Phe
Leu	Phe	His	Ser 20	Ala	Leu	Thr	Ala	Ala 25	Ala	Lys	Ala	Ala	Ala 30	Thr	Ala
Ala	Arg	Glu 35	Arg	Pro	Gly	Gly	Gln 40	Phe	Ser	Ser	Ser	Cys 45	Ala	Pro	Ala
Leu	Leu 50	Gly	Gln	Ser	Val	Gly 55	Gly	Arg	Arg	Pro	Ala 60	Cys	Ala	Gln	Thr
Ser 65	Arg	Leu	Arg	Arg	Pro 70	Gly	Pro	Ala	Ala	Val 75	Ala	Ser	Val	Trp	Pro 80
Glu	Asn	Leu	Gly	Ala 85	Pro	Ala	Ala	Arg	Ala 90	Pro	Arg	Ala	Glu	Pro 95	Arg
Ser	Gly	Ser	Arg 100	Gly	Gly	Arg	Arg	Val 105	Ser	Glu	Ser	Glu	Gly 110	Trp	Pro
Gly	Gln	Val 115	Val	Ala	Pro	Arg	Arg 120	Trp	Ser	Pro	Ser	Lys 125	Gly	Ser	Val
Trp	Pro 130	Thr	Arg	Ser	Thr	Ala 135	Arg	Thr	Ser	Pro	Ser 140	Ala	Ala	Thr	Ser
Pro 145	Arg	Pro	Arg	Glu	Met 150	Pro	Pro	Lys	Arg	Arg 155	Arg	Leu			

<210> 268  
 <211> 156  
 <212> PRT  
 <213> homo sapiens

<400> 268

Ser 1	Ser	Ala	Gln	Gly 5	Glu	Glu	Pro	Gly	Pro 10	Gly	Arg	Arg	Leu	Leu 15	Arg
Ala	Pro	Thr	Glu 20	Ser	Arg	Ser	Glu	Gly 25	Lys	Ser	Met	Phe	Ala 30	Gly	Val
Pro	Thr	Met 35	Arg	Glu	Ser	Ser	Pro 40	Lys	Gln	Tyr	Met	Gln 45	Leu	Gly	Gly
Arg	Val 50	Leu	Leu	Val	Leu	Met 55	Phe	Met	Thr	Leu	Leu 60	His	Phe	Asp	Ala
Ser	Phe	Phe	Ser	Ile	Val	Gln	Asn	Ile	Val	Gly	Thr	Ala	Leu	Met	Ile

00673395.122700

65				70				75				80			
Leu	Val	Ala	Ile	Gly 85	Phe	Lys	Thr	Lys	Leu 90	Ala	Ala	Leu	Thr	Leu 95	Val
Val	Trp	Leu	Phe 100	Ala	Ile	Asn	Val	Tyr 105	Phe	Asn	Ala	Phe	Trp 110	Thr	Ile
Pro	Val	Tyr 115	Lys	Pro	Met	His	Asp 120	Phe	Leu	Lys	Tyr	Asp 125	Phe	Phe	Gln
Thr	Met 130	Ser	Val	Ile	Gly	Gly 135	Leu	Leu	Leu	Val	Val 140	Ala	Leu	Gly	Pro
Gly 145	Gly	Val	Ser	Met	Asp 150	Glu	Lys	Lys	Lys	Glu 155	Trp				

<210> 269  
 <211> 112  
 <212> PRT  
 <213> homo sapiens

<400> 269

Leu 1	Gly	Ala	Cys	Ser 5	Trp	Trp	Trp	Pro	Trp 10	Ala	Leu	Gly	Val	Ser 15	Pro
Trp	Met	Arg	Arg 20	Arg	Arg	Ser	Gly	Asn 25	Ser	His	Arg	Ser	Leu 30	Pro	Ala
Trp	Leu	Arg 35	Pro	Val	Ala	Val	Lys 40	Asp	Trp	Phe	Gly	Val 45	Asp	Ser	Thr
Lys	Leu 50	Pro	Ala	Phe	Met	Tyr 55	Pro	Leu	Pro	Phe	Pro 60	Ser	Leu	Gly	Lys
Gly 65	Thr	Asp	Val	Leu	Arg 70	Thr	Leu	Phe	Ala	Glu 75	Thr	Pro	Glu	Asn	Arg 80
Trp	Leu	Ser	Leu	Leu 85	Trp	Ser	His	Ser	Leu 90	Ala	Ser	Asp	Pro	Ser 95	Val
Gln	Ala	Ser	Leu 100	Ala	Ala	Gly	Ser	Leu 105	Pro	His	Ala	Glu	Ala 110	Leu	Glu

<210> 270  
 <211> 130  
 <212> PRT  
 <213> homo sapiens

<400> 270

Ser 1	Gln	Arg	Val	Cys 5	Lys	Tyr	Ser	Pro	Gly 10	Ser	Leu	Leu	Pro	Tyr 15	Pro
Arg	Ile	Leu	Val 20	Arg	Ser	Ser	Asn	Gly 25	Phe	Arg	Thr	Trp	Val 30	Leu	Phe
Ser	Cys	Asp 35	His	Ser	Ser	Ala	His 40	Cys	Met	Lys	Thr	Gly 45	Leu	Ser	Gln
Cys	Phe 50	Asn	Leu	Thr	Arg	Ala 55	Val	Ser	Trp	Ser	Thr 60	Pro	Arg	Ser	Leu

002227-5622960

Leu 65	Val	Pro	Tyr	Asp	Ser 70	Pro	His	Gln	Met	Thr 75	Leu	Ala	Lys	Ser	Arg 80
Phe	Leu	Cys	Gly	Gln 85	Gly	Trp	Leu	Ala	Asp 90	Trp	Trp	Lys	Val	Gly 95	Trp
Thr	Lys	Gly	Gly 100	His	Val	Ser	Ser	Gln 105	His	Gln	Phe	Cys	Thr 110	Ser	Ser
Ala	Ser	Val 115	Leu	Val	Gly	Val	Pro 120	Val	Ser	Pro	Gly	Pro 125	Gly	Trp	Ala
Arg	Ala 130														

<210> 271

<211> 267

<212> PRT

<213> homo sapiens

<400> 271

Gly 1	Thr	Ser	Gly	Thr 5	Ser	His	Leu	His	Pro 10	Arg	Ser	Ile	Cys	Met 15	Ile
Gln	Lys	Tyr	Asn 20	His	Asp	Gly	Glu	Ala 25	Gly	Arg	Leu	Glu	Ala 30	Phe	Ser
Gln	Gly	Glu 35	Ser	Val	Leu	Lys	Glu 40	Pro	Lys	Tyr	Gln	Glu 45	Glu	Leu	Glu
Asp	Arg 50	Leu	His	Phe	Tyr	Val 55	Glu	Glu	Cys	Asp	Tyr 60	Leu	Gln	Gly	Phe
Gln 65	Ile	Leu	Cys	Asp	Leu 70	His	Asp	Gly	Phe	Ser 75	Gly	Val	Gly	Ala	Lys 80
Ala	Ala	Glu	Leu	Leu 85	Gln	Asp	Glu	Tyr	Ser 90	Gly	Arg	Gly	Ile	Ile 95	Thr
Trp	Gly	Leu	Leu 100	Pro	Gly	Pro	Tyr	His 105	Arg	Gly	Glu	Ala	Gln 110	Arg	Asn
Ile	Tyr	Arg 115	Leu	Leu	Asn	Thr	Ala 120	Phe	Gly	Leu	Val	His 125	Leu	Thr	Ala
His	Ser 130	Ser	Leu	Val	Cys	Pro 135	Leu	Ser	Leu	Gly	Gly 140	Ser	Leu	Gly	Leu
Arg 145	Pro	Glu	Pro	Pro	Val 150	Ser	Phe	Pro	Tyr	Leu 155	His	Tyr	Asp	Ala	Thr 160
Leu	Pro	Phe	His	Cys 165	Ser	Ala	Ile	Leu	Ala 170	Thr	Ala	Leu	Asp	Thr 175	Val
Thr	Val	Pro	Tyr 180	Arg	Leu	Cys	Ser	Ser 185	Pro	Val	Ser	Met	Val 190	His	Leu
Ala	Asp	Met 195	Leu	Ser	Phe	Cys	Gly 200	Lys	Lys	Val	Val	Thr 205	Ala	Gly	Ala
Ile	Ile	Pro	Phe	Pro	Leu	Ala	Pro	Gly	Gln	Ser	Leu	Pro	Asp	Ser	Leu

00673305.122700

210					215					220					
Met	Gln	Phe	Gly	Gly	Ala	Thr	Pro	Trp	Thr	Pro	Leu	Cys	Ala	Cys	Gly
225					230					235					240
Glu	Pro	Ser	Gly	Thr	Arg	Cys	Phe	Ala	Gln	Ser	Val	Val	Leu	Arg	Gly
				245					250					255	
Tyr	Arg	Gln	Ser	Met	Pro	His	Lys	Pro	Gln	Thr					
			260					265							

<210> 272  
 <211> 118  
 <212> PRT  
 <213> homo sapiens

<400> 272

Gln	Val	Ala	Arg	Val	Ala	Gly	Pro	Gly	Ser	His	Pro	Arg	Thr	Arg	Gly
1				5					10					15	
Arg	Gln	Glu	Ser	Cys	Glu	Gln	Ser	Gly	Ala	Arg	Asp	Gln	Lys	Leu	Cys
			20					25					30		
Leu	Ile	Asp	Asp	Arg	Cys	Phe	Ser	Gly	Pro	Pro	His	Asp	Gly	Arg	Asp
		35					40					45			
Gln	Val	Ala	Gly	Pro	Arg	Leu	Leu	Phe	Pro	Ala	Leu	Asn	Ile	His	Leu
	50					55					60				
Val	Ala	Ala	Leu	Pro	Pro	Ser	Arg	Leu	Pro	Gln	Arg	Ser	His	Arg	Ala
	65				70					75					80
Gly	His	Thr	Gly	Ser	Gly	Ser	Pro	Ala	Ser	Ser	His	Ile	Pro	Pro	Arg
				85					90					95	
Arg	Asn	Ala	Ala	Cys	Pro	Pro	Ala	Leu	Pro	Gly	Thr	Trp	Val	Pro	Leu
			100					105					110		
Gly	His	Phe	Pro	Leu	Gly										
		115													

<210> 273  
 <211> 133  
 <212> PRT  
 <213> homo sapiens

<400> 273

Leu	Gly	Lys	Ala	Thr	Cys	Ser	Arg	Arg	Leu	Pro	Thr	Cys	Thr	Gln	Trp
1				5					10					15	
Gly	Pro	Trp	Gly	Ser	Ser	Lys	Leu	His	Gln	Gly	Ile	Arg	Lys	Gly	
			20				25					30			
Leu	Ala	Trp	Ser	Gln	Gly	Glu	Arg	Asp	Asp	Cys	Ser	Cys	Cys	His	His
		35					40					45			
Leu	Phe	Pro	Thr	Glu	Ala	Gln	His	Val	Ser	Gln	Met	Asn	His	Gly	Asn
	50					55					60				
Trp	Arg	Gly	Thr	Gln	Ala	Ile	Arg	Asn	Ser	Asp	Cys	Val	Gln	Gly	Cys
	65				70					75					80

Ser	Gln	Asp	Gly	Thr	Ala	Val	Glu	Gly	Gln	Ser	Gly	Ile	Ile	Met	Gln
				85					90					95	
Val	Arg	Glu	Ala	Asp	Arg	Trp	Leu	Gly	Ser	Gln	Ala	Gln	Ala	Pro	Thr
			100					105					110		
Gln	Gly	Gln	Gly	Ala	Asp	Lys	Arg	Ala	Val	Ser	Ser	Gln	Val	His	Glu
		115					120					125			
Thr	Lys	Ser	Cys	Val											
	130														

<210> 274  
 <211> 124  
 <212> PRT  
 <213> homo sapiens

<400> 274

Pro	Gln	Ala	Trp	Arg	Arg	Leu	Cys	Arg	Cys	Cys	Ser	Ala	Arg	Pro	Val
1				5					10					15	
Ala	Pro	Gly	Ala	Arg	Arg	Leu	Val	Pro	Cys	Arg	Thr	Pro	Thr	Arg	Gln
			20					25					30		
Pro	Ala	Gly	Gly	Thr	Cys	His	His	Pro	Ala	Ala	Phe	Arg	Gly	Arg	Ser
		35					40					45			
Arg	His	Ile	Pro	Val	Pro	His	Ala	Leu	Gly	Phe	Gly	Ala	Ser	Ala	Gly
	50					55					60				
Arg	Ser	Val	Pro	Leu	Gln	Ala	Leu	Ser	Gln	Ser	Pro	Gly	Ala	Ala	Asp
65					70					75					80
Leu	Gln	Val	Phe	Ser	Thr	Gly	Ala	Ala	Pro	Val	Ile	His	Thr	Arg	Leu
				85					90					95	
Leu	Glu	Asp	Pro	Ile	Leu	Gly	Ala	Thr	Leu	Pro	Ala	Gly	Pro	Ile	Arg
			100					105					110		
Cys	Arg	Ala	Val	Gly	Leu	Val	Pro	Arg	His	Cys	His				
		115					120								

<210> 275  
 <211> 426  
 <212> PRT  
 <213> homo sapiens

<400> 275

Gly	Ser	Ser	Arg	Arg	His	Gly	Gly	Gly	Tyr	Ala	Ala	Val	Ala	Leu	Leu
1				5					10					15	
Val	Leu	Leu	Leu	Leu	Gly	Pro	Gly	Gly	Trp	Cys	Leu	Ala	Glu	Pro	Pro
			20					25					30		
Arg	Asp	Ser	Leu	Arg	Glu	Glu	Leu	Val	Ile	Thr	Pro	Leu	Pro	Ser	Gly
		35					40					45			
Asp	Val	Ala	Ala	Thr	Phe	Gln	Phe	Arg	Thr	Arg	Trp	Asp	Ser	Glu	Leu
	50					55					60				

00673205.123700

Gln 65	Arg	Glu	Gly	Val	Ser 70	His	Tyr	Arg	Leu	Phe 75	Pro	Lys	Ala	Leu	Gly 80
Gln	Leu	Ile	Ser	Lys 85	Tyr	Ser	Leu	Arg	Glu 90	Leu	His	Leu	Ser	Phe 95	Thr
Gln	Gly	Phe	Trp 100	Arg	Thr	Arg	Tyr	Trp 105	Gly	Pro	Pro	Phe	Leu 110	Gln	Ala
Pro	Ser	Gly 115	Ala	Glu	Leu	Trp	Val 120	Trp	Phe	Gln	Asp	Thr 125	Val	Thr	Asp
Val	Asp 130	Lys	Ser	Trp	Lys	Glu 135	Leu	Ser	Asn	Val	Leu 140	Ser	Gly	Ile	Phe
Cys 145	Ala	Ser	Leu	Asn	Phe 150	Ile	Asp	Ser	Thr	Asn 155	Thr	Val	Thr	Pro	Thr 160
Ala	Ser	Phe	Lys	Pro 165	Leu	Gly	Leu	Ala	Asn 170	Asp	Thr	Asp	His	Tyr 175	Phe
Leu	Arg	Tyr	Ala 180	Val	Leu	Pro	Arg	Glu 185	Val	Val	Cys	Thr	Glu 190	Asn	Leu
Thr	Pro	Trp 195	Lys	Lys	Leu	Leu	Pro 200	Cys	Ser	Ser	Lys	Ala 205	Gly	Leu	Ser
Val	Leu 210	Leu	Lys	Ala	Asp	Arg 215	Leu	Phe	His	Thr	Ser 220	Tyr	His	Ser	Gln
Ala 225	Val	His	Ile	Arg	Pro 230	Val	Cys	Arg	Asn	Ala 235	Arg	Cys	Thr	Ser	Ile 240
Ser	Trp	Glu	Leu	Arg 245	Gln	Thr	Leu	Ser	Val 250	Val	Phe	Asp	Ala	Phe 255	Ile
Thr	Gly	Gln	Gly 260	Lys	Lys	Asp	Trp	Ser 265	Leu	Phe	Arg	Met	Phe 270	Ser	Arg
Thr	Leu	Thr 275	Glu	Pro	Cys	Pro	Leu 280	Ala	Ser	Glu	Ser	Arg 285	Val	Tyr	Val
Asp	Ile 290	Thr	Thr	Tyr	Asn	Gln 295	Asp	Asn	Glu	Thr	Leu 300	Glu	Val	His	Pro
Pro 305	Pro	Thr	Thr	Thr	Tyr 310	Gln	Asp	Val	Ile	Leu 315	Gly	Thr	Arg	Lys	Thr 320
Tyr	Ala	Ile	Tyr	Asp 325	Leu	Leu	Asp	Thr	Ala 330	Met	Ile	Asn	Asn	Ser 335	Arg
Asn	Leu	Asn	Ile 340	Gln	Leu	Lys	Trp	Lys 345	Arg	Pro	Pro	Glu	Asn 350	Glu	Ala
Pro	Pro	Val 355	Pro	Phe	Leu	His	Ala 360	Gln	Arg	Tyr	Val	Ser 365	Gly	Tyr	Gly
Leu	Gln 370	Lys	Gly	Glu	Leu	Ser 375	Thr	Leu	Leu	Tyr	Asn 380	Thr	His	Pro	Tyr
Arg 385	Ala	Phe	Pro	Val	Leu 390	Leu	Leu	Asp	Thr	Val 395	Pro	Trp	Tyr	Leu	Arg 400

00573305-122700

Leu	Leu	His	Pro	Leu 405	Pro	Ala	Cys	Pro	Gly 410	Pro	Ala	Ala	Thr	Pro 415	Pro
Pro	Gly	Asp	Ala 420	Asp	Ser	Ala	Ala	Gly 425	Gln						

<210> 276  
 <211> 128  
 <212> PRT  
 <213> homo sapiens

<400> 276

Ser 1	Pro	Ser	Ile	Leu 5	Tyr	Gly	Ser	Cys	Thr 10	Cys	His	Ser	His	Lys 15	Ala
Phe	Gly	Gly	Pro 20	Asp	Thr	Gly	Gly	His 25	Pro	Ser	Cys	Arg	Pro 30	His	Gln
Val	Gln	Ser 35	Cys	Gly	Ser	Gly	Ser 40	Lys	Thr	Leu	Ser	Leu 45	Met	Trp	Ile
Asn 50	Leu	Gly	Arg	Ser	Ser	Val 55	Met	Ser	Ser	Gln	Gly 60	Ser	Ser	Ala	Pro
Leu 65	Ser	Thr	Ser	Ser	Thr 70	Pro	Pro	Thr	Gln	Ser 75	Leu	Pro	Leu	Pro	Pro 80
Ser	Asn	Pro	Trp	Val 85	Trp	Pro	Met	Thr	Leu 90	Thr	Thr	Thr	Phe	Cys 95	Ala
Met	Leu	Cys	Cys 100	Arg	Gly	Arg	Trp	Ser 105	Ala	Pro	Lys	Thr	Ser 110	Pro	Pro
Gly	Arg	Ser 115	Ser	Cys	Pro	Val	Val 120	Pro	Arg	Gln	Ala	Ser 125	Leu	Cys	Cys

<210> 277  
 <211> 481  
 <212> PRT  
 <213> homo sapiens

<400> 277

Ala 1	Gln	Asp	Thr	Gly 5	Gly	Pro	Gly	Arg	Gln 10	Ser	Gly	His	Gly 15	Asp
Leu	Gln	Ile	Pro 20	Ile	Ser	Leu	Phe	Leu 25	Arg	Arg	Leu	Asn	Thr 30	His
Trp	Arg	Pro 35	Gly	Ser	Arg	Lys	Val 40	Met	Ala	Val	Val	Pro 45	Ala	Ser
Ser	Gly 50	Gln	Asp	Val	Gly	Ser 55	Phe	Ala	Tyr	Leu	Thr 60	Ile	Lys	Asp
Ile 65	Pro	Gln	Ile	Leu	Thr 70	Lys	Val	Ile	Asp	Thr 75	Leu	His	Arg	His
Ser	Glu	Phe	Phe 85	Glu	Lys	His	Gly	Glu 90	Gly	Val	Glu	Ala	Glu 95	Lys
Lys	Ala	Ile	Ser	Leu	Leu	Ser	Lys	Leu	Arg	Asn	Glu	Leu	Gln	Thr

09673395.122700



			100							105						110					
Lys	Pro	Phe 115	Ile	Pro	Leu	Val	Glu 120	Lys	Phe	Val	Asp	Thr 125	Asp	Ile	Trp						
Asn	Gln	Tyr	Leu	Glu	Tyr	Gln	Gln	Ser	Leu	Leu	Asn 140	Glu	Ser	Asp	Gly						
Lys 145	Ser	Arg	Trp	Phe	Tyr 150	Ser	Pro	Trp	Leu	Leu 155	Val	Glu	Cys	Tyr	Met 160						
Tyr	Arg	Arg	Ile	His 165	Glu	Ala	Ile	Ile	Gln 170	Ser	Pro	Pro	Ile	Asp 175	Tyr						
Phe	Asp	Val	Phe 180	Lys	Glu	Ser	Lys	Glu 185	Gln	Asn	Phe	Tyr	Gly 190	Ser	Gln						
Glu	Ser	Ile 195	Ile	Ala	Leu	Cys	Thr 200	His	Leu	Gln	Gln	Leu 205	Ile	Arg	Thr						
Ile	Glu 210	Asp	Leu	Asp	Glu	Asn 215	Gln	Leu	Lys	Asp	Glu 220	Phe	Phe	Lys	Leu						
Leu 225	Gln	Ile	Ser	Leu	Trp 230	Gly	Asn	Lys	Cys	Asp 235	Leu	Ser	Leu	Ser	Gly 240						
Gly	Glu	Ser	Ser	Ser 245	Gln	Asn	Thr	Asn	Val 250	Leu	Asn	Ser	Leu	Glu 255	Asp						
Leu	Lys	Pro	Phe 260	Ile	Leu	Leu	Asn	Asp 265	Met	Glu	His	Leu	Trp 270	Ser	Leu						
Leu	Ser	Asn 275	Cys	Lys	Lys	Thr	Arg 280	Glu	Lys	Ala	Ser	Ala 285	Thr	Arg	Val						
Tyr	Ile 290	Val	Leu	Asp	Asn	Ser 295	Gly	Phe	Glu	Leu	Val 300	Thr	Asp	Leu	Ile						
Leu 305	Ala	Asp	Phe	Leu	Leu 310	Ser	Ser	Glu	Leu	Ala 315	Thr	Glu	Val	His	Phe 320						
Tyr	Gly	Lys	Thr	Ile 325	Pro	Trp	Phe	Val	Ser 330	Asp	Thr	Thr	Ile	His 335	Asp						
Phe	Asn	Trp	Leu 340	Ile	Glu	Gln	Val	Lys 345	His	Ser	Asn	His	Lys 350	Trp	Met						
Ser	Lys	Cys 355	Gly	Ala	Asp	Trp	Glu 360	Glu	Tyr	Ile	Lys	Met 365	Gly	Lys	Trp						
Val	Tyr 370	His	Asn	His	Ile	Phe 375	Trp	Thr	Leu	Pro	His 380	Glu	Tyr	Cys	Ala						
Met 385	Pro	Gln	Val	Ala	Pro 390	Asp	Leu	Tyr	Ala	Glu 395	Leu	Gln	Lys	Ala	His 400						
Leu	Ile	Leu	Phe 405	Lys	Gly	Asp	Leu	Asn	Tyr 410	Arg	Lys	Leu	Thr	Gly 415	Asp						
Arg	Lys	Trp	Glu 420	Phe	Ser	Val	Pro	Phe 425	His	Gln	Ala	Leu	Asn 430	Gly	Phe						
His	Pro	Ala	Pro	Leu	Cys	Thr	Ile	Arg	Thr	Leu	Lys	Ala	Glu	Ile	Gln						

435					440					445					
Val	Gly	Leu	Gln	Pro	Gly	Gln	Gly	Glu	Gln	Leu	Leu	Ala	Ser	Glu	Pro
	450					455					460				
Ser	Trp	Trp	Thr	Thr	Gly	Lys	Tyr	Gly	Ile	Phe	Gln	Tyr	Asp	Gly	Pro
465					470					475					480

Leu

<210> 278  
 <211> 128  
 <212> PRT  
 <213> homo sapiens

<400> 278

Phe	His	Ile	Ser	Val	Ser	Thr	Asn	Phe	Ser	Thr	Lys	Gly	Ile	Asn	Gly
1				5					10					15	
Leu	Ser	Val	Cys	Asn	Ser	Phe	Arg	Asn	Leu	Glu	Arg	Arg	Glu	Ile	Ala
			20					25					30		
Phe	Phe	Ser	Ala	Ser	Thr	Pro	Ser	Ser	Pro	Cys	Phe	Ser	Lys	Asn	Ser
		35					40					45			
Leu	Leu	Cys	Arg	Cys	Asn	Val	Ser	Ile	Thr	Leu	Val	Lys	Ile	Cys	Gly
	50					55					60				
Ile	Leu	Ser	Leu	Ile	Val	Arg	Tyr	Ala	Asn	Asp	Pro	Thr	Ser	Cys	Pro
65					70					75					80
Glu	Arg	Asp	Ala	Gly	Thr	Thr	Ala	Ile	Thr	Phe	Arg	Asp	Pro	Gly	Arg
				85					90					95	
Gln	Cys	Trp	Val	Phe	Asn	Arg	Arg	Arg	Asn	Arg	Glu	Ile	Gly	Ile	Cys
			100					105					110		
Lys	Ser	Pro	Pro	Cys	Pro	Asp	Cys	Arg	Pro	Gly	Pro	Pro	Val	Ser	Cys
		115					120					125			

<210> 279  
 <211> 83  
 <212> PRT  
 <213> homo sapiens

<400> 279

Glu	Leu	Leu	Asn	Gln	Val	Lys	Gly	Asp	His	Arg	Thr	Glu	Ile	Phe	His
1				5					10					15	
Ile	Phe	Gln	Trp	Ser	Thr	Ser	Trp	Ala	Gln	Arg	Pro	Gly	Ala	Val	Pro
			20					25					30		
Leu	Ala	Gln	Ala	Ala	Asp	Gln	Pro	Glu	Phe	Gln	Leu	Leu	Met	Phe	Leu
		35					40					45			
Trp	Tyr	Arg	Val	Val	Gln	Asp	Gly	Ser	His	Ser	Glu	Pro	Asp	Glu	Met
	50					55					60				
Glu	Gln	Lys	Thr	Pro	Ile	Phe	Cys	His	Leu	Ser	Thr	Ser	Cys	Asn	Ser
65					70					75					80

Asn His Pro

<210> 280  
<211> 168  
<212> PRT  
<213> homo sapiens

<400> 280

Phe 1	Tyr	Asp	Arg	Arg 5	Asp	Cys	Phe	Val	Ala 10	Val	Ser	Phe	Leu	Arg 15	Gly
Leu	Ser	Leu	Trp 20	Leu	His	Phe	Tyr	Leu 25	Trp	Trp	Leu	Cys	Tyr 30	Gly	Gly
Ala	Glu	Met 35	Arg	Gln	Lys	Arg	Lys 40	Gly	Asp	Leu	Ser	Pro 45	Ala	Glu	Leu
Met	Met 50	Leu	Thr	Ile	Gly	Asp 55	Val	Ile	Lys	Gln	Leu 60	Ile	Glu	Ala	His
Glu 65	Gln	Gly	Lys	Asp	Ile 70	Asp	Leu	Asn	Lys	Val 75	Lys	Thr	Lys	Thr	Ala 80
Ala	Lys	Tyr	Gly	Leu 85	Ser	Ala	Gln	Pro	Arg 90	Leu	Val	Asp	Ile	Ile 95	Ala
Ala	Val	Pro	Pro 100	Gln	Tyr	Arg	Lys	Val 105	Leu	Met	Pro	Lys	Leu 110	Lys	Ala
Lys	Pro	Ile 115	Arg	Thr	Ala	Ser	Gly 120	Ile	Ala	Val	Val	Ala 125	Val	Met	Cys
Lys	Pro 130	His	Arg	Cys	Pro	His 135	Ile	Ser	Phe	Thr	Gly 140	Asn	Ile	Cys	Val
Tyr 145	Cys	Pro	Gly	Gly	Pro 150	Asp	Ser	Asp	Phe	Glu 155	Tyr	Ser	Thr	Gln	Ser 160
Tyr	Thr	Gly	Tyr	Glu 165	Gln	Pro	Pro								

<210> 281  
<211> 70  
<212> PRT  
<213> homo sapiens

<400> 281

Gly 1	Gly	Thr	Ala	Ala 5	Met	Ile	Ser	Thr	Arg 10	Arg	Gly	Trp	Ala	Glu 15	Arg
Pro	Tyr	Leu	Ala 20	Ala	Val	Leu	Val	Phe 25	Thr	Leu	Phe	Arg	Ser 30	Met	Ser
Phe	Pro	Cys 35	Ser	Trp	Ala	Ser	Ile 40	Ser	Cys	Leu	Ile	Thr 45	Ser	Pro	Ile
Val	Ser 50	Ile	Ile	Ser	Ser	Ala 55	Gly	Leu	Arg	Ser	Pro 60	Phe	Arg	Phe	Cys
Leu 65	Ile	Ser	Ala	Pro	Pro 70										

00673305.122700

<210> 282  
 <211> 71  
 <212> PRT  
 <213> homo sapiens

<400> 282

Ile	Asp	Val	Phe	Pro	Leu	Leu	Val	Gly	Phe	Asn	Gln	Leu	Phe	Asn	Asn
1				5					10					15	
Ile	Ser	Tyr	Ser	Gln	His	His	Gln	Leu	Ser	Arg	Ala	Glu	Ile	Ser	Phe
			20					25					30		
Pro	Leu	Leu	Pro	His	Phe	Cys	Ala	Ala	Val	Ala	Glu	Pro	Pro	Glu	Ile
		35					40					45			
Lys	Met	Gln	Pro	Gln	Thr	Gln	Thr	Thr	Glu	Lys	Ala	Asp	Ser	His	Lys
	50					55					60				
Thr	Ile	Pro	Pro	Val	Val	Lys									
65					70										

<210> 283  
 <211> 114  
 <212> PRT  
 <213> homo sapiens

<400> 283

Lys	Pro	Arg	Gln	Leu	Pro	Asn	Met	Ala	Phe	Leu	Pro	Ser	Pro	Ala	Trp
1				5					10					15	
Trp	Ile	Ser	Leu	Leu	Ala	Val	Pro	Pro	Gln	Tyr	Arg	Lys	Val	Leu	Met
			20					25					30		
Pro	Lys	Leu	Lys	Ala	Lys	Pro	Ile	Arg	Thr	Ala	Ser	Gly	Ile	Ala	Val
		35					40					45			
Val	Ala	Val	Met	Cys	Lys	Pro	His	Arg	Cys	Pro	His	Ile	Ser	Phe	Thr
	50					55					60				
Gly	Asn	Ile	Cys	Val	Tyr	Cys	Pro	Gly	Trp	Asp	Leu	Ile	Leu	Ile	Leu
					70					75					80
Ser	Ile	Pro	Pro	Ser	Leu	Thr	Leu	Gly	Tyr	Glu	Pro	Thr	Ser	Met	Arg
				85					90					95	
Ser	Tyr	Ser	Val	Pro	Asp	Met	Asp	Pro	Phe	Pro	Tyr	Arg	Thr	Arg	Thr
			100					105					110		
Pro	Asp														

<210> 284  
 <211> 127  
 <212> PRT  
 <213> homo sapiens

<400> 284

Trp	Val	Ser	Pro	Leu	Thr	Trp	Ala	Ser	Arg	Pro	Cys	Asp	Thr	Glu	Glu
1				5					10					15	

00673305.122700

Gly	Arg	Gln	Ala 20	Met	Ile	Ser	Thr	Arg 25	Arg	Gly	Trp	Ala	Glu 30	Arg	Pro	
Tyr	Leu	Ala 35	Ala	Val	Leu	Val	Phe 40	Thr	Leu	Phe	Arg	Ser 45	Met	Ser	Phe	
Pro	Cys 50	Ser	Trp	Ala	Ser	Ile 55	Ser	Cys	Leu	Ile	Thr 60	Ser	Pro	Ile	Val	
Ser 65	Ile	Ile	Ser	Ser	Ala 70	Gly	Leu	Arg	Ser	Pro 75	Asp	Tyr	Gly	Gly	Phe 80	
Thr	Thr	Arg	Pro	Gly 85	Ser	Asn	Ile	Leu	Gly 90	Ser	Arg	Val	Gly	His 95	Tyr	
Thr	His	Gln	Thr 100	Met	Glu	Asp	Ser	Pro 105	Pro	Asp	Gln	Glu	Ala 110	Thr	Ala	
Trp	Ala	Pro 115	Glu	Leu	Ala	Thr	Pro 120	Pro	Cys	Thr	Asp	Glu 125	Asp	Arg		

<210> 285

<211> 92

<212> PRT

<213> homo sapiens

<400> 285

Pro 1	His	Thr	Thr	Asn 5	Pro	Thr	Cys	Phe	Lys 10	Leu	Phe	Leu	Ile	Arg 15	Cys	
Pro	Cys	Pro	Val 20	Arg	Lys	Arg	Val	His 25	Ile	Trp	His	Gly	Ile 30	Ala	Pro	
His	Gly	Gly 35	Trp	Leu	Ile	Ala	Gln 40	Cys	Lys	Thr	Gly	Trp 45	Asn	Thr	Gln	
Asn 50	Gln	Asn	Gln	Val	Pro	Pro 55	Arg	Ala	Val	Tyr	Thr 60	Tyr	Ile	Ser	Cys	
Lys 65	Thr	Asp	Val	Trp	Thr 70	Ser	Val	Gly	Phe 75	Ala	His	His	Ser	His	Asp 80	
Ser	Asn	Pro	Thr	Ser 85	Ser	Ser	Asp	Gly	Phe 90	Arg	Leu					

<210> 286

<211> 76

<212> PRT

<213> homo sapiens

<400> 286

Asp 1	Leu	Ser	Arg	Pro 5	Gly	Gly	Thr	Arg	Phe 10	Val	Leu	Thr	Ile	Gln 15	Gln	
Thr	Phe	Phe	Ser 20	Lys	Val	Phe	Val	Gln 25	Asp	Asn	Phe	Lys	Asn 30	Asn	Ile	
Lys	Ile	Asn 35	Asn	Gly	Phe	Asp	Phe 40	Ser	Leu	Lys	Ile	Glu 45	Lys	Lys	Gly	
Val	Gly	Gly	Gly	Val	Asn	His	Trp	Pro	Phe	Phe	Phe	Trp	Arg	Gly	Pro	

00673305-122700

00673305-122700

50					55					60				
Ile 65	Gly	Ile	Val	Arg	Pro 70	Trp	Gly	Ser	Gly	Leu 75	Ser			

<210> 287  
 <211> 97  
 <212> PRT  
 <213> homo sapiens  
 <400> 287

Arg 1	Thr	Phe	Val	Leu 5	Phe	Tyr	His	Arg	Leu 10	Thr	Leu	Gln	Leu 15	Ile
Asn	Thr	Ser	Phe 20	Gly	Asp	Val	Trp	Cys 25	Lys	Thr	His	Lys	His 30	Gln
Lys	Ser	Thr 35	Ser	Pro	Leu	His	Asp 40	Pro	Ser	Leu	Leu	Ser 45	Gly	Ile
Ser	Ala 50	Ala	Ser	Cys	Thr	Leu 55	Leu	Gly	Pro	Pro	Pro 60	Ile	His	Arg
Phe 65	Arg	Gly	Thr	Gln	Ile 70	Thr	Ala	Gly	Phe	Gln 75	Phe	Phe	Phe	Asn 80
Thr	Phe	Leu	Trp	Ser 85	Val	Pro	Thr	Ala	Leu 90	Ser	Val	Leu	Leu	Lys 95

Glu  
 <210> 288  
 <211> 77  
 <212> PRT  
 <213> homo sapiens  
 <400> 288

Ile 1	Leu	His	Leu	Glu 5	Met	Tyr	Gly	Val	Lys 10	His	Thr	Asn	Thr	His 15
Lys	Ala	Gln	Ala 20	Arg	Cys	Met	Thr	Arg 25	Leu	Ser	Phe	Leu	Gly 30	Phe
Leu	Leu	Arg 35	Pro	Ala	Pro	Ser	Trp 40	Ala	His	Leu	Arg	Phe 45	Thr	Val
Ser	Gly 50	Gly	Pro	Lys	Ser	Leu 55	Leu	Val	Phe	Asn	Phe 60	Phe	Leu	Ile
His 65	Phe	Cys	Gly	Gln	Phe 70	Gln	Gln	His	Cys	Pro 75	Tyr	Phe		

<210> 289  
 <211> 28  
 <212> PRT  
 <213> homo sapiens  
 <400> 289

Ile 1	Leu	Ile	Asp	Gly 5	Val	Arg	Ala	Ala	Phe 10	Ile	Pro	Tyr	Arg	Glu 15
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------

Asn Gly Ala Arg Leu Ser Arg Asp Phe Ile Ser Ala  
20 25

<210> 290

&lt;211&gt; 28

<212> PRT

<213> homo sapiens

<400> 290

His Gln Phe His Asn Tyr Phe Asn Leu Leu Gly Phe Ile His Leu Ile  
1 5 10 15

Ile Leu Lys Phe His Gln Gln Trp Gly Thr Glu Lys  
20 25

<210> 291

<211> 29

&lt;212&gt; PRT

<213> homo sapiens

&lt;400&gt; 291

Ala   Pro   Gly   Pro   Gln   Ala   Ile   Leu   Ile   Ile   Asn   Leu   Asn   Arg   Trp   Gly  
1                      5                      10                      15

Lys   Ser   Cys   Leu<sub>20</sub>   His   Pro   Ile   Gln<sub>25</sub>   Arg   Ile   Gln   Trp   Cys

&lt;210&gt; 292

<211> 30

<212> PRT

<213> homo sapiens

&lt;400&gt; 292

Ala Glu Ile Lys Ser Leu Leu Ser Leu Ala Pro Leu Tyr Ser Leu Tyr  
1 5 10 15

Gly Met Lys Ala Ala Leu Thr Pro Ser Ile Lys Ile Tyr Tyr  
20 25 30

&lt;210&gt; 293

<211> 33

<212> PRT

<213> homo sapiens

&lt;400&gt; 293

Ala Met Lys Val Leu Ser Phe Leu Leu Cys Ile Arg Ile Ser Phe Leu  
1 5 10 15

Phe Val Val Glu Ser Ile Val Arg Gly Ile Ser Lys Leu Asn Glu Val  
20 25 30

Asn

&lt;210&gt; 294

&lt;211&gt; 38

&lt;212&gt; PRT

<213> homo sapiens

<400> 294

Ala	Ile	Asn	Lys	Val	Ser	Ser	Gly	Tyr	Gly	Pro	Leu	Ala	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Val	Ser	Val	Glu	Ala	Ala	Gln	Arg	Ile	Ser	Leu	Asn	Phe	Ser
			20					25					30		
Gln	Lys	Trp	Leu	Leu	Thr										
		35													

<210> 295

<211> 40

<212> PRT

<213> homo sapiens

<400> 295

Phe	Thr	Ser	Phe	Asn	Leu	Leu	Ile	Pro	Arg	Thr	Ile	Leu	Ser	Thr	Thr
1				5					10					15	
Asn	Arg	Asn	Glu	Ile	Leu	Ile	His	Lys	Arg	Lys	Leu	Lys	Thr	Phe	Ile
			20					25					30		
Ala	Tyr	Val	Gly	Leu	Ser	Asn	Lys								
		35					40								

<210> 296

<211> 71

<212> PRT

<213> homo sapiens

<400> 296

Val	Asn	Leu	Leu	Lys	Tyr	Gly	Gln	Ile	His	Leu	Ala	Val	Lys	Gln	Leu
1				5					10					15	
Asn	Ile	His	Cys	Tyr	Leu	Ile	Lys	Val	Phe	Val	Ser	Val	Leu	Pro	Gly
			20					25					30		
Pro	Asn	Ile	Lys	Thr	Thr	Ser	Val	Gln	Lys	Ile	Asn	Val	Gln	Arg	Ala
			35				40					45			
Val	Cys	Ser	Leu	Phe	Trp	Tyr	Val	His	Phe	Lys	Lys	Thr	Pro	Leu	Ser
	50					55					60				
Ser	Leu	Ala	Asn	Gln	Glu	Tyr									
65					70										

<210> 297

<211> 67

<212> PRT

<213> homo sapiens

<400> 297

Arg	Phe	Tyr	Leu	Tyr	Phe	Ile	Leu	Ser	Arg	Gly	Thr	Asn	Ser	Arg	His
1				5					10					15	
Thr	Phe	Ala	Arg	Pro	Ser	Cys	Arg	Lys	Thr	Gln	Ser	Arg	Lys	Gly	Lys
			20					25					30		
Asn	Lys	Ile	Ala	Ile	Lys	Tyr	Met	Val	Leu	Gly	Ala	Gly	Arg	Thr	Arg

00673395.122700



35					40					45					
Asn	Pro	Gln	Gly	Asp	Gln	Phe	Leu	Ala	Arg	Ser	Phe	Phe	Arg	Val	Tyr
	50					55					60				
Pro	Val	Glu													
65															
<210> 298															
<211> 56															
<212> PRT															
<213> homo sapiens															
<400> 298															
Lys	Asn	Leu	Glu	Phe	Phe	Ser	Pro	Ser	Thr	Ser	Tyr	Leu	Leu	Leu	Gln
1				5					10					15	
Asn	Ser	Ser	Glu	Gly	Phe	Ile	Tyr	Ile	Leu	Ser	Tyr	Pro	Glu	Gly	Pro
			20					25					30		
Thr	Ala	Gly	Ile	Pro	Leu	Pro	Gly	Leu	Leu	Ala	Glu	Arg	His	Arg	Ala
		35					40					45			
Val	Lys	Ala	Lys	Ile	Lys	Leu	Gln								
	50					55									
<210> 299															
<211> 140															
<212> PRT															
<213> homo sapiens															
<400> 299															
Thr	Pro	Asn	Ser	Arg	Gly	Ala	Gly	Arg	Val	Val	Arg	Gly	Ser	Ala	Arg
1				5					10					15	
Gly	Val	Gly	Arg	Ser	Cys	Ala	Ser	Trp	Leu	Pro	Val	Gly	Arg	Arg	Cys
			20					25					30		
Arg	Thr	Ser	Glu	Thr	Gly	Ser	Gly	Ala	Ser	Arg	Arg	Ser	Arg	Ala	Ile
		35					40					45			
Gly	Ser	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Trp	Ser	Ala	Asn	Ser	Ala	Ser
	50					55					60				
Ser	Ala	Arg	Pro	Thr	Ser	Ser	Gly	Pro	Lys	Pro	Ser	Phe	Ile	Ala	
65				70					75					80	
Phe	Arg	Phe	Gly	Gly	Gln	Ser	Leu	Pro	Pro	Phe	Ile	Ser	Leu	Trp	Val
				85					90					95	
Gln	Glu	Leu	Asp	Phe	Phe	Ile	Trp	Ser	Ile	Tyr	Ile	Ser	Tyr	Ile	Ser
			100					105					110		
Ile	Leu	Arg	Asp	Leu	Lys	Gln	Glu	Leu	Leu	Met	Gly	Gly	Gln	Gln	Thr
		115					120					125			
Ile	Tyr	Ser	Cys	Ser	Ser	Leu	Thr	Gly	Phe	Ala	Ser				
	130					135					140				
<210> 300															
<211> 279															

<212> PRT  
<213> homo sapiens

<400> 300

Gln 1	Ser	Arg	Ser	Arg 5	Pro	Arg	Arg	Glu	Gly 10	Val	Gly	Thr	Gly	Ser 15	Arg
Ala	Val	Leu	Cys 20	Ile	Leu	Ala	Thr	Cys 25	Gly	Ser	Lys	Met	Ser 30	Asp	Ile
Gly	Asp	Trp 35	Phe	Arg	Ser	Ile	Pro 40	Ala	Ile	Thr	Arg	Tyr 45	Trp	Phe	Ala
Ala	Thr 50	Val	Ala	Val	Pro	Leu 55	Val	Gly	Lys	Leu	Gly 60	Leu	Ile	Ser	Pro
Ala 65	Tyr	Leu	Phe	Leu	Trp 70	Pro	Glu	Ala	Phe	Leu 75	Tyr	Arg	Phe	Gln	Ile 80
Trp	Arg	Pro	Ile	Thr 85	Ala	Thr	Phe	Tyr	Phe 90	Pro	Val	Gly	Pro	Gly 95	Thr
Gly	Phe	Leu	Tyr 100	Leu	Val	Asn	Leu	Tyr 105	Phe	Leu	Tyr	Gln	Tyr 110	Ser	Thr
Arg	Leu	Glu 115	Thr	Gly	Ala	Phe	Asp 120	Gly	Arg	Pro	Ala	Asp 125	Tyr	Leu	Phe
Met	Leu 130	Leu	Phe	Asn	Trp 135	Ile	Cys	Ile	Val	Ile	Thr 140	Gly	Leu	Ala	Met
Asp 145	Met	Gln	Leu	Leu	Met 150	Ile	Pro	Leu	Ile	Met 155	Ser	Val	Leu	Tyr	Val 160
Trp	Ala	Gln	Leu	Asn 165	Arg	Asp	Met	Ile	Val 170	Ser	Phe	Trp	Phe	Gly 175	Thr
Arg	Phe	Lys	Ala 180	Cys	Tyr	Leu	Pro	Trp 185	Val	Ile	Leu	Gly	Phe 190	Asn	Tyr
Ile	Ile	Gly 195	Gly	Ser	Val	Ile	Asn 200	Glu	Leu	Ile	Gly	Asn 205	Leu	Val	Gly
His 210	Leu	Tyr	Phe	Phe	Leu	Met 215	Phe	Arg	Tyr	Pro	Met 220	Asp	Leu	Gly	Gly
Arg 225	Asn	Phe	Leu	Ser	Thr 230	Pro	Gln	Phe	Leu	Tyr 235	Arg	Trp	Leu	Pro	Ser 240
Arg	Arg	Gly	Gly	Val 245	Ser	Gly	Phe	Gly	Val 250	Pro	Pro	Ala	Ser	Met 255	Arg
Arg	Ala	Ala	Asp 260	Gln	Asn	Gly	Gly	Gly 265	Gly	Arg	His	Asn	Trp 270	Gly	Gln
Gly	Phe	Arg 275	Leu	Gly	Asp	Gln									

<210> 301  
<211> 106  
<212> PRT  
<213> homo sapiens

00673305.122700

<400> 301

Ile 1	Asp	Gln	Ile	Lys 5	Lys	Ser	Ser	Ser	Trp 10	Thr	His	Arg	Glu	Ile 15	Lys	
Gly	Gly	Ser	Asp 20	Trp	Pro	Pro	Asn	Leu 25	Lys	Ala	Ile	Lys	Glu 30	Gly	Phe	
Gly	Pro	Glu 35	Glu	Glu	Val	Gly	Arg 40	Ala	Asp	Glu	Ala	Glu 45	Phe	Ala	Asp	
Gln	Gly 50	His	Gly	Asp	Gly	Gly 55	Gly	Glu	Pro	Ile	Ala 60	Arg	Asp	Arg	Arg	
Asp 65	Ala	Pro	Glu	Pro	Val 70	Ser	Asp	Val	Arg	His 75	Leu	Arg	Pro	Thr	Gly 80	
Ser	Gln	Asp	Ala	Gln 85	Asp	Arg	Pro	Thr	Pro 90	Arg	Ala	Asp	Pro	Leu 95	Thr	
Thr	Arg	Pro	Ala 100	Pro	Arg	Leu	Leu	Gly 105	Val							

<210> 302

<211> 207

<212> PRT

<213> homo sapiens

<400> 302

Leu 1	Glu	Pro	Leu	Glu 5	Pro	Asn	Arg	Leu	Glu 10	Leu	Lys	Lys	Gly	Tyr 15	Leu	
Thr	Leu	Ser	Asp 20	Ser	Gly	Asp	Lys	Val 25	Ala	Val	Glu	Trp	Asp 30	Lys	Asp	
His	Gly	Val 35	Leu	Glu	Ser	His	Leu 40	Ala	Glu	Lys	Gly	Arg 45	Gly	Met	Glu	
Leu 50	Ser	Asp	Leu	Ile	Val	Phe 55	Asn	Gly	Lys	Leu	Tyr 60	Ser	Val	Asp	Asp	
Arg 65	Thr	Gly	Val	Val	Tyr 70	Gln	Ile	Glu	Gly	Ser 75	Lys	Ala	Val	Pro	Trp 80	
Val	Ile	Leu	Ser	Asp 85	Gly	Asp	Gly	Thr	Val 90	Glu	Lys	Gly	Phe	Lys 95	Ala	
Glu	Trp	Leu	Ala 100	Val	Lys	Asp	Glu	Arg 105	Leu	Tyr	Val	Gly	Gly 110	Leu	Gly	
Lys	Glu	Trp 115	Thr	Thr	Thr	Thr	Gly 120	Asp	Val	Val	Asn	Glu 125	Asn	Pro	Glu	
Trp	Val 130	Lys	Val	Val	Gly	Tyr 135	Lys	Gly	Ser	Val	Asp 140	His	Glu	Asn	Trp	
Val 145	Ser	Asn	Tyr	Asn	Ala 150	Leu	Arg	Ala	Ala	Ala 155	Gly	Ile	Gln	Pro	Pro 160	
Gly	Asn	Leu	Ile	His 165	Glu	Ser	Ala	Cys	Trp 170	Ser	Asp	Thr	Leu	Gln 175	Arg	

09673395.122700

Trp	Phe	Phe	Leu 180	Pro	Arg	Arg	Ala	Ser 185	Gln	Glu	Arg	Tyr	Ser 190	Glu	Glu
Gly	Arg	Arg 195	Ala	Gln	Gly	Arg	Gln 200	Pro	Ala	Ala	Glu	Arg 205	Leu	Pro	

<210> 303  
 <211> 153  
 <212> PRT  
 <213> homo sapiens

<400> 303

Arg 1	Trp	Trp	Ala	Thr 5	Arg	Ala	Ala	Trp	Thr 10	Thr	Arg	Thr	Gly	Cys 15	Pro
Thr	Thr	Thr	Pro 20	Cys	Gly	Leu	Leu	Pro 25	Ala	Ser	Ser	Arg	Gln 30	Val	Thr
Ser	Ser	Met 35	Ser	Leu	Pro	Ala	Gly 40	Val	Thr	Arg	Cys	Ser 45	Ala	Gly	Ser
Ser	Cys 50	Arg	Ala	Ala	Pro	Ala 55	Arg	Ser	Ala	Thr	Ala 60	Arg	Lys	Asp	Asp
Glu 65	Arg	Lys	Gly	Ala	Asn 70	Leu	Leu	Leu	Ser	Ala 75	Ser	Pro	Asp	Phe	Gly 80
Asp	Ile	Ala	Val	Ser 85	His	Val	Gly	Ala	Val 90	Val	Pro	Thr	His	Gly 95	Phe
Ser	Ser	Phe	Lys 100	Phe	Ile	Pro	Asn	Thr 105	Asp	Asp	Gln	Ile	Ile 110	Val	Ala
Leu	Lys	Ser 115	Glu	Glu	Asp	Ser	Gly 120	Arg	Val	Ala	Ser	Tyr 125	Ile	Met	Ala
Phe	Thr 130	Leu	Asp	Gly	Arg	Phe 135	Leu	Leu	Pro	Glu	Thr 140	Lys	Ile	Gly	Ser
Val 145	Lys	Tyr	Glu	Gly	Ile 150	Glu	Phe	Ile							

<210> 304  
 <211> 174  
 <212> PRT  
 <213> homo sapiens

<400> 304

Val 1	Gly	Thr	Thr	Ala 5	Pro	Thr	Trp	Leu	Thr 10	Ala	Met	Ser	Pro	Lys 15	Ser
Gly	Glu	Ala	Leu 20	Ser	Ser	Arg	Leu	Ala 25	Pro	Leu	Arg	Ser	Ser 30	Ser	Phe
Leu	Ala	Val 35	Ala	Leu	Leu	Ala	Gly 40	Ala	Ala	Arg	Gln	Glu 45	Glu	Pro	Ala
Leu	Gln 50	Arg	Val	Thr	Pro	Ala 55	Gly	Arg	Leu	Met	Asp 60	Glu	Val	Thr	Trp

00673305.122700

Arg 65	Leu	Asp	Ala	Gly	Ser 70	Ser	Pro	Gln	Gly	Val 75	Val	Val	Gly	His	Pro 80
Val	Leu	Val	Val	His 85	Ala	Ala	Leu	Val	Ala 90	His	His	Leu	His	Pro 95	Leu
Arg	Val	Leu	Val 100	His	His	Ile	Thr	Arg 105	Ser	Gly	Arg	Pro	Leu 110	Leu	Ala
Gln	Ala	Ala 115	His	Val	Gln	Thr	Leu 120	Val	Leu	His	Cys	Gln 125	Pro	Phe	Gly
Leu	Glu 130	Ala	Phe	Leu	His	Gly 135	Ala	Val	Ala	Val	Gly 140	Gln	Asn	His	Pro
Gly 145	His	Gly	Phe	Ala	Ala 150	Phe	Asp	Leu	Val	Asp 155	Asp	Pro	Arg	Pro	Val 160
Ile	His	Gly	Val	Glu 165	Phe	Pro	Ile	Glu	Asn 170	Asn	Gln	Val	Gly		

```
<210> 305
<211> 61
<212> PRT
<213> homo sapiens
```

<400> 305

Lys 1	Leu	Val	Cys	Leu 5	Glu	Ala	Asp	Ser	Lys 10	Ser	Ser	Phe	Ser	Ser	Glu 15
His	Leu	Phe	Ser 20	Tyr	His	Leu	Ile	Ser 25	Ile	Leu	Lys	His	His 30	Gly	Cys
Ser	Cys	Ser 35	Lys	Met	Gly	Asp	Val 40	Lys	Glu	Asn	Tyr	Leu 45	Glu	Thr	Phe
Ile	Ser 50	Ser	Pro	Lys	Trp	Ser 55	Phe	Ile	Leu	Cys	Leu 60	Ser			

```
<210> 306
<211> 144
<212> PRT
<213> homo sapiens
```

<400> 306

Asn 1	Thr	Met	Ala	Val 5	Ala	Ala	Val	Lys	Trp 10	Val	Met	Ser	Lys	Arg 15	Thr
Ile	Leu	Lys	His 20	Leu	Phe	Pro	Val	Gln 25	Asn	Gly	Ala	Leu	Tyr 30	Cys	Val
Cys	His	Lys 35	Ser	Thr	Tyr	Ser	Pro 40	Leu	Pro	Asp	Asp	Tyr 45	Asn	Cys	Asn
Val	Glu 50	Leu	Ala	Leu	Thr	Ser 55	Asp	Gly	Arg	Thr	Ile 60	Val	Cys	Tyr	His
Pro 65	Ser	Val	Asp	Ile	Pro 70	Tyr	Glu	His	Thr	Lys 75	Pro	Ile	Pro	Arg	Pro 80
Asp	Pro	Val	His	Asn	Asn	Glu	Glu	Thr	His	Asp	Gln	Val	Leu	Lys	Thr

85

90

95

Arg	Leu	Glu	Glu	Lys	Val	Glu	His	Leu	Glu	Glu	Gly	Pro	Met	Ile	Glu
			100					105					110		
Gln	Leu	Ser	Lys	Met	Phe	Phe	Thr	Thr	Lys	His	Arg	Trp	Tyr	Pro	His
		115					120					125			
Gly	Arg	Tyr	His	Arg	Cys	Arg	Lys	Asn	Leu	Asn	Pro	Pro	Lys	Asp	Arg
	130					135					140				

&lt;210&gt; 307

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 307

Ile	His	Gln	Thr	Ala	Phe	Ser	Gln	Met	Ala	Asn	Glu	Ala	His	Phe	Ser
1				5					10					15	
Leu	Ile	Pro	Pro	Gly	Thr	Ser	Ala	Ser	Ser	Val	Phe	Trp	Arg	Ile	Gln
			20					25					30		
Ile	Leu	Thr	Thr	Ser	Val	Ile	Pro	Ser	Met	Arg	Ile	Pro	Thr	Val	Leu
		35					40					45			
Ser	Ser	Lys	Glu	His	Phe	Ala	Lys	Leu	Phe	Tyr	His	Arg	Ser	Phe	Leu
	50					55					60				
Lys	Val	Phe	Asn	Phe	Phe	Phe	Gln	Ser	Gly	Phe	Gln	His	Leu	Ile	Met
	65				70					75					80
Cys	Phe	Phe	Ile	Ile	Met	His	Arg	Ile	Trp	Pro	Arg	Asp	Arg	Phe	Cys
				85					90					95	
Val	Phe	Ile	Trp	Asn	Val	His	Arg	Arg	Val	Val	Ala	Tyr	Tyr	Cys	Pro
			100					105					110		
Ala	Ile	Arg	Ser	Gln	Ser	Lys	Leu	Tyr	Val	Ala	Ile	Ile	Val	Ile	Trp
		115					120					125			

&lt;210&gt; 308

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 308

Ser	Arg	Ser	Lys	Met	Ala	Ala	Leu	Arg	Ala	Leu	Cys	Gly	Phe	Arg	Gly
1				5					10					15	
Val	Ala	Ala	Gln	Val	Leu	Arg	Pro	Gly	Ala	Gly	Val	Arg	Leu	Pro	Ile
			20					25					30		
Gln	Pro	Ser	Arg	Gly	Val	Arg	Gln	Trp	Gln	Pro	Asp	Val	Glu	Trp	Ala
		35					40					45			
Gln	Gln	Phe	Gly	Gly	Ala	Val	Met	Tyr	Pro	Ser	Lys	Glu	Thr	Ala	His
	50					55					60				
Trp	Lys	Pro	Pro	Pro	Trp	Asn	Asp	Val	Asp	Pro	Pro	Lys	Asp	Thr	Ile
	65				70					75					80

00573305.122700

Val	Lys	Asn	Ile	Thr 85	Leu	Asn	Phe	Gly	Pro 90	Gln	His	Pro	Ala	Ala 95	His	
Gly	Val	Leu	Arg 100	Leu	Val	Met	Glu	Leu 105	Ser	Gly	Glu	Met	Val 110	Arg	Lys	
Cys	Asp	Pro 115	His	Ile	Gly	Leu	Leu 120	His	Arg	Gly	Thr	Glu 125	Lys	Leu	Ile	
Glu	Tyr 130	Lys	Thr	Tyr	Leu	Gln 135	Ala	Leu	Pro	Tyr	Phe 140	Asp	Arg	Leu	Asp	
Tyr 145	Val	Ser	Met	Met	Cys 150	Asn	Glu	Gln	Ala	Tyr 155	Ser	Leu	Ala	Val	Glu 160	
Lys	Leu	Leu	Asn	Ile 165	Arg	Pro	Pro	Pro	Arg 170	Ala	Gln	Trp	Ile	Arg 175	Val	
Leu	Phe	Gly	Glu 180	Ile	Thr	Arg	Leu	Leu 185	Asn	His	Ile	Met	Ala 190	Val	Thr	
Thr	His	Ala 195	Leu	Asp	Leu	Gly	Ala 200	Met	Thr	Pro	Phe	Phe 205	Trp	Leu	Phe	
Glu	Glu 210	Arg	Glu	Lys	Met	Phe 215	Glu	Phe	Tyr	Glu	Arg 220	Val	Ser	Gly	Ala	
Arg 225	Met	His	Ala	Ala	Tyr 230	Ile	Arg	Pro	Gly	Gly 235	Val	His	Gln	Asp	Leu 240	
Pro	Leu	Gly	Leu	Met 245	Asp	Asp	Ile	Tyr	Gln 250	Phe	Ser	Lys	Asn	Phe 255	Ser	
Leu	Arg	Leu	Asp 260	Glu	Leu	Glu	Glu	Leu 265	Leu	Thr	Asn	Asn	Arg 270	Ile	Trp	
Arg	Asn	Arg 275	Thr	Ile	Asp	Ile	Gly 280	Val	Val	Thr	Ala	Glu 285	Glu	Ala	Leu	
Asn	Tyr 290	Gly	Phe	Ser	Gly	Val 295	Met	Leu	Arg	Gly	Ser 300	Gly	Ile	Gln	Trp	
Asp 305	Leu	Arg	Lys	Thr	Gln 310	Pro	Tyr	Asp	Val	Tyr 315	Asp	Gln	Val	Glu	Phe 320	
Asp	Val	Pro	Val	Gly 325	Ser	Arg	Gly	Asp	Cys 330	Tyr	Asp	Arg	Tyr	Leu 335	Cys	
Arg	Val	Glu	Glu 340	Met	Arg	Gln	Ser	Leu 345	Arg	Ile	Ile	Ala	Gln 350	Cys	Leu	
Asn	Lys	Met 355	Pro	Pro	Gly	Glu	Ile 360	Lys	Val	Asp	Asp	Ala 365	Lys	Val	Ser	
Pro	Pro 370	Lys	Arg	Ala	Glu	Met 375	Lys	Thr	Ser	Met	Glu 380	Ser	Leu	Ile	His	
His 385	Phe	Lys	Leu	Tyr	Thr 390	Glu	Gly	Tyr	Gln	Val 395	Pro	Pro	Gly	Ala	Thr 400	
Tyr	Thr	Ala	Ile	Glu 405	Ala	Pro	Lys	Gly	Glu 410	Phe	Gly	Val	Tyr	Leu 415	Val	

00673305.122700

Ser	Asp	Gly	Ser	Ser	Arg	Pro	Tyr	Arg	Cys	Lys	Ile	Lys	Ala	Pro	Gly
			420					425					430		
Phe	Ala	His	Leu	Ala	Gly	Leu	Asp	Lys	Met	Ser	Lys	Gly	His	Met	Leu
		435					440					445			
Ala	Asp	Val	Val	Ala	Ile	Ile	Gly	Thr	Gln	Asp	Ile	Val	Phe	Gly	Glu
	450					455					460				
Val	Asp	Arg													
465															

<210> 309  
 <211> 131  
 <212> PRT  
 <213> homo sapiens

<400> 309

Gln	Pro	Ser	Val	His	Glu	His	Thr	His	Thr	His	Thr	His	Thr	His	Thr
1				5					10					15	
His	Thr	Gln	Arg	Pro	Ile	Ser	Ser	Glu	Glu	Gln	Ala	Pro	Gln	Lys	Lys
			20					25					30		
Leu	Ile	Gly	Arg	Gly	Asp	Gln	Thr	Leu	Leu	Pro	Cys	Ser	Pro	Ile	Tyr
		35					40					45			
Phe	Ser	Lys	Tyr	Asn	Ile	Leu	Gly	Thr	Tyr	Asp	Gly	Asn	Asp	Ile	Cys
	50					55					60				
Gln	His	Val	Ser	Leu	Arg	His	Leu	Val	Gln	Thr	Ser	Gln	Met	Gly	Lys
65					70					75					80
Thr	Arg	Ser	Leu	Asp	Leu	Ala	Ser	Ile	Arg	Ala	Ala	Ala	Ala	Ile	Arg
				85					90					95	
His	Gln	Val	His	Pro	Lys	Leu	Ser	Leu	Gly	Ser	Leu	Asn	Gly	Ser	Ile
			100					105					110		
Cys	Gly	Ser	Trp	Arg	Asn	Leu	Val	Ala	Leu	Ser	Ile	Gln	Leu	Lys	Val
		115					120					125			
Met	Asn	Gln													
	130														

<210> 310  
 <211> 100  
 <212> PRT  
 <213> homo sapiens

<400> 310

Ser	Gln	Asp	Thr	Met	Arg	Cys	Trp	Val	Leu	Gly	Pro	Lys	Val	Gln	Gly
1				5					10					15	
Asn	Val	Leu	His	Asn	Cys	Val	Leu	Trp	Arg	Val	His	Ile	Ile	Pro	Arg
			20					25					30		
Trp	Arg	Leu	Pro	Val	Gly	Cys	Phe	Phe	Ala	Trp	Val	His	Asn	Ser	Ser
		35					40					45			

00673605-122700



Pro	Lys	Leu	Leu	Cys	Pro	Phe	His	Ile	Trp	Leu	Pro	Leu	Pro	Asn	Thr
	50					55					60				
Ser	Ala	Gly	Leu	Asn	Arg	Gln	Ser	Asp	Ser	Ser	Pro	Arg	Pro	Gln	His
65					70					75					80
Leu	Gly	Arg	Asp	Ala	Pro	Glu	Ala	Ala	Gln	Ser	Pro	Gln	Arg	Arg	His
				85					90					95	
Leu	Thr	Pro	Ala												
			100												

<210> 311  
 <211> 162  
 <212> PRT  
 <213> homo sapiens

<400> 311

Arg	Arg	Leu	Arg	Gly	Gly	Glu	Pro	Ser	Thr	Asp	Arg	Arg	Arg	Asp	Pro
1				5					10					15	
Glu	Ser	Arg	Thr	Pro	Ala	Pro	Pro	Pro	Thr	Pro	Arg	Ala	Met	Asp	Pro
			20						25				30		
Lys	Asp	Arg	Lys	Lys	Ile	Gln	Phe	Ser	Val	Pro	Ala	Pro	Pro	Ser	Gln
		35					40					45			
Leu	Asp	Pro	Arg	Gln	Val	Glu	Met	Ile	Arg	Arg	Arg	Arg	Pro	Thr	Pro
	50					55					60				
Ala	Met	Leu	Phe	Arg	Leu	Ser	Glu	His	Ser	Ser	Pro	Glu	Glu	Glu	Ala
65					70					75					80
Ser	Pro	His	Gln	Arg	Ala	Ser	Gly	Glu	Gly	His	His	Leu	Lys	Ser	Lys
				85					90					95	
Arg	Pro	Asn	Pro	Cys	Ala	Tyr	Thr	Pro	Pro	Ser	Leu	Lys	Ala	Val	Gln
			100					105					110		
Arg	Ile	Ala	Glu	Ser	His	Leu	Gln	Ser	Ile	Ser	Asn	Leu	Asn	Glu	Asn
		115					120					125			
Gln	Ala	Ser	Glu	Glu	Glu	Asp	Glu	Leu	Gly	Glu	Leu	Arg	Glu	Leu	Gly
	130					135					140				
Tyr	Pro	Arg	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Ala	Arg	Leu
145					150					155					160
Lys	Ser														

<210> 312  
 <211> 154  
 <212> PRT  
 <213> homo sapiens

<400> 312

Val	Ser	Leu	Gly	Arg	Asn	Leu	Ser	Ala	Leu	Pro	Pro	Leu	Ser	Leu	Ala
1				5					10					15	
His	Arg	His	Pro	Ala	Cys	Ile	Ser	Gln	Glu	Glu	Val	Glu	Gly	Thr	Ser
			20					25					30		

00673305-122700

Leu	Phe	Pro 35	Arg	Asn	Pro	Leu	Tyr 40	Pro	His	Pro	Val	Leu 45	Cys	Ser	Ser	
Pro	Arg 50	Leu	Leu	Gly	Leu	Arg 55	Leu	Leu	Thr	Ser	Arg 60	Arg	Leu	Arg	Leu	
Val 65	Cys	Val	Cys	Leu	Phe 70	Ala	His	Leu	Trp	Leu 75	Ile	Pro	Arg	Glu	Pro 80	
Gly	His	Leu	Leu	Pro 85	Asp	Ala	His	Pro	Cys 90	Gln	Ser	Phe	Leu	His 95	Ser	
Pro	Ser	Gly	Arg 100	Trp	Asp	Val	Arg	Gln 105	Pro	Thr	Leu	Glu	Asn 110	Pro	Glu	
Asn	Arg	Glu 115	Gln	Gly	Phe	Ala	Leu 120	His	Asn	Ser	Thr	Pro 125	Gln	Ile	Leu	
Ser	Pro 130	Gly	His	Arg	Arg	Pro 135	Thr	Gly	Gln	Asp	Pro 140	Lys	Ile	Trp	Gly	
Lys 145	Glu	Val	Leu	Arg	Thr 150	Leu	Arg	Tyr	Pro							

<210> 313  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 313

Ala 1	Gln	Gly	Leu	Gly 5	Leu	Phe	Asp	Leu	Arg 10	Trp	Cys	Pro	Ser	Pro 15	Glu	
Ala	Leu	Trp	Trp 20	Gly	Glu	Ala	Ser	Ser 25	Ser	Gly	Glu	Glu	Cys 30	Ser	Glu	
Ser	Arg	Asn 35	Ser	Met	Ala	Gly	Val 40	Gly	Leu	Leu	Arg	Arg 45	Ile	Ile	Ser	
Thr	Trp 50	Arg	Gly	Ser	Ser	Trp 55	Leu	Gly	Gly	Ala	Gly 60	Thr	Glu	Asn	Trp	
Ile 65	Phe	Leu	Arg	Ser	Leu 70	Gly	Ser	Met	Ala	Arg 75	Gly	Val	Gly	Gly	Gly 80	
Ala	Gly	Val	Arg	Asp 85	Ser	Gly	Ser	Arg	Arg 90	Arg	Ser	Val	Leu	Gly 95	Ser	
Pro	Pro	Arg	Arg 100													

<210> 314  
 <211> 162  
 <212> PRT  
 <213> homo sapiens

<400> 314

Ser 1	Asp	Arg	Trp	Thr 5	Cys	Ser	Pro	Pro	Leu 10	Gly	Ala	Arg	Ser	Met 15	Ser	
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	--

00573385-132700

Arg	Phe	Pro	Ala	Val	Ala	Gly	Arg	Ala	Pro	Arg	Arg	Gln	Glu	Glu	Gly	
			20					25					30			
Glu	Arg	Ser	Arg	Asp	Leu	Gln	Glu	Glu	Arg	Leu	Ser	Ala	Val	Cys	Ile	
		35					40					45				
Ala	Asp	Arg	Glu	Glu	Lys	Gly	Cys	Thr	Ser	Gln	Glu	Gly	Gly	Thr	Thr	
	50					55					60					
Pro	Thr	Phe	Pro	Ile	Gln	Lys	Gln	Arg	Lys	Lys	Ile	Ile	Gln	Ala	Val	
	65				70					75					80	
Arg	Asp	Asn	Ser	Phe	Leu	Ile	Val	Thr	Gly	Asn	Thr	Gly	Ser	Gly	Lys	
				85					90					95		
Thr	Thr	Gln	Leu	Pro	Lys	Tyr	Leu	Tyr	Glu	Ala	Gly	Phe	Ser	Gln	His	
			100					105					110			
Gly	Met	Ile	Gly	Val	Thr	Gln	Pro	Arg	Lys	Val	Ala	Ala	Ile	Ser	Val	
		115					120					125				
Ala	Gln	Arg	Val	Ala	Glu	Glu	Met	Lys	Cys	Thr	Leu	Gly	Ser	Lys	Val	
	130					135					140					
Gly	Tyr	Gln	Val	Arg	Phe	Asp	Asp	Cys	Ser	Ser	Lys	Glu	Thr	Ala	Ile	
	145				150					155					160	
Lys	Tyr															

<210> 315  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 315

Gln	Ile	Gly	Gly	Arg	Ala	Arg	Leu	His	Ser	Gly	Pro	Gly	Leu	Cys	Pro	
1				5					10					15		
Gly	Phe	Pro	Gln	Ser	Arg	Ala	Gly	Arg	Gln	Gly	Gly	Arg	Arg	Arg	Val	
			20					25					30			
Ser	Gly	Gln	Glu	Thr	Ser	Arg	Lys	Ser	Gly	Ser	Arg	Leu	Phe	Ala	Ser	
		35					40					45				
Pro	Ile	Glu	Lys	Arg	Lys	Asp	Ala	Arg	Pro	Arg	Arg	Glu	Glu	Leu	Leu	
	50					55					60					
Gln	Leu	Phe	Leu	Phe	Arg	Asn	Lys	Glu	Lys	Arg	Leu	Phe	Lys	Leu		
	65				70					75						

<210> 316  
 <211> 69  
 <212> PRT  
 <213> homo sapiens

<400> 316

Ile	Gly	Lys	Val	Gly	Val	Val	Pro	Pro	Ser	Trp	Asp	Val	His	Pro	Phe	
1				5					10					15		
Ser	Ser	Leu	Ser	Ala	Met	Gln	Thr	Ala	Glu	Ser	Arg	Ser	Ser	Trp	Arg	
			20					25					30			

00573305.122700

Ser	Leu	Asp 35	Arg	Ser	Pro	Ser	Ser 40	Cys	Arg	Leu	Gly	Ala 45	Leu	Pro	Ala
Thr	Ala 50	Gly	Asn	Arg	Asp	Ile 55	Asp	Leu	Ala	Pro	Ser 60	Gly	Gly	Glu	His
Val 65	His	Arg	Ser	Glu											

<210> 317  
 <211> 173  
 <212> PRT  
 <213> homo sapiens

<400> 317

Ala 1	Gln	Glu	Ser	Pro 5	Trp	Gln	Leu	Cys	Arg 10	Gly	Ala	Arg	Thr	Ser 15	Lys
Arg	Lys	Leu	Pro 20	Lys	Leu	Gly	Met	Glu 25	Gln	His	Cys	Asn	Glu 30	Met	Cys
Pro	Pro	Ser 35	Ser	Leu	Phe	Leu	Pro 40	Gly	Ala	Tyr	Lys	Ala 45	Gln	Met	Tyr
Ser	Asp 50	Val	Trp	Thr	Asn	Thr 55	Lys	Lys	Lys	Lys	Lys 60	Lys	Lys	Lys	Lys
Lys 65	Ala	Phe	Leu	Ser	His 70	Arg	His	Lys	Thr	Gln 75	Ile	Ile	Tyr	Cys	Tyr 80
Glu	Ala	Leu	Phe	Thr 85	Asn	Gly	Gln	Phe	Leu 90	His	Phe	Ile	Ala	Ala 95	Cys
Glu	Arg	Leu	Pro 100	Asp	Gly	Arg	Pro	Ile 105	Ser	Leu	Val	Leu	Gln 110	Thr	Ser
Ser	Gln	Ala 115	Ala	Phe	Tyr	Gln	Lys 120	Gly	Glu	Asn	Ser	Cys 125	Leu	Ser	Phe
Leu	Lys 130	Asn	Ala	Phe	Leu	Tyr 135	Leu	Ser	Ile	Arg	His 140	Tyr	Thr	Ser	Glu
Leu 145	Tyr	Lys	Arg	Pro	Gly 150	Gly	Thr	Met	Ser	Leu 155	Val	Asp	Thr	Phe	His 160
Cys	Ser	Val	Ala	Pro 165	Phe	Leu	Ala	Trp	Glu 170	Ala	Ser	Ala			

<210> 318  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 318

Ala 1	Gln	Glu	Ser	Pro 5	Trp	Gln	Leu	Cys	Arg 10	Gly	Ala	Arg	Thr	Ser 15	Lys
Arg	Lys	Leu	Pro 20	Lys	Leu	Gly	Met	Glu 25	Gln	His	Cys	Asn	Glu 30	Met	Cys

00673305-122700

Pro	Pro	Ser	Ser	Leu	Phe	Leu	Pro	Gly	Ala	Tyr	Lys	Ala	Gln	Met	Tyr
		35					40					45			
Ser	Asp	Val	Trp	Thr	Asn	Thr	Lys	Lys	His	Phe	Leu	Lys	Arg	Lys	Gly
	50					55					60				
Met	Ser	Phe	Pro	Leu	Phe	Asp	Lys	Lys	Gln	Pro	Val	Met	Lys	Ser	Gly
	65				70					75					80
Ala	Gln	Glu	Arg	Trp	Val	Ser	His	Leu	Glu	Ala	Phe	Arg	Thr	Gln	Leu
				85					90					95	

<210> 319  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 319

Thr	Cys	Glu	Pro	Phe	Arg	Asn	Pro	Gln	Val	Gly	Lys	Asp	Pro	Thr	Pro
1				5					10					15	
Ser	Leu	Arg	Ile	Ile	Cys	Leu	Ala	Ile	Thr	Gly	Ser	Trp	Lys	Cys	Phe
			20					25					30		
Leu	Gly	Cys	Val	Lys	Ile	Asn	Gln	Gly	Gly	Met	Lys	His	Ile	Phe	Leu
		35					40					45			
Ala	Thr	Lys	Leu	Glu	Phe	Leu	Arg	Glu	Gln	Met	Gln	Arg	Asp	Leu	Leu
	50					55					60				
Leu	Leu	Ala	Arg	Leu	Gln	Gly	Pro	Leu	Trp	Ser	His	Thr	Glu	Ala	Val
	65				70					75					80
Thr	Gly	His	Lys	Pro	Arg	Arg	Ala	Arg	Gly	Ser	Cys	Ala	Glu	Ala	Pro
				85					90					95	
Gly	Pro	Leu	Ser	Gly	Ser	Phe	Pro	Ser							
			100					105							

<210> 320  
 <211> 82  
 <212> PRT  
 <213> homo sapiens

<400> 320

Ile	Arg	Lys	Arg	Glu	Gln	Gly	Arg	Ser	Ser	Pro	Ala	Pro	Trp	Glu	Ser
1				5					10					15	
Val	Phe	Ala	Ser	Val	Pro	Phe	Arg	Gly	Asp	Asp	Gly	Ile	Phe	Asp	Asp
			20					25					30		
Asn	Phe	Ile	Glu	Glu	Arg	Lys	Gln	Gly	Leu	Glu	Gln	Phe	Ile	Asn	Lys
		35					40					45			
Val	Ala	Gly	His	Pro	Leu	Ala	Gln	Asn	Glu	Arg	Cys	Leu	His	Met	Phe
	50					55					60				
Leu	Gln	Asp	Glu	Ile	Ile	Asp	Lys	Ser	Tyr	Thr	Pro	Ser	Lys	Ile	Arg
	65				70					75					80
His	Ala														

00673395.122700

<210> 321  
 <211> 159  
 <212> PRT  
 <213> homo sapiens

<400> 321

Arg	Ala	Ser	Pro	Cys	Pro	His	Gly	Gly	Gln	Gln	Arg	Arg	Arg	Arg	Arg
1				5					10					15	
Leu	Asn	Ala	Glu	Gly	Ala	Glu	Gly	Ala	Arg	Gly	Gly	Gly	Ser	Ser	Tyr
			20					25					30		
Ser	Glu	Met	Ala	Glu	Thr	Val	Ala	Asp	Thr	Arg	Arg	Leu	Ile	Thr	Lys
		35					40					45			
Pro	Gln	Asn	Leu	Asn	Asp	Ala	Tyr	Gly	Pro	Pro	Ser	Asn	Phe	Leu	Glu
	50					55					60				
Ile	Asp	Val	Ser	Asn	Pro	Gln	Thr	Val	Gly	Val	Gly	Arg	Gly	Arg	Phe
65					70					75					80
Thr	Thr	Tyr	Glu	Ile	Arg	Val	Lys	Thr	Asn	Leu	Pro	Ile	Phe	Lys	Leu
				85					90					95	
Lys	Glu	Ser	Thr	Val	Arg	Arg	Arg	Tyr	Ser	Asp	Phe	Glu	Trp	Leu	Arg
			100					105					110		
Ser	Glu	Leu	Glu	Arg	Glu	Ser	Lys	Val	Val	Val	Pro	Pro	Leu	Pro	Gly
		115					120					125			
Lys	Ala	Phe	Leu	Arg	Gln	Phe	Leu	Leu	Glu	Glu	Met	Met	Glu	Tyr	Leu
	130					135					140				
Met	Thr	Ile	Leu	Leu	Arg	Lys	Glu	Asn	Lys	Gly	Trp	Ser	Ser	Leu	
145					150					155					

<210> 322  
 <211> 114  
 <212> PRT  
 <213> homo sapiens

<400> 322

Phe	Thr	Ser	Gln	Pro	Phe	Lys	Val	Thr	Val	Ser	Ser	Ser	Asn	Ser	Arg
1				5					10					15	
Phe	Phe	Gln	Leu	Glu	Asn	Arg	Lys	Ile	Cys	Leu	Asp	Pro	Asp	Phe	Val
			20					25					30		
Ser	Gly	Glu	Ala	Ala	Pro	Ala	Asp	Pro	His	Arg	Leu	Arg	Val	Ala	His
		35					40					45			
Ile	Asp	Leu	Glu	Glu	Val	Ala	Gly	Gly	Ser	Val	Gly	Val	Ile	Gln	Val
50						55					60				
Leu	Arg	Leu	Gly	Asp	Gln	Pro	Pro	Gly	Val	Ser	His	Gly	Leu	Arg	His
65					70					75					80
Phe	Ala	Val	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Ser	Leu	Arg	Pro	Leu	Arg
				85					90					95	

00673305.122700

Val Gln Pro Pro Pro Pro Pro Leu Leu Pro Ala Val Gly Thr Arg Ala  
100 105 110

Arg Ala

<210> 323

<211> 374

<212> PRT

<213> homo sapiens

<400> 323

Arg 1	Arg	Ala	Gln	Glu 5	Ser	Pro	Leu	Gly	Arg 10	Gln	Ser	His	Leu	Pro 15	Arg
Ile	Tyr	Gln	Ala 20	Phe	Leu	Met	Ser	Ala 25	Thr	Phe	Asn	Glu	Asp 30	Val	Gln
Ala	Leu	Lys 35	Glu	Leu	Ile	Leu	His 40	Asn	Pro	Val	Thr	Leu 45	Lys	Leu	Gln
Glu	Ser 50	Gln	Leu	Pro	Gly	Pro 55	Asp	Gln	Leu	Gln	Gln 60	Phe	Gln	Val	Val
Cys 65	Glu	Thr	Glu	Glu	Asp 70	Lys	Phe	Leu	Leu	Leu 75	Tyr	Ala	Leu	Leu	Lys 80
Leu	Ser	Leu	Ile	Arg 85	Gly	Lys	Ser	Leu	Leu 90	Phe	Val	Asn	Thr	Leu 95	Glu
Arg	Ser	Tyr	Arg 100	Leu	Arg	Leu	Phe	Leu 105	Glu	Gln	Phe	Ser	Ile 110	Pro	Thr
Cys	Val	Leu 115	Asn	Gly	Glu	Leu	Pro 120	Leu	Arg	Ser	Arg	Cys 125	His	Ile	Ile
Ser	Gln 130	Phe	Asn	Gln	Gly	Phe 135	Tyr	Asp	Cys	Val	Ile 140	Ala	Thr	Asp	Ala
Glu 145	Val	Leu	Gly	Ala	Pro 150	Val	Lys	Gly	Lys	Arg 155	Arg	Gly	Arg	Gly	Pro 160
Lys	Gly	Asp	Lys	Ala 165	Ser	Asp	Pro	Glu	Ala 170	Gly	Val	Ala	Arg	Gly 175	Ile
Asp	Phe	His	His 180	Val	Ser	Ala	Val	Leu 185	Asn	Phe	Asp	Leu	Pro 190	Pro	Thr
Pro	Glu	Ala 195	Tyr	Ile	His	Arg	Ala 200	Gly	Arg	Thr	Ala	Arg 205	Ala	Asn	Asn
Pro	Gly 210	Ile	Val	Leu	Thr	Phe 215	Val	Leu	Pro	Thr	Glu 220	Gln	Phe	His	Leu
Gly 225	Lys	Ile	Glu	Glu	Leu 230	Leu	Ser	Gly	Glu	Asn 235	Arg	Gly	Pro	Ile	Leu 240
Leu	Pro	Tyr	Gln	Phe 245	Arg	Met	Glu	Glu	Ile 250	Glu	Gly	Phe	Arg	Tyr 255	Arg
Cys	Arg	Asp	Ala 260	Met	Arg	Ser	Val	Thr 265	Lys	Gln	Ala	Ile	Arg 270	Glu	Ala

09673305.122700

Arg	Leu	Lys 275	Glu	Ile	Lys	Glu	Glu 280	Leu	Leu	His	Ser	Glu 285	Lys	Leu	Lys
Thr	Tyr 290	Phe	Glu	Asp	Asn	Pro 295	Arg	Asp	Leu	Gln	Leu 300	Leu	Arg	His	Asp
Leu 305	Pro	Leu	His	Pro	Ala 310	Val	Val	Lys	Pro	His 315	Leu	Gly	His	Val	Pro 320
Asp	Tyr	Leu	Val	Pro 325	Pro	Ala	Leu	Arg	Gly 330	Leu	Val	Arg	Pro	His 335	Lys
Lys	Arg	Lys	Lys 340	Leu	Ser	Ser	Ser	Cys 345	Arg	Lys	Ala	Lys	Arg 350	Ala	Lys
Ser	Gln	Asn 355	Pro	Leu	Arg	Ser	Phe 360	Lys	His	Lys	Gly	Lys 365	Lys	Phe	Arg
Pro	Thr 370	Ala	Lys	Pro	Ser										

<210> 324

<211> 224

<212> PRT

<213> homo sapiens

<400> 324

Gln 1	Arg	Val	Arg	Ala 5	Ala	Leu	Leu	Ser	Ser 10	Ala	Met	Glu	Asp	Ser 15	Glu
Ala	Leu	Gly	Phe 20	Glu	His	Met	Gly	Leu 25	Asp	Pro	Arg	Leu	Leu 30	Gln	Ala
Val	Thr	Asp 35	Leu	Gly	Trp	Ser	Arg 40	Pro	Thr	Leu	Ile	Gln 45	Glu	Lys	Ala
Ile	Pro 50	Leu	Ala	Leu	Glu	Gly 55	Lys	Asp	Leu	Leu	Ala 60	Arg	Ala	Arg	Thr
Gly 65	Ser	Gly	Lys	Thr	Ala 70	Ala	Tyr	Ala	Ile	Pro 75	Met	Leu	Gln	Leu	Leu 80
Leu	His	Arg	Lys	Ala 85	Thr	Gly	Pro	Val	Val 90	Glu	Gln	Ala	Val	Arg 95	Gly
Leu	Val	Leu	Val 100	Pro	Thr	Lys	Glu	Leu 105	Ala	Arg	Gln	Ala	Gln 110	Ser	Met
Ile	Gln	Gln 115	Leu	Ala	Thr	Tyr	Cys 120	Ala	Arg	Asp	Val	Arg 125	Val	Ala	Asn
Val	Ser 130	Ala	Ala	Glu	Asp	Ser	Val	Ser	Gln	Arg	Ala 140	Val	Leu	Met	Glu
Lys 145	Pro	Asp	Val	Val	Val 150	Gly	Thr	Pro	Ser	Arg 155	Ile	Leu	Ser	His	Leu 160
Gln	Gln	Asp	Ser	Leu 165	Lys	Leu	Arg	Asp	Ser 170	Leu	Glu	Leu	Leu	Val 175	Val
Asp	Glu	Ala	Asp 180	Leu	Leu	Phe	Ser	Phe 185	Gly	Phe	Glu	Glu	Glu 190	Leu	Lys

09673305-122700



Ser	Leu	Leu 195	Trp	Glu	Gly	Arg	Val 200	Thr	Cys	Pro	Gly	Phe 205	Thr	Arg	Leu
Phe	Ser 210	Cys	Gln	Leu	Leu	Leu 215	Thr	Arg	Thr	Tyr	Lys 220	His	Ser	Arg	Ser

<210> 325  
 <211> 115  
 <212> PRT  
 <213> homo sapiens

<400> 325

Phe 1	Phe	Phe	Phe	Phe 5	Phe	Phe	Phe	Phe	Gly 10	Ala	Ala	Lys	Ile	Phe 15	Ile
Leu	Leu	Ser	Arg 20	Gly	Lys	Met	Pro	Ala 25	Trp	Lys	Cys	Gln	Gly 30	Ala	Lys
Gly	Pro	Ser 35	Thr	Ala	Gly	Pro	Arg 40	Thr	Val	Cys	Ser	Gly 45	Cys	Ala	Val
Ser	Thr 50	Arg	Ala	Ser	Pro	Val 55	His	Glu	Gly	Cys	Lys 60	Pro	Val	Leu	His
Asn 65	Val	Leu	Ser	Ser	Arg 70	Glu	Ala	Gln	Gln	Pro 75	Gln	Glu	Gly	Leu	Ala 80
Val	Gly	Leu	Asn	Phe 85	Phe	Pro	Leu	Cys	Leu 90	Lys	Leu	Arg	Ser	Gly 95	Phe
Trp	Asp	Phe	Ala 100	Leu	Leu	Ala	Phe	Leu 105	Gln	Glu	Glu	Asp	Ser 110	Phe	Phe
Arg	Phe	Leu 115													

<210> 326  
 <211> 66  
 <212> PRT  
 <213> homo sapiens

<400> 326

Tyr 1	Leu	Gln	Cys	Gln 5	Arg	Ser	Leu	Cys	Gly 10	Ala	Lys	Cys	Val	Thr 15	Trp
Ala	Val	Glu	Thr 20	Arg	His	Leu	Leu	Ser 25	Pro	Ala	Leu	Met	Thr 30	Leu	Arg
Lys	Glu	Asp 35	Val	Ile	Gln	Gly	Lys 40	Phe	Leu	Ile	Pro	Lys 45	Leu	Pro	Val
His	Val 50	Asn	Arg	Thr	Ser	Phe 55	Tyr	Ser	Ser	Arg	Cys 60	Thr	Gly	Ser	Leu
Ala 65	Pro														

<210> 327  
 <211> 90  
 <212> PRT

00673305.122700

<213> homo sapiens

<400> 327

Phe 1	Arg	Ser	Cys	Leu 5	Phe	Met	Leu	Thr	Gly 10	Leu	Leu	Phe	Ile	Arg 15	Gln
Asp	Val	Leu 20	Val	Pro	Trp	His	Leu	Lys 25	Gly	Asn	Pro	Asp	Lys 30	Gly	Lys
Pro	Val	Glu 35	Pro	Phe	Gly	Pro	Ile 40	Gly	Ser	Gln	Asp	Pro 45	Ser	Pro	Val
Phe	His 50	Arg	Tyr	Tyr	His	Val 55	Phe	Arg	Glu	Gly	Glu 60	Leu	Glu	Gly	Ala
Cys 65	Arg	Thr	Val	Ser	Asp 70	Val	Arg	Ile	Leu	Gln 75	Ser	Tyr	Tyr	Asp	Gln 80
Gly	Asn	Trp	Cys	Val 85	Ile	Leu	Gln	Lys	Ala 90						

<210> 328

<211> 83

<212> PRT

<213> homo sapiens

<400> 328

Ser 1	Gly	Leu	Leu	Lys 5	Asn	His	Thr	Pro	Val 10	Ser	Leu	Ile	Val 15	Val	Ala
Leu	Gln	Asn	Ser 20	Asp	Ile	Thr	His	Ser 25	Pro	Ala	Gly	Thr	Phe 30	Gln	Phe
Ser	Leu	Thr 35	Glu	His	Met	Val	Val 40	Thr	Met	Lys	His	Arg 45	Thr	Trp	Val
Leu	Gly 50	Ser	Tyr	Gly	Thr	Lys 55	Trp	Leu	Asn	Arg	Phe 60	Ala	Phe	Ile	Arg
Ile 65	Ser	Leu	Lys	Val	Pro 70	Gly	Asn	Gln	Tyr	Ile 75	Leu	Thr	Asn	Lys	Lys 80
Lys	Ser	Cys													

<210> 329

<211> 185

<212> PRT

<213> homo sapiens

<400> 329

Glu 1	Arg	Arg	Ser	Lys 5	Ser	Arg	Glu	Glu	Arg 10	Glu	Lys	Glu	Arg	Glu 15	Arg
Glu	Arg	Glu	Glu 20	Arg	Glu	Arg	Lys	Arg 25	Arg	Arg	Glu	Glu	Glu 30	Glu	Arg
Glu	Lys	Glu 35	Arg	Ala	Arg	Asp	Arg 40	Glu	Arg	Arg	Lys	Arg 45	Ser	Arg	Ser
Arg	Ser	Arg	His	Ser	Ser	Arg	Thr	Ser	Asp	Arg	Arg	Cys	Ser	Arg	Ser

00573305.122700

50				55				60							
Arg 65	Asp	His	Lys	Arg	Ser 70	Arg	Ser	Arg	Glu	Arg 75	Arg	Arg	Ser	Arg	Ser 80
Arg	Asp	Arg	Arg	Arg 85	Ser	Arg	Ser	His	Asp 90	Arg	Ser	Glu	Arg	Lys 95	His
Arg	Ser	Arg	Ser 100	Arg	Asp	Arg	Arg	Arg 105	Ser	Lys	Ser	Arg	Asp 110	Arg	Lys
Ser	Tyr	Lys 115	His	Arg	Ser	Lys	Ser 120	Arg	Asp	Arg	Glu	Gln 125	Asp	Arg	Lys
Ser	Lys 130	Glu	Lys	Glu	Lys	Arg 135	Gly	Ser	Asp	Asp	Lys 140	Lys	Ser	Ser	Val
Lys 145	Ser	Gly	Ser	Arg	Glu 150	Lys	Gln	Ser	Glu	Asp 155	Thr	Asn	Thr	Glu	Ser 160
Lys	Glu	Ser	Asp	Thr 165	Lys	Asn	Glu	Val	Asn 170	Gly	Thr	Ser	Glu	Asp 175	Ile
Lys	Ser	Glu	Gly 180	Asp	Thr	Gln	Ser	Asn 185							

<210> 330  
 <211> 178  
 <212> PRT  
 <213> homo sapiens

<400> 330

Tyr 1	His	Phe	Pro	Ser 5	Ile	Gln	Cys	Leu	Cys 10	Leu	His	Ser	Ala	Phe 15	Leu
Asp	Tyr	Arg	Thr 20	Ser	His	Tyr	Phe	Phe 25	Tyr	His	Gln	Ile	Pro 30	Ser	Phe
Leu	Ser	Pro 35	Trp	Ile	Phe	Tyr	Leu 40	Val	Leu	Cys	Pro	Asp 45	Phe	Cys	Ser
Cys	Ala 50	Tyr	Met	Thr	Phe	Asp 55	Pro	Gly	Phe	Leu	Ile 60	Phe	Phe	Asp	Pro
Asp 65	Phe	Glu	Ile	Cys	Val 70	Phe	Phe	Leu	Ile	Asp 75	His	Gly	Phe	Cys	Phe 80
Phe	Val	Asp	Leu 85	Tyr	Phe	Cys	Ser	Ala	Phe 90	Phe	Leu	Tyr	Phe	Val 95	Thr
Phe	Cys	Gly	Pro 100	Glu	Thr	Cys	Cys	Ile 105	Phe	Cys	Leu	Met	Phe 110	Gly	Leu
Ser	Val	Tyr 115	Phe	Val	Asn	Asp	Phe 120	Ser	Phe	Phe	Phe	Leu 125	Cys	His	Glu
Pro	Phe 130	Leu	Phe	Leu	Phe	Leu 135	Pro	Leu	Pro	Phe	Val 140	Phe	Ser	Phe	Leu
Phe 145	Leu	Pro	Phe	Leu	Ser	Pro	Val	Leu	Ser	Leu 155	Ser	Leu	Leu	Cys	Ser 160

00672305-122700

Cys Phe Ser Phe Leu Arg Arg Ser Ser Arg Ile Arg Leu Phe Gly Ser  
165 170 175

Ser Pro

<210> 331

<211> 182

<212> PRT

<213> homo sapiens

<400> 331

Val Ser Pro Ser Asp Leu Met Ser Ser Leu Val Pro Leu Thr Ser Phe  
1 5 10 15

Leu Val Ser Leu Ser Phe Asp Ser Val Phe Val Ser Ser Leu Cys Phe  
20 25 30

Ser Arg Leu Pro Asp Phe Thr Leu Leu Phe Leu Ser Ser Asp Pro Leu  
35 40 45

Phe Ser Phe Ser Leu Asp Phe Leu Ser Cys Ser Leu Ser Arg Leu Leu  
50 55 60

Leu Leu Cys Leu Tyr Asp Phe Arg Ser Arg Leu Phe Asp Leu Leu Arg  
65 70 75 80

Ser Arg Leu Arg Asp Leu Cys Phe Leu Ser Asp Arg Ser Trp Leu Leu  
85 90 95

Leu Leu Arg Arg Ser Leu Leu Leu Arg Leu Leu Ser Leu Leu Arg  
100 105 110

Asp Leu Leu Trp Ser Arg Asp Leu Leu His Leu Leu Ser Asp Val Arg  
115 120 125

Leu Glu Cys Leu Leu Arg Glu Arg Leu Leu Phe Leu Leu Ser Leu Ser  
130 135 140

Arg Ala Leu Ser Phe Ser Leu Ser Ser Ser Ser Leu Arg Leu Phe Leu  
145 150 155 160

Ser Leu Ser Ser Leu Ser Leu Ser Arg Ser Phe Ser Leu Ser Ser Leu  
165 170 175

Leu Leu Leu Leu Leu Ser  
180

<210> 332

<211> 88

<212> PRT

<213> homo sapiens

<400> 332

Gly Phe Gly Met Gln Leu Val Ile Leu Arg Val Thr Ile Phe Leu Pro  
1 5 10 15

Trp Cys Phe Ala Val Pro Val Pro Pro Ala Ala Asp His Lys Gly Trp  
20 25 30

Asp Phe Val Glu Gly Tyr Phe His Gln Phe Phe Leu Thr Glu Lys Glu  
35 40 45

00673305.122700

Ser	Pro	Leu	Leu	Thr	Gln	Glu	Thr	Gln	Thr	Gln	Leu	Leu	Gln	Gln	Phe
	50					55					60				
His	Arg	Asn	Gly	Thr	Asp	Leu	Leu	Asp	Met	Gln	Met	His	Ala	Ser	Ala
65					70					75					80
Thr	Ala	Ala	Pro	Leu	Trp	Gly	Ala								
				85											

<210> 333  
 <211> 61  
 <212> PRT  
 <213> homo sapiens

<400> 333

Pro	Arg	Arg	Ser	Arg	His	Ser	Leu	Pro	Arg	Arg	His	Lys	His	Ser	Ser
1				5					10					15	
Cys	Asn	Asn	Ser	Ile	Gly	Met	Gly	Gln	Thr	Tyr	Leu	Thr	Cys	Arg	Cys
			20					25					30		
Met	Leu	Leu	Leu	Gln	Gln	Pro	His	Cys	Gly	Val	Pro	Asp	Gly	Ser	Asp
		35					40					45			
Asn	Cys	Ile	Ser	Pro	Gly	Arg	Cys	Lys	Trp	Ile	Lys	His			
	50					55					60				

<210> 334  
 <211> 62  
 <212> PRT  
 <213> homo sapiens

<400> 334

Ser	Thr	Cys	Ile	Phe	Leu	Ala	Arg	Cys	Ser	Cys	Arg	Thr	His	Gln	Ala
1				5					10					15	
Pro	His	Ser	Gly	Ala	Ala	Val	Ala	Glu	Ala	Cys	Ile	Cys	Met	Ser	Ser
			20					25					30		
Arg	Ser	Val	Pro	Phe	Arg	Trp	Asn	Cys	Cys	Arg	Ser	Cys	Val	Cys	Val
		35					40					45			
Ser	Trp	Val	Arg	Ser	Gly	Asp	Ser	Phe	Ser	Val	Arg	Lys	Asn		
	50					55					60				

<210> 335  
 <211> 61  
 <212> PRT  
 <213> homo sapiens

<400> 335

Val	Cys	Pro	Ile	Pro	Met	Glu	Leu	Leu	Gln	Glu	Leu	Cys	Leu	Cys	Leu
1				5					10					15	
Leu	Gly	Lys	Glu	Trp	Arg	Leu	Leu	Leu	Gly	Gln	Glu	Lys	Leu	Met	Glu
			20					25					30		
Ile	Ala	Leu	Asn	Lys	Val	Pro	Ser	Phe	Met	Val	Cys	Ser	Arg	Gly	His
		35					40					45			

00673395.122700

Trp Asn Gly Glu Thr Pro Gly Gln Glu Asp Ser Asn Ser  
50 55 60

<210> 336  
<211> 63  
<212> PRT  
<213> homo sapiens

<400> 336

Ala Glu Asp Thr Ile Gln Lys Arg Asn Ser Gln Phe Glu Thr Val Thr  
1 5 10 15  
Pro Pro Ala Pro Asn Cys Gly Asp Glu 25 Glu Arg Lys Gln Trp 30 Leu Trp  
Phe Leu Ser 35 Glu Gly Arg Leu Arg 40 Thr Glu Arg Ser Asn 45 His Gln Gly  
His Arg 50 Phe Trp Lys Ser Ser 55 Arg Gly Gly Trp Leu 60 Glu Glu Gln

<210> 337  
<211> 65  
<212> PRT  
<213> homo sapiens

<400> 337

Lys Gly Trp Arg Ser Asp Phe Thr Val Gly 10 Gly Arg Gln Arg Asp Gly  
1 5 15  
Gln His Val Gln Thr Gly Ser Phe Phe 25 Ser Ile Ser Leu 30 Leu Ser Lys  
Ser Arg Thr 35 Ala Gln Trp Leu Cys 40 Gln Gly Gly Ser Ser 45 Ser Tyr Ser  
His Phe 50 Ser Gly Ser Leu Lys 55 Ser Thr Arg Tyr Tyr 60 Arg Gly Ser Arg  
Ser  
65

<210> 338  
<211> 249  
<212> PRT  
<213> homo sapiens

<400> 338

Ser Cys Gly Asp Val Glu Gln Lys Ile Gln Phe Lys Arg Glu Thr Ala  
1 5 10 15  
Ser Leu Lys Leu 20 Leu Pro His Gln Pro 25 Arg Ile Val Glu 30 Met Lys Lys  
Gly Ser Asn Gly Tyr Gly Phe Tyr 40 Leu Arg Ala Gly Ser 45 Glu Gln Lys  
Gly Gln 50 Ile Ile Lys Asp Ile 55 Asp Ser Gly Ser Pro 60 Ala Glu Glu Ala

00673205-122700

Gly 65	Leu	Lys	Asn	Asn	Asp 70	Leu	Val	Val	Ala	Val 75	Asn	Gly	Glu	Ser	Val 80
Glu	Thr	Leu	Asp	His 85	Asp	Ser	Val	Val	Glu 90	Met	Ile	Arg	Lys	Gly 95	Gly
Asp	Gln	Thr	Ser 100	Leu	Leu	Val	Val	Asp 105	Lys	Glu	Thr	Asp	Asn 110	Met	Tyr
Arg	Leu	Ala 115	His	Phe	Ser	Pro	Phe 120	Leu	Tyr	Tyr	Gln	Ser 125	Gln	Glu	Leu
Pro	Asn 130	Gly	Ser	Val	Lys	Glu 135	Ala	Pro	Ala	Pro	Thr 140	Pro	Thr	Ser	Leu
Glu 145	Val	Ser	Ser	Pro	Pro 150	Asp	Thr	Thr	Glu	Glu 155	Val	Asp	His	Lys	Pro 160
Lys	Leu	Cys	Arg	Leu 165	Ala	Lys	Gly	Glu	Asn 170	Gly	Tyr	Gly	Phe	His 175	Leu
Asn	Ala	Ile	Arg 180	Gly	Leu	Pro	Gly	Ser 185	Phe	Ile	Lys	Glu	Val 190	Gln	Lys
Gly	Gly	Pro 195	Ala	Asp	Leu	Ala	Gly 200	Leu	Glu	Asp	Glu	Asp 205	Val	Ile	Ile
Glu	Val 210	Asn	Gly	Val	Asn	Val 215	Leu	Asp	Glu	Pro	Tyr 220	Glu	Lys	Val	Val
Asp 225	Arg	Ile	Gln	Ser	Ser 230	Gly	Lys	Asn	Val	Thr 235	Leu	Leu	Val	Cys	Gly 240
Lys	Lys	Ala	Tyr	Asp 245	Tyr	Phe	Gln	Ala							

<210> 339  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 339

Ile 1	Thr	Gly	Val	Gln 5	Pro	Glu	His	Ile	Gln 10	Tyr	Leu	Lys	Asn	Tyr 15	Phe
His	Leu	Trp	Thr 20	Arg	Gln	Leu	Ala	His 25	Ile	Tyr	His	Tyr	Tyr 30	Ile	His
Gly	Pro	Lys 35	Gly	Asn	Glu	Ile	Arg 40	Thr	Ser	Lys	Glu	Val 45	Glu	Pro	Phe
Asn	Asn 50	Ile	Asp	Ile	Glu	Ile 55	Ser	Met	Phe	Glu	Lys 60	Gly	Lys	Val	Pro
Lys 65	Ile	Val													

<210> 340  
 <211> 44  
 <212> PRT  
 <213> homo sapiens

00673305-12700

<400> 340

Arg	Ile	Phe	Ile	Thr	Thr	Ile	Phe	Met	Ala	Gln	Lys	Glu	Met	Lys	Tyr
1				5					10					15	
Glu	His	Gln	Lys	Lys	Leu	Asn	Leu	Ser	Thr	Ile	Leu	Ile	Leu	Lys	Phe
			20					25					30		
Leu	Cys	Leu	Lys	Lys	Gly	Arg	Tyr	Leu	Arg	Leu	Ser				
		35					40								

<210> 341

<211> 46

<212> PRT

<213> homo sapiens

<400> 341

Lys	Val	Gln	Leu	Leu	Leu	Met	Phe	Val	Phe	His	Phe	Leu	Leu	Gly	His
1				5					10					15	
Glu	Tyr	Ser	Ser	Asp	Lys	Tyr	Ala	Leu	Thr	Val	Val	Ser	Lys	Gly	Gly
			20					25					30		
Asn	Asn	Phe	Ser	Ser	Thr	Val	Cys	Val	Leu	Val	Val	Pro	Leu		
		35					40					45			

<210> 342

<211> 237

<212> PRT

<213> homo sapiens

<400> 342

Gly	Arg	Trp	Arg	Arg	Arg	Leu	Arg	His	Gly	Arg	Gly	Ser	Ala	Glu	Ala
1				5					10					15	
Val	Gly	Pro	Thr	Ala	Met	Ala	Glu	Leu	Leu	Gln	Glu	Glu	Leu	Ser	Val
			20					25					30		
Leu	Ala	Ala	Ile	Phe	Cys	Arg	Pro	His	Glu	Trp	Glu	Val	Leu	Ser	Arg
		35					40					45			
Ser	Glu	Thr	Asp	Gly	Thr	Val	Phe	Arg	Ile	His	Thr	Lys	Ala	Glu	Gly
	50				55						60				
Phe	Met	Asp	Ala	Asp	Ile	Pro	Leu	Glu	Leu	Val	Phe	His	Leu	Pro	Val
	65				70					75					80
Asn	Tyr	Pro	Ser	Cys	Leu	Pro	Gly	Ile	Ser	Ile	Asn	Ser	Glu	Gln	Leu
				85					90					95	
Thr	Arg	Ala	Gln	Cys	Val	Thr	Val	Lys	Glu	Lys	Leu	Leu	Glu	Gln	Ala
			100					105					110		
Glu	Ser	Leu	Leu	Ser	Glu	Pro	Met	Val	His	Glu	Leu	Val	Leu	Trp	Ile
		115					120					125			
Gln	Gln	Asn	Leu	Arg	His	Ile	Leu	Ser	Gln	Pro	Glu	Thr	Gly	Ser	Gly
	130					135					140				
Ser	Glu	Lys	Cys	Thr	Phe	Ser	Thr	Ser	Thr	Thr	Met	Asp	Asp	Gly	Leu

00673395.122700



145					150					155					160
Trp	Ile	Thr	Leu	Leu 165	His	Leu	Asp	His	Met 170	Arg	Ala	Lys	Thr	Lys 175	Tyr
Val	Lys	Ile	Val 180	Glu	Lys	Trp	Ala	Ser 185	Asp	Leu	Arg	Leu	Thr 190	Gly	Arg
Leu	Met	Phe 195	Met	Gly	Lys	Ile	Ile 200	Leu	Asp	Phe	Thr	Thr 205	Gly	Arg	Gln
Lys	Gln 210	Pro	Gln	Gly	Val	Leu 215	Asp	Ser	Ser	Glu	Asn 220	Leu	Gln	Ser	Arg
Cys 225	Gly	Leu	Lys	Trp	Lys 230	Glu	Met	Gln	Arg	Glu 235	Asn	Asp			

<210> 343  
 <211> 89  
 <212> PRT  
 <213> homo sapiens

<400> 343

Tyr 1	Leu	Ile	Leu	Leu 5	Gln	Gly	Asp	Arg	Asn 10	Asn	Leu	Lys	Val	Tyr 15	Leu
Ile	Leu	Gln	Lys 20	Thr	Ser	Lys	Val	Asp 25	Val	Asp	Ser	Ser	Gly 30	Lys	Lys
Cys	Lys	Glu 35	Lys	Met	Ile	Ser	Val 40	Leu	Phe	Glu	Thr	Lys 45	Val	Gln	Thr
Glu	His 50	Lys	Arg	Phe	Leu	Ala 55	Phe	Glu	Val	Lys	Glu 60	Tyr	Ser	Ala	Leu
Asp 65	Glu	Leu	Gln	Lys	Glu 70	Phe	Glu	Thr	Ala	Gly 75	Leu	Lys	Lys	Leu	Phe 80
Ser	Glu	Phe	Val	Leu 85	Ala	Leu	Val	Lys							

<210> 344  
 <211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 344

Pro 1	Leu	Pro	Lys	Ser 5	Asn	Ala	Lys	Thr	Thr 10	Lys	Asn	Thr	Ala	Ile 15	Leu
Leu	Lys	Asp	Ser 20	Cys	Leu	Pro	Phe	His 25	Phe	Thr	Arg	Ala	Ser 30	Thr	Asn
Ser	Glu	Lys 35	Ser	Phe	Leu	Ser	Pro 40	Ala	Val	Ser	Asn	Ser 45	Phe	Cys	Asn
Ser	Ser 50	Asn	Ala	Glu	Tyr	Ser 55	Leu	Thr	Ser	Asn	Ala 60	Arg	Asn	Leu	Leu
Cys 65	Ser	Val	Cys	Thr	Phe 70	Val	Ser	Asn	Ser	Thr 75	Leu	Ile	Ile	Phe	Ser 80

09573305.122700

Leu	His	Phe	Phe	Pro	Leu	Glu	Ser	Thr	Ser	Thr	Leu	Glu	Val	Phe
				85					90					95

<210> 345  
 <211> 72  
 <212> PRT  
 <213> homo sapiens

<400> 345

Arg	Ala	Gly	Leu	Phe	Pro	Gly	Arg	Arg	Val	Gly	Leu	Glu	Ala	Glu	Asn
1				5					10					15	
Gly	Pro	Cys	Cys	His	Gln	His	Gly	Asp	Phe	Val	Pro	Cys	Pro	Val	Leu
			20					25					30		
Ser	Ala	Arg	Met	Ser	Gln	Pro	Glu	Ala	Glu	Glu	Ala	Ala	Leu	Val	Ala
		35					40					45			
His	Ala	Val	Gly	His	Asp	Cys	Val	Cys	Ser	Gly	Gly	Gly	Val	Leu	Leu
	50					55					60				
Pro	His	His	Arg	Arg	Asn	Asn	Leu								
65					70										

<210> 346  
 <211> 171  
 <212> PRT  
 <213> homo sapiens

<400> 346

Gly	Arg	Ala	Cys	Phe	Arg	Gly	Gly	Ala	Trp	Gly	Leu	Arg	Pro	Arg	Thr
1				5					10					15	
Ala	Leu	Ala	Ala	Thr	Asn	Met	Glu	Thr	Leu	Tyr	Arg	Val	Pro	Phe	Leu
			20					25					30		
Val	Leu	Glu	Cys	Pro	Asn	Leu	Lys	Leu	Lys	Lys	Pro	Pro	Trp	Leu	His
		35					40					45			
Met	Pro	Ser	Ala	Met	Thr	Val	Tyr	Ala	Leu	Val	Val	Val	Ser	Tyr	Phe
	50					55					60				
Leu	Ile	Thr	Gly	Gly	Ile	Ile	Tyr	Asp	Val	Ile	Val	Glu	Pro	Pro	Ser
65					70					75					80
Val	Gly	Ser	Met	Thr	Asp	Glu	His	Gly	His	Gln	Arg	Pro	Val	Ala	Phe
				85					90					95	
Leu	Ala	Tyr	Arg	Val	Asn	Gly	Gln	Tyr	Ile	Met	Glu	Gly	Leu	Ala	Ser
			100					105					110		
Ser	Phe	Leu	Phe	Thr	Met	Gly	Gly	Leu	Gly	Phe	Ile	Ile	Leu	Asp	Arg
		115					120					125			
Ser	Asn	Ala	Pro	Asn	Ile	Pro	Lys	Leu	Asn	Arg	Phe	Leu	Leu	Leu	Phe
	130					135					140				
Ile	Gly	Phe	Val	Cys	Val	Leu	Leu	Ser	Phe	Phe	Met	Ala	Arg	Val	Phe
145					150					155					160

00573395-122700

Met Arg Met Lys Leu Pro Gly Tyr Leu Met Gly  
165 170

<210> 347  
<211> 82  
<212> PRT  
<213> homo sapiens

<400> 347

Glu 1	Ala	Gly	Cys	Lys 5	Ser	Phe	His	Asn	Ile 10	Leu	Ser	Ile	Tyr	Ser 15	Val
Gly	Gln	Glu	Ser 20	Tyr	Trp	Pro	Leu	Met 25	Pro	Met	Phe	Ile	Ser 30	His	Arg
Thr	Asp	Thr 35	Trp	Arg	Phe	Asn	Asn 40	Asn	Ile	Ile	Asn	Tyr 45	Ser	Ser	Gly
Asp	Glu 50	Glu	Val	Arg	His	His 55	His	Gln	Ser	Ile	His 60	Ser	His	Gly	Arg
Arg 65	His	Val	Gln	Pro	Gly 70	Arg	Leu	Leu	Gln	Leu 75	Gln	Val	Gly	Thr	Phe 80
Glu	His														

<210> 348  
<211> 103  
<212> PRT  
<213> homo sapiens

<400> 348

His 1	Lys	Val	Ile	Val 5	Val	Trp	Asn	Asn	Ile 10	Gly	Glu	Lys	Ala	Pro 15	Asp
Glu	Leu	Trp	Asn 20	Ser	Leu	Gly	Pro	His 25	Pro	Ile	Pro	Val	Ile 30	Phe	Lys
Gln	Gln	Thr 35	Ala	Asn	Arg	Met	Arg 40	Asn	Arg	Leu	Gln	Val 45	Phe	Pro	Glu
Leu 50	Glu	Thr	Asn	Ala	Val	Leu 55	Met	Val	Asp	Asp	Asp 60	Thr	Leu	Ile	Ser
Thr 65	Pro	Asp	Leu	Val	Phe 70	Ala	Phe	Ser	Val	Trp 75	Gln	Gln	Phe	Pro	Asp 80
Gln	Ile	Val	Gly	Ile 85	Cys	Phe	Leu	Glu	Ser 90	Thr	Ser	Phe	Thr	Phe 95	Ile
Gln	Gly	Ile	Tyr 100	Ser	Tyr	Trp									

<210> 349  
<211> 50  
<212> PRT  
<213> homo sapiens

<400> 349

Glu	Ser	Lys	Asn	Lys	Val	Trp	Gly	Ala	Asp	Glu	Cys	Val	Ile	Ile	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

00673305-122700

1				5					10					15		
His	Gln	His	Cys 20	Ile	Gly	Phe	Gln	Phe 25	Arg	Lys	Asp	Leu	Glu 30	Ser	Ile	
Ser	His	Pro 35	Val	Cys	Cys	Leu	Leu 40	Phe	Glu	Asp	His	Arg 45	Asp	Arg	Val	
Gly	Pro 50															

<210> 350  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 350

Ser 1	Gly	Asn	Cys	Cys 5	Gln	Thr	Glu	Lys	Ala 10	Lys	Thr	Arg	Ser	Gly 15	Val
Leu	Met	Ser	Val 20	Ser	Ser	Ser	Thr	Ile 25	Asn	Thr	Ala	Leu	Val 30	Ser	Ser
Ser	Gly	Lys 35	Thr	Trp	Ser	Arg	Phe 40	Leu	Ile	Leu	Phe	Ala 45	Val	Cys	Cys
Leu	Lys 50	Ile	Thr	Gly	Ile	Gly 55	Trp	Gly	Pro	Arg	Glu 60	Phe	His	Asn	Ser
Ser 65	Gly	Ala	Phe	Ser	Pro 70	Ile	Leu	Phe	His	Thr 75	Thr	Ile	Thr	Leu	

<210> 351  
 <211> 70  
 <212> PRT  
 <213> homo sapiens

<400> 351

Gly 1	Thr	Leu	Arg	His 5	Ser	Val	His	Val	Val 10	Pro	Pro	Lys	His	Gly 15	His
His	Lys	Val	Leu 20	Ser	Ser	Gly	Val	Cys 25	Ser	Arg	Leu	Leu	Gly 30	Ile	Gln
Arg	Glu	Gly 35	Arg	Asn	Gln	Glu	Phe 40	Gln	Lys	His	Ile	His 45	Val	Ala	Thr
Pro	Ala 50	Thr	Ser	Gly	Ile	Leu 55	Cys	Ser	Asp	Lys	Leu 60	His	Gly	Trp	Glu
Val 65	Phe	Phe	Leu	Ala	Arg 70										

<210> 352  
 <211> 71  
 <212> PRT  
 <213> homo sapiens

<400> 352

His	Leu	Ile	Pro	Phe	Met	Ala	Lys	Ser	Ser	Phe	Arg	Val	Gly	Asn	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

00673305-122700

1				5				10				15			
Gln	Thr	Phe	Cys 20	Ala	Cys	Cys	Ser	Pro 25	Lys	Ala	Trp	Ser	Ser 30	Gln	Ser
Pro	Glu	Phe 35	Trp	Cys	Val	Leu	Pro 40	Pro	Pro	Gly	Tyr	Thr 45	Glu	Arg	Arg
Gln	Glu 50	Ser	Gly	Val	Pro	Glu 55	Ala	Tyr	Thr	Cys	Gly 60	Tyr	Pro	Ser	Asn
Lys 65	Arg	His	Pro	Val	Leu 70	Arg									

<210> 353  
 <211> 60  
 <212> PRT  
 <213> homo sapiens

<400> 353

Ser 1	Gly	Gln	Cys	Gly 5	Met	Gln	Leu	Gly	Pro 10	Asp	Gln	Pro	Ser	Ser 15	Glu
Gln	Met	Ala	Val 20	Val	Pro	Ile	Ser	Thr 25	Lys	Pro	Gln	Arg	Ala 30	Arg	Lys
Asn	Thr	Ser 35	Gln	Pro	Cys	Ser	Leu 40	Ser	Glu	His	Arg	Met 45	Pro	Leu	Val
Ala	Gly 50	Val	Ala	Thr	Cys	Ile 55	Cys	Phe	Trp	Asn	Ser 60				

<210> 354  
 <211> 225  
 <212> PRT  
 <213> homo sapiens

<400> 354

Gly 1	Leu	Pro	Ala	Arg 5	Arg	Pro	Gln	Cys	Phe 10	Leu	Arg	Ala	Glu	Met 15	Ala
Asn	Ser	Gly	Leu 20	Gln	Leu	Leu	Gly	Phe 25	Ser	Met	Ala	Leu	Leu 30	Gly	Trp
Val	Gly	Leu 35	Val	Ala	Cys	Thr	Ala 40	Ile	Pro	Gln	Trp	Gln 45	Met	Ser	Ser
Tyr	Ala 50	Gly	Asp	Asn	Ile	Ile 55	Thr	Ala	Gln	Ala	Met 60	Tyr	Lys	Gly	Leu
Trp 65	Met	Asp	Cys	Val	Thr 70	Gln	Ser	Thr	Gly	Met 75	Met	Ser	Cys	Lys	Met 80
Tyr	Asp	Ser	Val	Leu 85	Ala	Leu	Ser	Ala	Ala 90	Leu	Gln	Ala	Thr	Arg 95	Ala
Leu	Met	Val	Val 100	Ser	Leu	Val	Leu	Gly 105	Phe	Leu	Ala	Met	Phe 110	Val	Ala
Thr	Met	Gly 115	Met	Lys	Cys	Thr	Arg 120	Cys	Gly	Gly	Asp	Asp 125	Lys	Val	Lys

09673395-122700

Lys	Ala 130	Arg	Ile	Ala	Met	Gly 135	Gly	Gly	Ile	Ile	Phe 140	Ile	Val	Ala	Gly
Leu	Ala	Ala	Leu	Val	Ala 150	Cys	Ser	Trp	Tyr	Gly 155	His	Gln	Ile	Val	Thr 160
Asp	Phe	Tyr	Asn	Pro 165	Leu	Ile	Pro	Thr	Asn 170	Ile	Lys	Tyr	Glu	Phe 175	Gly
Pro	Ala	Ile	Phe 180	Ile	Gly	Trp	Ala	Gly 185	Ser	Ala	Leu	Val	Ile 190	Leu	Gly
Gly	Ala	Leu 195	Leu	Ser	Cys	Ser	Cys 200	Pro	Gly	Asn	Glu	Ser 205	Lys	Ala	Gly
Tyr	Arg 210	Ala	Pro	Arg	Ser	Tyr 215	Pro	Lys	Ser	Asn	Ser 220	Ser	Lys	Glu	Tyr
Val															
225															

<210> 355  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 355

Gln 1	His	His	His	Gly 5	Pro	Gly	His	Val	Gln 10	Gly	Ala	Val	Asp	Gly 15	Leu
Arg	His	Ala	Glu 20	His	Gly	Asp	Asp	Glu 25	Leu	Gln	Asn	Val	Arg 30	Leu	Gly
Ala	Arg	Pro 35	Val	Arg	Gly	Leu	Ala 40	Gly	His	Ser	Ser	Pro 45	Asn	Gly	Gly
Leu	Pro 50	Gly	Ala	Gly	Leu	Pro 55	Gly	His	Val	Cys	Gly 60	His	Asp	Gly	His
Glu 65	Val	His	Ala	Leu	Trp 70	Gly	Arg	Arg	Gln	Ser 75	Glu	Glu	Gly	Pro	Tyr 80
Ser	His	Gly	Trp	Arg 85	His	Asn	Phe	His	Arg 90	Gly	Arg	Ser	Cys	Arg 95	Leu
Gly	Ser	Leu	Leu 100	Leu	Val	Trp	Pro	Ser 105	Asp	Cys	His	Arg	Leu 110	Leu	

<210> 356  
 <211> 154  
 <212> PRT  
 <213> homo sapiens

<400> 356

Cys 1	Cys	His	Pro	His 5	Arg	Ser	Ser	Ser	Ala 10	Thr	Ala	Gly	Trp	Arg 15	Cys
Arg	Pro	Pro	Asp 20	Pro	Pro	Ser	Pro	Ala 25	Gly	Pro	Trp	Arg	Ser 30	Pro	Ala

00673305.122700

Thr	Ala	Gly 35	Pro	Asn	Trp	Pro	Phe 40	Pro	Pro	Ser	Glu	Asn 45	Thr	Gly	Gly
Ala	Gly 50	Arg	Gly	Asp	Pro	Thr 55	Val	Lys	Gln	Thr	Thr 60	Leu	Gly	Gly	Gln
Pro 65	His	Lys	Arg	Lys	Leu 70	Glu	Val	Glu	Phe	Ser 75	Gly	His	Pro	Lys	Arg 80
Gln	Lys	Gly	Phe	Gly 85	Pro	Gly	Glu	Cys	Lys 90	Ser	Cys	His	Gln	Thr 95	Thr
His	Lys	Ser	Thr 100	Pro	Pro	Val	Lys	Arg 105	Trp	Pro	Arg	Gly	Thr 110	Gly	Ser
Arg	Ile	Arg 115	Arg	Glu	Gly	Gly	Ser 120	Arg	Gln	Asn	Trp	Trp 125	Ser	Pro	Lys
Ala	Arg 130	Arg	Phe	Pro	Pro	Gly 135	Ala	Leu	Gly	Asp	Pro 140	Leu	Ser	Pro	Pro
Ala 145	Ser	Arg	Leu	Leu	Thr 150	Gly	Val	Gly	Pro						

<210> 357  
 <211> 72  
 <212> PRT  
 <213> homo sapiens

<400> 357

Asn 1	Leu	Thr	Gln	Val 5	Thr	Phe	Leu	Phe	Phe 10	Cys	Pro	Pro	Asn	Val 15	His
Ala	Ser	Tyr	Arg 20	Leu	His	Phe	Glu	Ala 25	Leu	Met	Asn	Ile	Pro 30	Val	Leu
Val	Leu	Asp 35	Val	Asn	Asp	Asp	Phe 40	Ala	Glu	Glu	Val	Thr 45	Lys	Gln	Glu
Asp	Leu 50	Met	Arg	Glu	Val	Gly 55	Arg	Thr	Leu	Thr	Pro 60	Val	Phe	Leu	Val
Val 65	Ser	Leu	Trp	Leu	Tyr 70	Leu	Leu								

<210> 358  
 <211> 69  
 <212> PRT  
 <213> homo sapiens

<400> 358

Ser 1	Pro	Ser	His	Leu 5	Ser	His	Glu	Val	Phe 10	Leu	Phe	Gly	Tyr	Phe 15	Leu
Ser	Lys	Ile	Ile 20	Ile	Asp	Ile	Gln	His 25	Gln	His	Trp	Asn	Val 30	His	Gln
Ser	Leu	Lys 35	Val	Glu	Pro	Ile	Arg 40	Ser	Val	Asn	Val	Trp 45	Gly	Thr	Glu
Lys	Lys	Lys	Cys	Asn	Leu	Ser	Gln	Val	Ser	His	Thr	Arg	Gln	Val	Leu

09672395.122700

50

55

60

Leu Arg Glu Gln Ile  
65

&lt;210&gt; 359

&lt;400&gt; 359

000

&lt;210&gt; 360

&lt;211&gt; 53

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 360

Lys Arg Tyr Asn Gln Arg Glu Thr Thr Arg Lys Thr Gly Val Lys Val  
1 5 10 15

Leu Pro Thr Ser Leu Met Arg Ser Ser Cys Leu Val Thr Ser Ala  
20 25 30

Lys Ser Ser Leu Thr Ser Asn Thr Ser Thr Gly Met Phe Ile Arg Ala  
35 40 45

Ser Lys Trp Ser Leu  
50

&lt;210&gt; 361

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 361

Ser Cys Trp Glu Thr Lys Trp Thr Ser Cys Pro Arg Met Leu Leu Ala  
1 5 10 15

Thr Gly Arg Gly Cys Gly Ser Asp Cys Gly Arg Thr Val Pro Ala Pro  
20 25 30

Gly Ser Cys Trp Pro Leu Ala Pro Arg Ala Thr Ala Pro Arg Gln Gly  
35 40 45

Arg Ala Thr Gly Arg Gly Glu Ser Glu Ser Ala Glu Leu Val Pro His  
50 55 60

Ser Gly Gln Gly Arg Ala Ala Asp Gln Arg Gln Asp Arg Leu Trp Ser  
65 70 75 80

Gly Arg Val Asp Leu Cys Pro Ser Ala Leu Leu Ala Leu Pro Trp Gly  
85 90 95

Arg Leu Leu Ser Gly Arg His Gln Arg Arg Gln Ile His Ser Leu  
100 105 110

&lt;210&gt; 362

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 362

00673305-122700



Thr 1	Arg	Asn	Gly	Ser 5	Val	Phe	Gly	Cys	Tyr 10	Arg	Pro	His	Arg	Phe 15	Pro
Ala	Gly	Lys	Ser 20	Val	Ser	Leu	Val	Tyr 25	Ser	Arg	Gly	Phe	Gln 30	His	Pro
Pro	Cys	Ala 35	Tyr	His	Leu	Leu	Gly 40	Gln	Gly	Arg	Arg	Ser 45	Val	Ser	Glu
Ala	Cys 50	Arg	Ser	Tyr	Val	Thr 55	Pro	Asp	Ser	Asn	Gly 60	Trp	Lys	Arg	Thr
Asn 65	Gly	Gln	Asp	Phe	Leu 70	Leu	Leu	Leu	Lys 75	Thr	Leu	Met	Val	Lys 80	
Arg	Lys	Asp	Trp	Gly 85	Gln	Pro	Gly	Ser	Ser 90	Gly	Pro	Thr	Ser	Lys 95	Phe
Pro	Leu	Gln	Val 100	Ile	Leu	Cys	Gln	Ala 105	Leu	Phe	Lys	Lys			

<210> 363

<211> 381

<212> PRT

<213> homo sapiens

<400> 363

Gly 1	Pro	Ala	Arg	Arg 5	Pro	Ala	Ala	Arg	Leu 10	Ala	Arg	Ala	Gly	Gly 15	Pro
Gln	Ala	Ala	Asp 20	Arg	Ala	Gly	Lys	Gln 25	Ser	Gly	Pro	Pro	Ala 30	Pro	Gly
Cys	Ser	Trp 35	Leu	Pro	Ala	Glu	Ala 40	Ala	Gly	Ala	Thr	Val 45	Gly	Gly	Leu
Cys	Pro 50	Arg	Arg	Ala	Pro	Ala 55	Gly	Pro	Trp	His	Gln 60	Gly	Pro	Gln	Arg
Pro 65	Val	Lys	Asp	Glu	Pro 70	Gln	Asp	Gly	Glu	Asn 75	Pro	Asn	Pro	Pro	Asn 80
Trp	Ser	Arg	Thr 85	Val	Val	Arg	Asp	Val	Arg 90	Leu	Ile	Ser	Ala	Lys 95	Thr
Gly	Tyr	Gly	Val 100	Glu	Glu	Leu	Ile	Ser 105	Ala	Leu	Gln	Arg	Ser 110	Trp	Arg
Tyr	Arg	Gly 115	Asp	Val	Tyr	Leu	Val 120	Gly	Ala	Thr	Asn	Ala 125	Gly	Lys	Ser
Thr	Leu 130	Phe	Asn	Thr	Leu 135	Glu	Ser	Asp	Tyr	Cys 140	Thr	Ala	Lys	Gly	
Ser 145	Glu	Ala	Ile	Asp	Arg 150	Ala	Thr	Ile	Ser	Pro 155	Trp	Pro	Gly	Thr	Thr 160
Leu	Asn	Leu	Leu	Lys 165	Phe	Pro	Ile	Cys	Asn 170	Pro	Thr	Pro	Tyr	Arg 175	Met
Phe	Lys	Arg	His 180	Gln	Arg	Leu	Lys	Lys 185	Asp	Ser	Thr	Gln	Ala 190	Glu	Glu

00573305.122700

Asp	Leu	Ser	Glu	Gln	Glu	Gln	Asn	Gln	Leu	Asn	Val	Leu	Lys	Lys	His
		195					200					205			
Gly	Tyr	Val	Val	Gly	Arg	Val	Gly	Arg	Thr	Phe	Leu	Tyr	Ser	Glu	Glu
	210					215					220				
Gln	Lys	Asp	Asn	Ile	Pro	Phe	Glu	Phe	Asp	Ala	Asp	Ser	Leu	Ala	Phe
	225				230					235					240
Asp	Met	Glu	Asn	Asp	Pro	Val	Met	Gly	Thr	His	Lys	Ser	Thr	Lys	Gln
				245					250					255	
Val	Glu	Leu	Thr	Ala	Gln	Asp	Val	Lys	Asp	Ala	His	Trp	Phe	Tyr	Asp
			260					265					270		
Thr	Pro	Gly	Ile	Thr	Lys	Glu	Asn	Cys	Ile	Leu	Asn	Leu	Leu	Thr	Glu
		275					280					285			
Lys	Glu	Val	Asn	Ile	Val	Leu	Pro	Thr	Gln	Ser	Ile	Val	Pro	Arg	Thr
		290				295					300				
Phe	Val	Leu	Lys	Pro	Gly	Met	Val	Leu	Phe	Leu	Gly	Ala	Ile	Gly	Arg
	305				310					315					320
Ile	Asp	Phe	Leu	Gln	Gly	Asn	Gln	Ser	Ala	Trp	Phe	Thr	Val	Val	Ala
				325					330					335	
Ser	Asn	Ile	Leu	Pro	Val	His	Ile	Thr	Ser	Leu	Asp	Arg	Ala	Asp	Ala
			340					345					350		
Leu	Tyr	Gln	Lys	His	Ala	Gly	His	Thr	Leu	Leu	Gln	Ile	Pro	Met	Gly
		355					360					365			
Gly	Lys	Glu	Arg	Met	Gly	Arg	Ile	Ser	Ser	Ser	Cys	Cys			
	370					375					380				

<210> 364

<211> 182

<212> PRT

<213> homo sapiens

<400> 364

Gln	Pro	Ser	Thr	Thr	Cys	Thr	Ser	Val	Leu	Val	Cys	Leu	Leu	Ser	Ala
1				5					10					15	
Met	Pro	Leu	Pro	Val	Ala	Leu	Gln	Thr	Arg	Leu	Ala	Lys	Arg	Gly	Ile
			20					25					30		
Leu	Lys	His	Leu	Glu	Pro	Glu	Pro	Glu	Glu	Glu	Ile	Ile	Ala	Glu	Asp
		35					40					45			
Tyr	Asp	Asp	Asp	Pro	Val	Asp	Tyr	Glu	Ala	Thr	Arg	Leu	Glu	Gly	Leu
	50					55					60				
Pro	Pro	Ser	Trp	Tyr	Lys	Val	Phe	Asp	Pro	Ser	Cys	Gly	Leu	Pro	Tyr
	65				70					75					80
Tyr	Trp	Asn	Ala	Asp	Thr	Asp	Leu	Val	Ser	Trp	Leu	Ser	Pro	His	Asp
				85					90					95	
Pro	Asn	Ser	Val	Val	Thr	Lys	Ser	Ala	Lys	Lys	Leu	Arg	Ser	Ser	Asn

00573305-122700

100						105						110					
Ala	Asp	Ala	Glu	Glu	Lys	Leu	Asp	Arg	Ser	His	Asp	Lys	Ser	Asp	Arg		
		115					120					125					
Gly	His	Asp	Lys	Ser	Asp	Arg	Ser	His	Glu	Lys	Leu	Asp	Arg	Gly	His		
	130					135					140						
Asp	Lys	Ser	Asp	Arg	Gly	His	Asp	Lys	Ser	Asp	Arg	Asp	Arg	Glu	Arg		
	145				150					155					160		
Gly	Tyr	Asp	Lys	Ser	Arg	Asn	Gly	Ile	Arg	Asp	Arg	Gly	Tyr	Asp	Gln		
				165					170					175			
Ala	Asp	Arg	Glu	Glu	Gly												
			180														

<210> 365  
 <211> 149  
 <212> PRT  
 <213> homo sapiens

<400> 365

Arg	Arg	His	Glu	Arg	Asp	Gly	Arg	Cys	Asp	Ser	Leu	Pro	Leu	Pro	Ala
1				5					10					15	
Arg	Val	Tyr	Trp	Ser	Val	Cys	Tyr	Gln	Leu	Cys	Arg	Cys	Pro	Leu	Arg
			20					25					30		
Cys	Arg	Pro	Ala	Trp	Pro	Arg	Glu	Ala	Ser	Ser	Asn	Ile	Trp	Ser	Leu
		35					40					45			
Asn	Gln	Arg	Lys	Arg	Ser	Leu	Pro	Arg	Thr	Met	Thr	Met	Ile	Leu	Trp
	50					55					60				
Thr	Thr	Arg	Pro	Pro	Gly	Trp	Arg	Ala	Tyr	His	Gln	Ala	Gly	Thr	Arg
	65				70					75					80
Cys	Ser	Thr	Leu	Pro	Ala	Gly	Ser	Leu	Thr	Thr	Gly	Met	Gln	Thr	Gln
			85						90					95	
Thr	Leu	Tyr	Pro	Gly	Ser	Pro	His	Met	Thr	Pro	Thr	Pro	Trp	Leu	Pro
			100					105					110		
Asn	Arg	Pro	Arg	Ser	Ser	Glu	Ala	Val	Met	Gln	Met	Leu	Lys	Lys	Ser
		115					120					125			
Trp	Thr	Gly	Ala	Met	Thr	Ser	Arg	Thr	Gly	Ala	Met	Thr	Ser	Arg	Thr
	130					135					140				
Ala	Ala	Met	Arg	Asn											
	145														

<210> 366  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 366

Pro	Arg	Ser	Arg	Ser	Leu	Ser	Asp	Leu	Ser	Trp	Pro	Arg	Ser	Asp	Leu
1				5					10					15	

Ser	Trp	Pro	Leu 20	Ser	Ser	Phe	Ser	Trp 25	Leu	Arg	Ser	Asp	Leu 30	Ser	Trp
Pro	Leu	Ser 35	Asp	Leu	Ser	Trp	Leu 40	Arg	Ser	Asn	Phe	Ser 45	Ser	Ala	Ser
Ala	Leu 50	Leu	Leu	Leu	Ser	Phe 55	Leu	Ala	Asp	Leu	Val 60	Thr	Thr	Glu	Leu
Gly 65	Ser	Cys	Gly	Glu	Ser 70	Gln	Asp	Thr	Arg	Ser 75	Val	Ser	Ala	Phe	Gln 80

<210> 367  
 <211> 160  
 <212> PRT  
 <213> homo sapiens

<400> 367

Val 1	Ala	Gln	Gln	Pro 5	Ala	Leu	Ile	His	Gly 10	Tyr	Arg	Lys	Ala	Val 15	Leu
Thr	Pro	Asn	His 20	Val	Glu	Phe	Ser	Arg 25	Leu	Tyr	Asp	Ala	Val 30	Leu	Arg
Gly	Pro	Met 35	Asp	Ser	Asp	Asp	Ser 40	His	Gly	Ser	Val	Leu 45	Arg	Leu	Ser
Gln	Ala 50	Leu	Gly	Asn	Val	Thr 55	Val	Val	Gln	Lys	Gly 60	Glu	Arg	Asp	Ile
Leu 65	Ser	Asn	Gly	Gln	Gln 70	Val	Leu	Val	Cys 75	Gln	Glu	Gly	Ser	Ser 80	
Arg	Arg	Cys	Gly 85	Gln	Gly	Asp	Leu	Leu 90	Ser	Gly	Ser	Leu	Gly 95	Val	
Leu	Val	His	Trp 100	Ala	Leu	Leu	Ala	Gly 105	Pro	Gln	Lys	Thr	Asn 110	Gly	Ser
Ser	Pro	Leu 115	Leu	Val	Ala	Ala	Phe 120	Gly	Ala	Cys	Ser	Leu 125	Thr	Arg	Gln
Cys	Asn 130	His	Gln	Ala	Phe	Gln 135	Lys	His	Gly	Arg	Ser 140	Thr	Thr	Thr	Ser
Asp 145	Met	Ile	Ala	Glu	Val 150	Gly	Ala	Ala	Phe	Ser 155	Lys	Leu	Phe	Glu	Thr 160

<210> 368  
 <211> 164  
 <212> PRT  
 <213> homo sapiens

<400> 368

Ile 1	Leu	Asn	Gly	Asn 5	Gln	Phe	Met	Leu	Lys 10	Leu	Lys	Ile	Trp	Gln 15	Ala
Pro	Tyr	Ala	Phe 20	Ser	Thr	Arg	Val	Gly 25	Pro	Asp	Phe	Pro	Ile 30	Thr	His

00673305-122700

Thr	Leu	Ser 35	Pro	Val	Gln	Gly	Ala 40	Cys	Leu	Leu	Leu	Val 45	Cys	Ala	Gly	
Ser	Gly 50	Phe	Lys	Glu	Leu	Ala 55	Glu	Gly	Gly	Pro	His 60	Leu	Gly	Asp	His	
Val 65	Gly	Gly	Gly	Gly	Gly 70	Ala	Thr	Val	Leu	Leu 75	Glu	Gly	Leu	Val	Val 80	
Ala	Leu	Pro	Gly	Glu 85	Arg	Ala	Gly	Ala	Lys 90	Arg	Gly	His	Gln	Glu 95	Arg	
Ala	Gly	Pro	Ile 100	Cys	Phe	Leu	Trp	Ser 105	Ser	Lys	Glu	Arg	Pro 110	Val	Tyr	
Gln	Asp	Ala 115	Gln	Gly	Ala	Arg	Gln 120	Glu	Val	Pro	Leu	Pro 125	Ser	Thr	Pro	
Ala	Ala 130	Ala	Ala	Phe	Leu	Ala 135	Ala	His	Lys	His	Leu 140	Leu	Ala	Val	Gly	
Glu 145	Asp	Val	Ala	Leu	Ser 150	Phe	Leu	Asp	His	Arg 155	His	Val	Ala	Gln	Gly 160	
Leu	Ala	Glu	Ser													

<210> 369

<211> 187

<212> PRT

<213> homo sapiens

<400> 369

Lys 1	Ser	Gly	Lys	His 5	Arg	Thr	Pro	Ser	Ala 10	His	Ala	Trp	Val	Arg 15	Ile	
Phe	Pro	Ser	His 20	Thr	Arg	Ser	Pro	Pro 25	Ser	Lys	Val	Pro	Val 30	Tyr	Phe	
Trp	Ser	Ala 35	Arg	Ala	Gln	Val	Ser 40	Lys	Ser	Leu	Leu	Lys 45	Ala	Ala	Pro	
Thr	Ser 50	Ala	Ile	Met	Ser	Glu 55	Val	Val	Val	Glu	Arg 60	Pro	Cys	Phe	Trp	
Lys 65	Ala	Trp	Trp	Leu	His 70	Cys	Leu	Val	Arg	Glu 75	Gln	Ala	Pro	Asn	Ala 80	
Ala	Thr	Arg	Arg	Gly 85	Leu	Asp	Pro	Phe	Val 90	Phe	Cys	Gly	Pro	Ala 95	Arg	
Ser	Ala	Gln	Cys 100	Thr	Arg	Thr	Pro	Arg 105	Glu	Pro	Asp	Arg	Arg 110	Ser	Pro	
Cys	Pro	Pro 115	His	Leu	Arg	Leu	Leu 120	Pro	Ser	Trp	Leu	His 125	Thr	Ser	Thr	
Cys	Trp 130	Pro	Leu	Glu	Arg	Met 135	Ser	Arg	Ser	Pro	Phe 140	Trp	Thr	Thr	Val	
Thr 145	Leu	Pro	Arg	Ala	Trp 150	Leu	Ser	Leu	Ser	Thr 155	Asp	Pro	Trp	Leu	Ser 160	

00672305-122700

Ser Leu Ser Ile Gly Pro Leu Ser Thr Ala Ser Tyr Ser Leu Leu Asn  
165 170 175

Ser Thr Trp Leu Gly Val Ser Thr Ala Phe Arg  
180 185

<210> 370

<211> 40

<212> PRT

<213> homo sapiens

<400> 370

Leu Phe Leu Phe Thr Asn His Asn Asp Ser Gly Lys Pro Gly Cys Lys  
1 5 10 15

His Gln His Cys His Gln Leu Arg Ile Cys Asp Gln Glu Cys His Leu  
20 30

Thr Val Thr Gly Arg Arg Gln Lys  
35 40

<210> 371

<211> 34

<212> PRT

<213> homo sapiens

<400> 371

Gln Ala Glu Asp Lys Ser Glu Thr Gly Leu Met Arg Ile Thr Gly Lys  
1 5 10 15

Leu Ala Leu Ala Pro Pro Glu Asn Glu Leu Phe His Ser Leu Ala Asp  
20 25 30

His Pro

<210> 372

<211> 38

<212> PRT

<213> homo sapiens

<400> 372

Asn Ser Ser Phe Ser Gly Gly Ala Lys Ala Ser Phe Pro Val Ile Arg  
1 5 10 15

Ile Ser Pro Val Ser Leu Leu Ser Ser Ala Cys Tyr Arg Glu Met Ala  
20 25 30

Leu Leu Ile Thr Asp Pro  
35

<210> 373

<211> 123

<212> PRT

<213> homo sapiens

<400> 373

Arg Gln Leu Phe Gly Ile Val Ser Ile Ala Thr Leu Thr Val Leu Ala  
1 5 10 15

00673305.122700

Tyr	Glu	Arg	Tyr 20	Ile	Arg	Val	Val	His 25	Ala	Arg	Val	Ile	Asn 30	Phe	Ser	
Trp	Ala	Trp 35	Arg	Ala	Ile	Thr	Tyr 40	Ile	Trp	Leu	Tyr	Ser 45	Leu	Ala	Trp	
Ala	Gly 50	Ala	Pro	Leu	Leu	Gly 55	Trp	Asn	Arg	Tyr	Ile 60	Leu	Asp	Val	His	
Gly 65	Leu	Gly	Cys	Thr 70	Val	Asp	Trp	Lys	Ser	Lys 75	Asp	Ala	Asn	Asp	Ser 80	
Ser	Phe	Val	Leu	Phe 85	Leu	Phe	Leu	Gly	Cys 90	Leu	Val	Val	Pro	Leu 95	Gly	
Val	Ile	Ala	His 100	Cys	Tyr	Gly	His	Ile 105	Leu	Tyr	Phe	His	Ser 110	Asn	Ala	
Ser	Leu	Val 115	Trp	Lys	Ile	Phe	Arg 120	Gln	Phe	Lys						

<210> 374  
 <211> 121  
 <212> PRT  
 <213> homo sapiens

<400> 374

Thr 1	Val	His	Ser	Arg 5	Gly	Pro	Cys	Gln	Ser 10	Asp	Gln	Phe	Phe	Leu 15	Gly	
Leu	Glu	Gly	His 20	Tyr	Leu	His	Leu	Ala 25	Leu	Leu	Thr	Gly	Val 30	Gly	Arg	
Ser	Thr	Ser 35	Pro	Gly	Met	Glu	Gln 40	Val	His	Pro	Gly	Arg 45	Thr	Arg	Thr	
Arg	Leu 50	His	Cys	Gly	Leu	Glu 55	Ile	Gln	Gly	Cys	Gln 60	Arg	Phe	Leu	Leu	
Cys 65	Ala	Phe	Leu	Ile	Ser 70	Trp	Leu	Pro	Gly	Gly 75	Ala	Pro	Gly	Cys	His 80	
Ser	Pro	Leu	Leu	Trp 85	Pro	Tyr	Ser	Ile	Phe 90	Pro	Phe	Glu	Cys	Phe 95	Val	
Gly	Val	Glu	Asp 100	Leu	Gln	Thr	Ile	Gln 105	Val	Ile	Lys	Ile	Leu 110	Lys	Tyr	
Glu	Lys	Lys 115	Leu	Ala	Lys	Met	Cys 120	Phe								

<210> 375  
 <211> 58  
 <212> PRT  
 <213> homo sapiens

<400> 375

His 1	Pro	Gly	Ala	Pro 5	Pro	Gly	Ser	Gln	Glu 10	Ile	Arg	Lys	Ala	Gln 15	Arg	
Arg	Asn	Arg	Trp	His	Pro	Trp	Ile	Ser	Ser	Pro	Gln	Cys	Ser	Leu	Val	

00673305.122700

				20						25						30			
Arg	Val	Arg	Pro	Gly	Cys	Thr	Cys	Ser	Ile	Pro	Gly	Glu	Val	Leu	Leu				
		35					40					45							
Pro	Thr	Pro	Val	Ser	Arg	Ala	Arg	Cys	Arg										
	50					55													

<210> 376  
 <211> 49  
 <212> PRT  
 <213> homo sapiens

<400> 376

Ala	Phe	Thr	Cys	Asp	Phe	Val	Pro	Leu	Cys	Gly	Leu	Leu	Glu	Gln	Trp				
1				5					10					15					
Thr	Thr	Lys	Ser	Ala	Met	Gln	Phe	Ile	Lys	Val	Asp	Leu	Val	Ile	Cys				
		20						25					30						
His	Pro	Thr	Ala	Tyr	Gly	Pro	Cys	Lys	Pro	Val	Leu	Glu	Ala	Asn	Ile				
		35					40					45							

Leu

<210> 377  
 <211> 68  
 <212> PRT  
 <213> homo sapiens

<400> 377

Phe	Cys	Thr	Thr	Leu	Trp	Pro	Ser	Gly	Ala	Met	Asp	Asn	Gln	Val	Ser				
1				5					10					15					
Tyr	Ala	Val	His	Lys	Ser	Gly	Pro	Gly	Tyr	Met	Ser	Ser	Asn	Ser	Ile				
		20						25					30						
Trp	Ser	Leu	Gln	Ala	Cys	Phe	Gly	Ser	Gln	Tyr	Ser	Ile	Thr	Tyr	Arg				
		35					40					45							
Asn	Pro	Leu	Glu	Ser	Asp	Val	Phe	Gly	Ser	Asn	Ile	Phe	Ser	Gln	Gly				
	50					55					60								

Ser 65 Asn Gly Leu

<210> 378  
 <211> 64  
 <212> PRT  
 <213> homo sapiens

<400> 378

His	Ile	Thr	Arg	Ser	Thr	Phe	Met	Asn	Cys	Ile	Ala	Asp	Leu	Val	Val				
1				5					10					15					
His	Cys	Ser	Arg	Arg	Pro	Gln	Ser	Gly	Thr	Lys	Ser	Gln	Val	Lys	Ala				
		20						25					30						
Gln	Thr	Ala	Pro	Val	Ile	Leu	Val	Val	Leu	Ser	Leu	His	Ser	Ser	Pro				
		35					40					45							



Leu Ala Lys Thr Gly Leu Asn Met Lys Ser Pro Ala Pro Arg Pro Gln  
50 55 60

<210> 379  
<211> 144  
<212> PRT  
<213> homo sapiens

<400> 379

Ala Pro Ile Ser Ser Asn Phe Cys Ser Glu Ser Ile Trp Gly Tyr Cys  
1 5 15  
Asp Gln Leu Lys Val Ser Glu Ser Thr His Val Leu Gln Pro Phe Leu  
20 25 30  
Pro Ser Ile Leu Asp Gly Leu Ile His Leu Ala Ala Gln Phe Ser Ser  
35 40 45  
Glu Val Leu Asn Leu Val Met Glu Thr Leu Cys Ile Val Cys Thr Val  
50 55 60  
Asp Pro Glu Phe Thr Ala Ser Met Glu Ser Lys Ile Cys Pro Phe Thr  
65 70 75 80  
Ile Ala Ile Phe Leu Lys Tyr Ser Asn Asp Pro Val Val Ala Ser Leu  
85 90 95  
Ala Gln Asp Ile Phe Lys Glu Leu Ser Gln Ile Glu Ala Cys Gln Gly  
100 105 110  
Pro Met Gln Met Arg Leu Ile Pro Thr Leu Val Ser Ile Met Gln Ala  
115 120 125  
Pro Ala Asp Lys Ile Pro Ala Gly Leu Cys Ala Thr Pro Leu Ile Ser  
130 135 140

<210> 380  
<211> 254  
<212> PRT  
<213> homo sapiens

<400> 380

Tyr Glu Ile Gln Ser Leu Pro Phe Pro Ser Phe Ser Ser Ala Lys Leu  
1 5 15  
Ser Leu Leu Trp His Ser Val Pro Phe Thr Gln Met Thr Met Pro Ser  
20 25 30  
Val Gln Asn Gly Gly Glu Cys Leu Arg Ala Tyr Val Ser Val Thr Leu  
35 40 45  
Glu Gln Val Ala Gln Trp His Asp Glu Gln Gly His Asn Gly Leu Trp  
50 55 60  
Tyr Val Met Gln Val Val Ser Gln Leu Leu Asp Pro Arg Thr Ser Glu  
65 70 75 80  
Phe Thr Ala Ala Phe Val Gly Arg Leu Val Ser Thr Leu Ile Ser Lys  
85 90 95

00673305.122700

Ala	Gly	Arg	Glu 100	Leu	Gly	Glu	Asn	Leu 105	Asp	Gln	Ile	Leu	Arg 110	Ala	Ile	
Leu	Ser	Lys 115	Met	Gln	Gln	Ala	Glu 120	Thr	Leu	Ser	Val	Met 125	Gln	Ser	Leu	
Ile	Met 130	Val	Phe	Ala	His	Leu 135	Val	His	Thr	Gln	Leu 140	Glu	Pro	Leu	Leu	
Glu 145	Phe	Leu	Cys	Ser	Leu 150	Pro	Gly	Pro	Thr	Gly 155	Lys	Pro	Ala	Leu	Glu 160	
Phe	Val	Met	Ala	Glu 165	Trp	Thr	Ser	Arg	Gln 170	His	Leu	Phe	Tyr	Gly 175	Gln	
Tyr	Glu	Gly	Lys 180	Val	Ser	Ser	Val	Ala 185	Leu	Cys	Lys	Leu	Leu 190	Gln	His	
Gly	Ile	Asn 195	Ala	Asp	Asp	Lys	Arg 200	Leu	Gln	Asp	Ile	Arg 205	Val	Lys	Gly	
Glu	Glu 210	Ile	Tyr	Ser	Met	Asp 215	Glu	Gly	Ile	Arg	Thr 220	Arg	Ser	Lys	Ser	
Ala 225	Lys	Asn	Pro	Glu	Arg 230	Trp	Thr	Asn	Ile	Pro 235	Leu	Leu	Val	Lys	Ile 240	
Leu	Lys	Leu	Ile	Ile 245	Asn	Glu	Leu	Ser	Asn 250	Val	Met	Gly	Gly			

<210> 381

<211> 95

<212> PRT

<213> homo sapiens

<400> 381

Ser 1	Leu	Ser	Gly	Pro 5	Asn	Ala	Asn	Glu	Ala 10	Asp	Ser	His	Ser	Gly 15	Gln	
His	Asn	Ala	Gly 20	Pro	Ser	Arg	Gln	Asp 25	Ser	Cys	Arg	Ala	Leu 30	Cys	Asp	
Thr	Ile	Asp 35	Ile	Leu	Thr	Thr	Val 40	Val	Arg	Asn	Thr	Lys 45	Pro	Pro	Leu	
Ser	Gln 50	Leu	Leu	Ile	Cys	Gln 55	Ala	Phe	Pro	Ala	Val 60	Ala	Gln	Cys	Thr	
Leu 65	His	Thr	Asp	Asp	Asn 70	Ala	Ile	Ser	Ala	Glu 75	Trp	Arg	Arg	Val	Leu 80	
Ala	Gly	Leu	Cys	Val 85	Ser	Asp	Pro	Gly	Thr 90	Ser	Ser	Pro	Val	Ala 95		

<210> 382

<211> 263

<212> PRT

<213> homo sapiens

<400> 382

Ala	Pro	Ile	Ser	Ser	Asn	Phe	Cys	Ser	Glu	Ser	Ile	Trp	Gly	Tyr	Cys	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

00673305-122700

1				5				10				15			
Asp	Gln	Leu	Lys 20	Val	Ser	Glu	Ser	Thr 25	His	Val	Leu	Gln	Pro 30	Phe	Leu
Pro	Ser	Ile 35	Leu	Asp	Gly	Leu	Ile 40	His	Leu	Ala	Ala	Gln 45	Phe	Ser	Ser
Glu	Val 50	Leu	Asn	Leu	Val	Met 55	Glu	Thr	Leu	Cys	Ile 60	Val	Cys	Thr	Val
Asp 65	Pro	Glu	Phe	Thr	Ala 70	Ser	Met	Glu	Ser	Lys 75	Ile	Cys	Pro	Phe	Thr 80
Ile	Ala	Ile	Phe	Leu 85	Lys	Tyr	Ser	Asn	Asp 90	Pro	Val	Val	Ala	Ser 95	Leu
Ala	Gln	Asp	Ile 100	Phe	Lys	Glu	Leu	Ser 105	Gln	Ile	Glu	Ala	Cys 110	Gln	Gly
Pro	Met	Gln 115	Met	Arg	Leu	Ile	Pro 120	Thr	Leu	Val	Ser	Ile 125	Met	Gln	Ala
Pro	Ala 130	Asp	Lys	Ile	Pro	Ala 135	Gly	Leu	Cys	Ala	Thr 140	Pro	Ile	Asp	Ile
Leu 145	Thr	Thr	Val	Val	Arg 150	Asn	Thr	Lys	Pro	Pro 155	Leu	Ser	Gln	Leu	Leu 160
Ile	Cys	Gln	Ala	Phe 165	Pro	Ala	Val	Ala	Gln 170	Cys	Thr	Leu	His	Thr 175	Asp
Asp	Asn	Ala	Thr 180	Met	Gln	Asn	Gly	Gly 185	Glu	Cys	Leu	Arg	Ala 190	Tyr	Val
Ser	Val	Thr 195	Leu	Glu	Gln	Val	Ala 200	Gln	Trp	His	Asp	Glu 205	Gln	Gly	His
Asn	Gly 210	Leu	Trp	Tyr	Val	Met 215	Gln	Val	Val	Ser	Gln 220	Leu	Leu	Asp	Pro
Arg 225	Thr	Ser	Glu	Phe	Thr 230	Ala	Ala	Phe	Val	Gly 235	Arg	Leu	Cys	Phe	His 240
Pro	His	Leu	Gln	Gly 245	Arg	Ala	Gly	Thr	Arg 250	Gly	Glu	Ser	Arg	Pro 255	Asp
Phe	Phe	Val	Pro 260	Ser	Phe	Ser									

<210> 383

<211> 68

<212> PRT

<213> homo sapiens

<400> 383

Thr 1	Leu	Arg	Cys	Gly 5	Gly	Pro	Gly	Ala	Gly 10	Ser	Pro	Leu	Ala	Ser 15	His
Thr	Thr	Val	His 20	Cys	Gly	Pro	Ala	His 25	His	Ala	Thr	Gly	Leu 30	Leu	Val

00673705 122700

Pro	Gly	Ser	Leu	Thr	His	Arg	Pro	Ala	Ser	Thr	Leu	Arg	His	Ser	Ala
		35					40					45			
Trp	Trp	His	Cys	His	Leu	Cys	Glu	Gly	Tyr	Thr	Val	Pro	Gln	Gln	Gly
	50					55					60				
Lys	Leu	Gly	Arg												
65															

<210> 384  
 <211> 97  
 <212> PRT  
 <213> homo sapiens

<400> 384

His	Ile	Gly	Pro	Gln	Ala	Leu	Ser	Ala	Ile	Leu	His	Gly	Gly	Ile	Val
1				5					10					15	
Ile	Cys	Val	Lys	Gly	Thr	Leu	Cys	His	Ser	Arg	Glu	Ser	Leu	Ala	Asp
			20					25					30		
Glu	Lys	Leu	Gly	Lys	Gly	Arg	Leu	Cys	Ile	Ser	Tyr	Tyr	Cys	Cys	Gln
		35					40					45			
Asp	Ile	Asn	Gly	Cys	Arg	Thr	Lys	Pro	Cys	Arg	Asn	Leu	Val	Cys	Trp
	50					55					60				
Gly	Leu	His	Tyr	Ala	Asp	Gln	Ser	Gly	Asn	Gln	Pro	His	Leu	His	Trp
65					70					75					80
Ala	Leu	Thr	Gly	Phe	Asn	Leu	Gly	Gln	Leu	Leu	Glu	Asp	Val	Leu	Ser
				85					90					95	
Gln															

<210> 385  
 <211> 140  
 <212> PRT  
 <213> homo sapiens

<400> 385

Thr	Arg	Ser	Ser	Ser	Pro	Gln	Thr	Ile	Thr	Phe	Asp	Ala	Cys	Val	Val
1				5					10					15	
Ile	Pro	Cys	Gly	Asp	Leu	Gln	Ser	Gln	Lys	Gln	Leu	Ser	Asp	Ser	Glu
			20					25					30		
Lys	Tyr	Leu	Cys	Pro	Phe	Lys	Ile	Lys	Gly	Ser	Pro	Tyr	Gln	Asp	Pro
		35					40					45			
Cys	Ser	Leu	Thr	Asn	Ala	Gly	Lys	Gln	Val	Cys	His	Ser	Trp	Asn	Glu
	50					55					60				
Val	Val	Trp	Thr	Thr	Glu	Tyr	Gln	Gly	Trp	Thr	Ser	Ser	Thr	Gly	Gly
65					70					75					80
Cys	Met	Ser	Leu	Lys	Pro	Tyr	Ile	His	Phe	Thr	Lys	Glu	Ser	Thr	Pro
				85					90					95	
His	Asn	Cys	Gln	Tyr	Asn	Gln	Cys	Asn	Pro	Val	Gln	Ile	Ser	Ile	Leu
			100					105					110		

007227-5032990

Ile Pro Thr Ser Thr Asp Pro Lys Pro Thr Leu Ser Cys Gly Ile Trp  
115 120 125

His Gly Ser Arg Asn Ser Arg Gly Thr Ser Tyr Trp  
130 135 140

<210> 386

<211> 49

<212> PRT

<213> homo sapiens

<400> 386

Asp Val Pro Leu Leu Phe Arg Leu Pro Cys His Ile Pro Gln Leu Lys  
1 5 10 15

Val Gly Leu Gly Ser Val Glu Val Gly Met Arg Ile Glu Ile Cys Thr  
20 25 30

Gly Leu His Trp Leu Tyr Trp Gln Leu Trp Gly Val Leu Ser Leu Val  
35 40 45

Lys

<210> 387

<211> 51

<212> PRT

<213> homo sapiens

<400> 387

Ser Glu Cys Met Val Leu Arg Thr Tyr Asn His Arg Leu Thr Arg Ser  
1 5 10 15

Ser Leu Asp Ile Gln Leu Ser Thr Pro Pro His Ser Ser Tyr Gly Arg  
20 25 30

Pro Val Phe Leu His Ser Leu Arg Asn Lys Gly Leu Asp Arg Gly Ser  
35 40 45

Leu Leu Ser  
50

<210> 388

<211> 97

<212> PRT

<213> homo sapiens

<400> 388

Ser Ser Ser Pro Leu Ser Phe Cys Trp Phe Leu Pro Ser Pro Ala Ala  
1 5 10 15

Ser Cys Ser Ser Ser Cys Pro Ser Gly Met Thr Ser Trp Ser Arg Ser  
20 25 30

Gly Pro Ser Ile Ser Gly Phe Ser Trp Leu Thr Asp Arg Ala Ala Cys  
35 40 45

Thr Cys Gly Val Trp Pro Ser Ser Pro Ala Pro Pro Lys Pro Leu Pro  
50 55 60

00573305-122700

Pro 65	Thr	Gly	Leu	Ser	Ser 70	Thr	Pro	Ala	Pro	Gly 75	Leu	Ala	Pro	Ala	Ala 80
Ala	Cys	Pro	Ser	Glu 85	Ala	Pro	Ile	Asn	Thr 90	Asp	Leu	Met	Val	Pro 95	Phe

Pro

<210> 389  
 <211> 148  
 <212> PRT  
 <213> homo sapiens

<400> 389

Gly 1	Lys	Gly	Thr	Met 5	Arg	Ser	Val	Leu	Ile 10	Gly	Ala	Ser	Glu	Gly 15	Gln
Ala	Ala	Ala	Gly 20	Ala	Arg	Pro	Gly	Ala 25	Gly	Val	Glu	Asp	Arg 30	Pro	Val
Gly	Gly	Arg 35	Gly	Phe	Gly	Gly	Ala 40	Gly	Glu	Leu	Gly	Gln 45	Thr	Pro	Gln
Val	Gln 50	Ala	Ala	Leu	Ser	Val 55	Ser	Gln	Glu	Asn	Pro 60	Glu	Met	Glu	Gly
Pro 65	Glu	Arg	Asp	Gln	Leu 70	Val	Ile	Pro	Asp	Gly 75	Gln	Glu	Glu	Glu	Gln 80
Glu	Ala	Ala	Gly 85	Gly	Arg	Asn	Gln	Gln 90	Lys	Leu	Arg	Gly	Glu 95	Asp	
Asp	Tyr	Asn	Met 100	Asp	Glu	Asn	Glu	Ala 105	Glu	Ser	Glu	Thr	Asp 110	Lys	Gln
Ala	Ala	Leu 115	Ala	Gly	Asn	Asp	Arg 120	Asn	Ile	Asp	Val	Phe 125	Asn	Val	Glu
Asp	Gln 130	Lys	Arg	Asp	Thr	Ile 135	Asn	Leu	Leu	Asp	Gln 140	Arg	Glu	Lys	Arg
Asn 145	His	Thr	Leu												

<210> 390  
 <211> 84  
 <212> PRT  
 <213> homo sapiens

<400> 390

Gly 1	Pro	Arg	Asp	Arg 5	Leu	Ile	Gln	Pro	Ser 10	Tyr	Phe	Gln	Arg	Gly 15	Lys
Trp	Gly	Leu	Glu 20	Val	Thr	Glu	His	Leu 25	Ala	Gly	Ala	Leu	Ala 30	Pro	Leu
Ala	Ser	His 35	Arg	Leu	Pro	Ser	Ser 40	Trp	Asp	Tyr	Arg	His 45	Thr	Val	Thr
Glu	Ala 50	Gly	Pro	Val	Cys	Asn 55	Ser	Arg	Cys	His	Leu 60	Gln	Leu	Lys	His

00673305-122700

Ser 65 Ser Tyr Val Met Ser 70 Leu Val Thr Lys Val 75 Lys Leu Ser His Pro 80

Glu Lys Ala Thr

<210> 391

<211> 59

<212> PRT

<213> homo sapiens

<400> 391

Cys 1 Gly Lys Lys Cys 5 Ile Thr Leu Phe Leu 10 Phe Leu Ser Pro Ser 15 Leu

Pro Leu Trp Cys 20 Leu Arg Tyr Trp Gly 25 Ser His Ser Trp Gly 30 His Ser

Glu Ala Thr 35 Arg Asn Ala Ser Ser 40 Leu His Leu Ala Val 45 Ser Ala Arg

Thr Arg 50 Asn Pro Gln Thr Ser 55 Ser Gln Thr Ser

<210> 392

<211> 107

<212> PRT

<213> homo sapiens

<400> 392

Thr 1 Pro Arg Asn Leu 5 Asn Phe His Ser Lys 10 Leu Thr Gln Phe His 15 Cys

Val Asn Thr Val 20 Ser Leu Gly Ser Thr 25 Lys His Pro Ile Thr 30 Gln Phe

Cys Phe Ile 35 Val Trp Thr Pro Ser 40 Arg Leu Gln Gly His 45 His Gly Gln

Glu Val 50 Cys Glu Glu Val Cys 55 Gly Phe Leu Val Leu 60 Ala Leu Thr Ala

Arg 65 Cys Lys Leu Glu Ala 70 Phe Leu Val Ala Ser 75 Glu Trp Pro Gln Leu 80

Trp Asp Pro Gln Tyr 85 Leu Arg His His Arg 90 Gly Arg Glu Gly Asp 95 Arg

Asn Arg Asn Arg 100 Val Met His Phe Phe 105 Pro His

<210> 393

<211> 61

<212> PRT

<213> homo sapiens

<400> 393

Val 1 Ala Pro Ala Val 5 Gly Ser Pro Val Ser 10 Gln Ala Pro Gln Arg 15 Gln

00673305-122700

Arg	Gly	Gly	Gln 20	Glu	Gln	Lys	Gln	Ser 25	Tyr	Ala	Phe	Leu	Ser 30	Thr	Leu
Lys	Lys	Arg 35	Asn	Tyr	Thr	Phe	Arg 40	Gly	Met	Leu	Ser	Pro 45	Arg	Ser	Thr
Ser	Ser 50	Pro	Val	Phe	His	Asp 55	Leu	Pro	Thr	Lys	Lys 60	Ile			

<210> 394  
 <211> 74  
 <212> PRT  
 <213> homo sapiens

<400> 394

Cys 1	Asn	Cys	Ala	Pro 5	Ser	Leu	Pro	Asp	Phe 10	Ser	Pro	Leu	His	Pro 15	Gln
Cys	Gly	Ile	Ser 20	Leu	Val	Pro	Arg	Gly 25	Thr	Pro	Leu	Asp	Leu 30	Trp	Thr
Ser	Arg	Pro 35	Gly	Gln	Glu	Ala	Ala 40	Thr	Arg	Asn	Pro	Arg 45	Pro	Leu	Leu
Leu	Lys 50	Phe	Thr	Ala	Ser	Val 55	Val	Val	Pro	Asp	Ser 60	Ser	Pro	Ala	Pro
Gly 65	Thr	Thr	Ser	Thr	Trp 70	Gly	Gly	Ala	Phe						

<210> 395  
 <211> 112  
 <212> PRT  
 <213> homo sapiens

<400> 395

Ala 1	Thr	Val	His	Pro 5	Ala	Cys	Gln	Ile	Phe 10	Pro	His	Tyr	Thr	Pro 15	Ser
Val	Ala	Tyr	Pro 20	Trp	Ser	Pro	Glu	Ala 25	His	Pro	Leu	Ile	Cys 30	Gly	Pro
Pro	Gly	Leu 35	Asp	Lys	Arg	Leu	Leu 40	Pro	Glu	Thr	Pro	Gly 45	Pro	Cys	Tyr
Ser	Asn 50	Ser	Gln	Pro	Val	Trp 55	Leu	Cys	Leu	Thr	Pro 60	Arg	Gln	Pro	Leu
Glu 65	Pro	His	Pro	Pro	Gly 70	Glu	Gly	Pro	Ser	Glu 75	Trp	Ser	Ser	Asp	Thr 80
Ala	Glu	Gly	Arg	Pro 85	Cys	Pro	Tyr	Pro	His 90	Cys	Gln	Val	Leu	Ser 95	Ala
Gln	Pro	Gly	Ser 100	Glu	Glu	Glu	Leu	Glu 105	Glu	Leu	Cys	Glu	Gln 110	Ala	Val

<210> 396  
 <211> 45  
 <212> PRT  
 <213> homo sapiens

00673395-12700



<400> 396

Asp	Arg	Arg	Ser	His	Gly	Leu	Leu	Leu	Tyr	Asn	Leu	Pro	Gly	Glu	Gln
1				5					10					15	
Phe	Lys	Asn	Met	Asn	Gln	Asp	Pro	Phe	Asp	Pro	Leu	Ile	Ile	Gln	Lys
			20					25					30		
Ser	Thr	Gln	Lys	Tyr	Ala	Gln	Lys	Tyr	Val	Gly	Ile	His			
		35					40					45			

<210> 397

<211> 43

<212> PRT

<213> homo sapiens

<400> 397

Glu	Arg	Leu	Ser	His	Cys	Arg	Ser	Leu	Val	Met	Leu	Ala	Leu	Ile	Ser
1				5					10					15	
Leu	Cys	Thr	Pro	Cys	Thr	His	Ala	Phe	Ser	Pro	Val	Phe	Tyr	Gln	Ala
			20					25					30		
Ser	Val	Ser	Cys	Ile	Thr	Leu	Lys	Cys	Asp	His					
		35					40								

<210> 398

<211> 64

<212> PRT

<213> homo sapiens

<400> 398

Trp	Ile	Lys	Arg	Ile	Leu	Ile	His	Ile	Phe	Lys	Leu	Leu	Ser	Arg	Glu
1				5					10					15	
Val	Val	Lys	Gln	Gln	Ser	Met	Arg	Ala	Ser	Ile	Ser	Leu	Pro	Leu	Leu
			20					25					30		
Gly	Asp	Ala	Cys	Pro	His	Leu	Pro	Met	Tyr	Pro	Met	His	Ser	Cys	Leu
		35					40					45			
Leu	Ser	Cys	Phe	Leu	Ser	Ser	Leu	Ser	Phe	Met	Tyr	Tyr	Thr	Lys	Met
	50					55					60				

<210> 399

<211> 77

<212> PRT

<213> homo sapiens

<400> 399

His	Ile	Lys	Ile	Glu	Phe	Phe	Gly	Gln	Asn	Phe	Trp	Glu	Ala	Met	His
1				5					10					15	
Pro	Thr	Trp	Ala	Asp	Ile	Gln	Pro	Glu	Leu	Phe	Ser	Arg	Gly	Glu	Trp
			20					25					30		
Tyr	Trp	Gln	Phe	Met	Ala	Glu	Ile	His	Ser	Asp	Trp	Leu	Glu	Ser	Met
		35					40					45			

006733501.122700

Leu	Tyr	Gln	Leu	Leu	Asn	Ile	Leu	Ser	Ile	Thr	Leu	Ala	Tyr	Cys	Tyr
	50					55					60				
Tyr	Tyr	Ile	Ser	Ser	Ile	Tyr	Arg	Gln	Lys	Gly	His	Phe			
65					70					75					

<210> 400  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 400

Ser	Ser	Leu	Gly	Lys	Thr	Phe	Gly	Lys	Gln	Cys	Ile	Leu	His	Gly	Leu
1				5					10					15	
Ile	Phe	Ser	Leu	Ser	Cys	Ser	Gln	Glu	Glu	Ser	Gly	Thr	Gly	Ser	Leu
			20					25					30		
Trp	Leu	Lys	Ser	Ile	Leu	Ile	Gly	Trp	Ser	Leu	Cys	Tyr	Thr	Ser	Cys
		35					40					45			

<210> 401  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 401

Phe	Arg	Asn	Pro	Ala	Leu	Ile	Glu	Pro	Ser	Val	Gly	Ser	Thr	Ala	Glu
1				5					10					15	
Ile	Phe	Arg	Ala	Phe	Asn	Ile	Leu	Lys	Met	Ala	Phe	Leu	Ser	Ile	Tyr
			20					25					30		
Arg	Gly	Asn	Ile	Ile	Val	Thr	Val	Cys	Lys	Ser	Asp	Thr	Gln	Asn	Val
		35					40					45			

<210> 402  
 <211> 70  
 <212> PRT  
 <213> homo sapiens

<400> 402

Glu	Gln	Leu	Arg	Leu	Asn	Ile	Ser	Pro	Cys	Arg	Met	His	Cys	Phe	Pro
1				5					10					15	
Lys	Val	Leu	Pro	Lys	Glu	Leu	Tyr	Phe	Tyr	Val	Leu	Ser	His	Arg	Thr
			20					25					30		
Gly	Glu	Lys	Cys	Ser	Gly	His	Cys	Trp	Asp	Leu	Ile	Phe	Leu	Gly	Met
		35					40					45			
Gly	Ser	Gly	Leu	Met	Ile	Leu	Ala	Thr	Gly	Val	Gln	Glu	Asn	Gly	Ser
	50					55					60				
Pro	Gly	Ser	Asp	Ser	Trp										
65					70										

<210> 403  
 <211> 63  
 <212> PRT

00673395.122700

<213> homo sapiens

<400> 403

Met	Cys	Asp	Phe	Ile	Arg	Gly	Ile	Cys	Gln	Phe	Ser	His	Cys	Gly	Ser
1				5					10					15	
Phe	Ser	Asp	Phe	Ala	Cys	Ser	Ser	Ser	Lys	Glu	Ala	Arg	Ser	Phe	Ala
			20					25					30		
Asp	Phe	Thr	Ile	Pro	Gln	Thr	Cys	Lys	Phe	Leu	Thr	Ser	Ser	Lys	Leu
		35					40					45			
Ala	Leu	Ala	Leu	Ser	Ser	Thr	Phe	Pro	Phe	Lys	Ser	Asn	Leu	Cys	
	50					55					60				

<210> 404

<211> 71

<212> PRT

<213> homo sapiens

<400> 404

Met	Gly	Ile	Thr	His	Glu	Cys	Val	Ile	Leu	Leu	Gly	Ala	Ser	Ala	Asn
1				5					10					15	
Ser	Leu	Thr	Val	Val	Pro	Ser	Leu	Thr	Leu	Pro	Val	His	His	Leu	Arg
			20					25					30		
Arg	Leu	Asp	Pro	Ser	Leu	Thr	Ser	Pro	Phe	Leu	Lys	Pro	Val	Ser	Phe
		35					40					45			
Ser	Leu	Leu	Pro	Asn	Trp	Leu	Trp	Leu	Phe	Leu	Gln	Pro	Phe	His	Ser
	50					55					60				
Arg	Ala	Ile	Phe	Ala	Lys	Glu									
65					70										

<210> 405

<211> 63

<212> PRT

<213> homo sapiens

<400> 405

Leu	Gly	Asp	His	Ile	Tyr	Asn	Trp	Asp	Val	Asn	His	Phe	Phe	Ser	Gly
1				5					10					15	
Ile	Arg	Ala	Gln	Arg	His	Asn	Leu	Gln	Gly	His	Ile	Ile	Tyr	Tyr	Glu
			20					25					30		
His	Phe	Thr	Val	Arg	Leu	Phe	Ile	Leu	Pro	Ser	Thr	Cys	Ala	Glu	Met
		35					40					45			
Lys	Pro	Lys	Gln	Ala	Val	Gly	Phe	His	Lys	Ser	Ile	Tyr	Val	Gly	
	50					55					60				

<210> 406

<211> 88

<212> PRT

<213> homo sapiens

<400> 406

00673305-122700

Leu 1	Val	Glu	Pro	Asn 5	Gly	Leu	Phe	Trp	Phe 10	His	Phe	Ser	Ala	Ser 15	Arg
Arg	Gln	Asn	Lys 20	Glu	Ser	His	Ser	Lys 25	Met	Phe	Ile	Val	Asp 30	Asn	Met
Ser	Leu	Lys 35	Val	Val	Pro	Leu	Cys 40	Ser	Tyr	Ser	Thr	Glu 45	Glu	Met	Ile
His	Ile 50	Pro	Ile	Ile	Asp	Met 55	Val	Ser	Gln	Ser	Glu 60	Glu	Ser	Phe	Arg
Arg 65	Leu	His	Lys	Tyr	Val 70	Leu	Cys	Thr	Cys	Pro 75	Met	Leu	Gly	Asn	Arg 80
Lys	Ile	Ile	Val	Ile 85	Asp	Lys	Thr								

<210> 407

<211> 296

<212> PRT

<213> homo sapiens

<400> 407

Leu 1	Thr	Val	Val	Tyr 5	Thr	Val	Phe	Tyr	Ala 10	Leu	Leu	Phe	Val	Phe 15	Ile
Tyr	Val	Gln	Leu 20	Trp	Leu	Val	Leu	Arg 25	Tyr	Arg	His	Lys	Arg 30	Leu	Ser
Tyr	Gln	Ser 35	Val	Phe	Leu	Phe	Leu 40	Cys	Leu	Phe	Trp	Ala 45	Ser	Arg	Arg
Thr	Val 50	Leu	Phe	Ser	Phe	Tyr 55	Phe	Lys	Asp	Phe	Val 60	Ala	Ala	Asn	Ser
Leu 65	Ser	Pro	Phe	Val	Phe 70	Trp	Leu	Leu	Tyr	Cys 75	Phe	Pro	Val	Cys	Leu 80
Gln	Phe	Phe	Thr	Leu 85	Thr	Leu	Met	Asn	Leu 90	Tyr	Phe	Thr	Gln	Val 95	Ile
Phe	Lys	Ala	Lys 100	Ser	Lys	Tyr	Ser	Pro 105	Glu	Leu	Leu	Lys	Tyr 110	Arg	Leu
Pro	Leu	Tyr 115	Leu	Ala	Ser	Leu	Phe 120	Ile	Ser	Leu	Val	Phe 125	Leu	Leu	Val
Asn	Leu 130	Thr	Cys	Ala	Val	Leu 135	Val	Lys	Thr	Gly	Asn 140	Trp	Glu	Arg	Lys
Val 145	Ile	Val	Ser	Val	Arg 150	Val	Ala	Ile	Asn	Asp 155	Thr	Leu	Phe	Val	Leu 160
Cys	Ala	Val	Ser	Leu 165	Ser	Ile	Cys	Leu	Tyr 170	Lys	Ile	Ser	Lys	Met 175	Ser
Leu	Ala	Asn	Ile 180	Tyr	Leu	Glu	Ser	Lys 185	Gly	Ser	Ser	Val	Cys 190	Gln	Val
Thr	Ala	Ile	Gly	Val	Thr	Val	Ile	Leu	Leu	Tyr	Thr	Ser	Arg	Ala	Cys

09673395-122700

	195						200						205					
Tyr	Asn 210	Leu	Phe	Ile	Leu	Ser 215	Phe	Ser	Gln	Asn	Lys 220	Ser	Val	His	Ser			
Phe 225	Asp	Tyr	Asp	Trp	Tyr 230	Asn	Val	Ser	Asp	Gln 235	Ala	Asp	Leu	Lys	Asn 240			
Gln	Leu	Gly	Asp	Ala 245	Gly	Tyr	Val	Leu	Phe 250	Gly	Val	Val	Leu	Phe 255	Val			
Trp	Glu	Leu	Leu 260	Pro	Thr	Thr	Leu	Val 265	Val	Tyr	Phe	Phe	Arg 270	Val	Arg			
Asn	Pro	Thr 275	Lys	Asp	Leu	Thr	Asn 280	Pro	Gly	Met	Val	Pro 285	Ser	His	Gly			
Phe	Ser 290	Pro	Gln	Ile	Leu	Phe 295	Leu											

```
<210> 408
<211> 152
<212> PRT
<213> homo sapiens
```

<400> 408

His 1	Arg	Arg	Leu	His 5	Arg	Val	Leu	Arg	Ala 10	Ala	Leu	Arg	Val	His 15	Leu
Arg	Ala	Ala	Leu 20	Ala	Gly	Ala	Ala	Leu 25	Pro	Pro	Gln	Ala	Ala 30	Gln	Leu
Pro	Glu	Arg 35	Leu	Pro	Leu	Ser	Leu 40	Pro	Leu	Leu	Gly	Leu 45	Pro	Ala	Asp
Arg	Pro 50	Leu	Leu	Leu	Leu	Leu 55	Gln	Arg	Leu	Arg	Gly 60	Gly	Gln	Phe	Ala
Gln 65	Pro	Leu	Arg	Leu	Leu 70	Ala	Ala	Leu	Leu	Leu 75	Pro	Cys	Val	Pro	Ala 80
Val	Phe	His	Pro	His 85	Ala	Asp	Glu	Leu	Val 90	Leu	His	Ala	Gly	Asp 95	Phe
Gln	Ser	Gln	Val 100	Lys	Ile	Phe	Ser	Arg 105	Ile	Thr	Gln	Ile	Pro 110	Val	Ala
Pro	Leu	Pro 115	Gly	Leu	Pro	Leu	His 120	Gln	Pro	Cys	Phe	Pro 125	Val	Gly	Glu
Phe	Asn 130	Leu	Cys	Cys	Ala	Gly 135	Lys	Asp	Gly	Lys	Leu 140	Gly	Glu	Glu	Gly
Tyr 145	Arg	Leu	Cys	Ala	Ser 150	Gly	His								

```
<210> 409
<211> 100
<212> PRT
<213> homo sapiens
```

<400> 409

096735 Jan 00

Leu 1	Gly	Phe	Glu	Asn 5	His	Leu	Arg	Glu	Val 10	Gln	Val	His	Gln	Arg 15	Glu
Gly	Glu	Lys	Leu 20	Gln	Ala	His	Arg	Glu 25	Ala	Val	Glu	Gln	Pro 30	Glu	Asp
Glu	Gly	Ala 35	Glu	Arg	Ile	Gly	Arg 40	His	Glu	Val	Phe	Glu 45	Val	Glu	Gly
Glu	Glu 50	Asp	Gly	Pro	Pro	Gly 55	Gly	Pro	Glu	Glu	Ala 60	Glu	Lys	Glu	Glu
Asp 65	Ala	Leu	Val	Ala	Glu 70	Pro	Leu	Val	Ala	Val 75	Thr	Gln	His	Gln	Pro 80
Glu	Leu	His	Val	Asp 85	Glu	His	Glu	Glu	Gln 90	Arg	Val	Glu	His	Gly 95	Val
Asp	Asp	Gly	Glu 100												

<210> 410  
 <211> 268  
 <212> PRT  
 <213> homo sapiens

<400> 410

Ala 1	Pro	Ile	Ser	Ser 5	Asn	Phe	Cys	Ser	Glu 10	Ser	Ile	Trp	Gly	Tyr 15	Cys
Asp	Gln	Leu	Lys 20	Val	Ser	Glu	Ser	Thr 25	His	Val	Leu	Gln	Pro 30	Phe	Leu
Pro	Ser	Ile 35	Leu	Asp	Gly	Leu	Ile 40	His	Leu	Ala	Ala	Gln 45	Phe	Ser	Ser
Glu 50	Val	Leu	Asn	Leu	Val	Met 55	Glu	Thr	Leu	Cys	Ile 60	Val	Cys	Thr	Val
Asp 65	Pro	Glu	Phe	Thr	Ala 70	Ser	Met	Glu	Ser	Lys 75	Ile	Cys	Pro	Phe	Thr 80
Ile	Ala	Ile	Phe	Leu 85	Lys	Tyr	Ser	Asn	Asp 90	Pro	Val	Val	Ala	Ser 95	Leu
Ala	Gln	Asp	Ile 100	Phe	Lys	Glu	Leu	Ser 105	Gln	Ile	Glu	Ala	Cys 110	Gln	Gly
Pro	Met	Gln 115	Met	Arg	Leu	Ile	Pro 120	Thr	Leu	Val	Ser	Ile 125	Met	Gln	Ala
Pro	Ala 130	Asp	Lys	Ile	Pro	Ala 135	Gly	Leu	Cys	Ala	Thr 140	Ala	Ile	Asp	Ile
Leu 145	Thr	Thr	Val	Val	Arg 150	Asn	Thr	Lys	Pro	Pro 155	Leu	Ser	Gln	Leu	Leu 160
Ile	Cys	Gln	Ala	Phe 165	Pro	Ala	Val	Ala	Gln 170	Cys	Thr	Leu	His	Thr 175	Asp
Asp	Asn	Ala	Thr	Met	Gln	Asn	Gly	Gly	Glu	Cys	Leu	Arg	Ala	Tyr	Val

00673305.122700

180										185					190				
Ser	Val	Thr	Leu	Glu	Gln	Val	Ala	Gln	Trp	His	Asp	Glu	Gln	Gly	His				
		195					200					205							
Asn	Gly	Leu	Trp	Tyr	Val	Met	Gln	Val	Val	Ser	Gln	Leu	Leu	Asp	Pro				
	210					215					220								
Arg	Thr	Ser	Glu	Phe	Thr	Ala	Ala	Phe	Val	Gly	Ala	Phe	Val	Ser	Thr				
	225				230					235					240				
Leu	Ile	Ser	Lys	Ala	Gly	Arg	Glu	Leu	Gly	Glu	Asn	Leu	Asp	Gln	Ile				
				245					250					255					
Ser	Ser	Cys	His	Pro	Ser	Val	Lys	Met	Ala	Gly	Gly								
			260					265											

<210> 411  
 <211> 97  
 <212> PRT  
 <213> homo sapiens

<400> 411

His	Ile	Gly	Pro	Gln	Ala	Leu	Ser	Ala	Ile	Leu	His	Gly	Gly	Ile	Val
1				5					10					15	
Ile	Cys	Val	Lys	Gly	Thr	Leu	Cys	His	Ser	Arg	Glu	Ser	Leu	Ala	Asp
			20					25					30		
Glu	Lys	Leu	Gly	Lys	Gly	Arg	Leu	Cys	Ile	Ser	Tyr	Tyr	Cys	Cys	Gln
		35					40					45			
Asp	Ile	Asn	Gly	Cys	Arg	Thr	Lys	Pro	Cys	Arg	Asn	Leu	Val	Cys	Trp
	50					55					60				
Gly	Leu	His	Tyr	Ala	Asp	Gln	Ser	Gly	Asn	Gln	Pro	His	Leu	His	Trp
	65				70					75					80
Ala	Leu	Thr	Gly	Phe	Asn	Leu	Gly	Gln	Leu	Leu	Glu	Asp	Val	Leu	Ser
				85					90					95	

Gln

<210> 412  
 <211> 77  
 <212> PRT  
 <213> homo sapiens

<400> 412

Pro	Pro	Ala	Ile	Leu	Thr	Glu	Gly	Trp	His	Glu	Glu	Ile	Trp	Ser	Arg
1				5					10					15	
Phe	Ser	Pro	Ser	Ser	Arg	Pro	Ala	Leu	Glu	Met	Arg	Val	Glu	Thr	Lys
			20					25					30		
Ala	Pro	Thr	Lys	Ala	Ala	Val	Asn	Ser	Glu	Val	Arg	Gly	Ser	Arg	Ser
		35					40					45			
Trp	Leu	Thr	Thr	Cys	Ile	Thr	Tyr	His	Ser	Pro	Leu	Trp	Pro	Cys	Ser
	50					55					60				

Ser Cys His Trp Ala Thr Cys Ser Arg Val Thr Asp Thr  
65 70 75

<210> 413  
<211> 62  
<212> PRT  
<213> homo sapiens

<400> 413

Ile	Gly	Phe	Ala	Ser	Ile	Pro	Pro	Arg	Ile	Ser	Gly	Ser	Pro	Ser	Ile
1				5					10					15	
Leu	Leu	Ala	Phe	Tyr	Pro	His	Pro	Pro	Ser	Pro	Lys	Leu	Gly	Pro	Val
			20					25					30		
Leu	Leu	Cys	Ala	Arg	Glu	Thr	Pro	Lys	Phe	Arg	Arg	Lys	Ser	Ile	Phe
		35					40					45			
Tyr	Arg	Gly	Gly	Phe	Ile	Leu	Asp	Gln	Lys	Asn	Lys	Lys	Asn		
	50					55					60				

<210> 414  
<211> 65  
<212> PRT  
<213> homo sapiens

<400> 414

Asp	Leu	Ile	Tyr	Asn	Tyr	Tyr	Cys	Tyr	Pro	Ser	Asp	Leu	Ser	Phe	Ser
1				5					10					15	
Ala	Ile	Asp	Val	Ile	Ala	Ile	Ser	Arg	Ser	Ser	His	Asn	Val	Phe	Asn
			20					25					30		
Pro	Ala	Leu	Ile	Leu	Met	Leu	Arg	Met	Glu	Phe	Leu	Thr	Ser	Ser	Leu
		35					40					45			
Lys	Glu	Pro	Gln	Pro	Pro	Asn	Thr	Tyr	Thr	Tyr	Thr	Ser	Arg	Ile	Ala
	50					55					60				
Lys															
65															

<210> 415  
<211> 94  
<212> PRT  
<213> homo sapiens

<400> 415

Leu	Asp	Ser	Leu	Pro	Phe	His	His	Val	Phe	Pro	Asp	Pro	His	Pro	Ser
1				5					10					15	
Phe	Trp	Leu	Phe	Thr	Arg	Ile	Arg	His	Leu	Arg	Ser	Trp	Gly	Gln	Cys
			20					25					30		
Tyr	Tyr	Val	Pro	Gly	Lys	Pro	Arg	Asn	Leu	Gly	Glu	Asn	Gln	Tyr	Phe
		35					40					45			
Thr	Gly	Glu	Asp	Ser	Ser	Leu	Thr	Lys	Lys	Ile	Lys	Lys	Ile	Lys	Asn
	50					55					60				

00673305.122700



Thr Lys Lys Phe Met Phe Leu Tyr Cys Ile Pro Lys Glu Cys Leu Tyr  
 65 70 75 80  
 Thr Val Ile Ile Leu Lys Glu Asn Thr Ser Met Leu Asp Ile  
 85 90

<210> 416  
 <211> 83  
 <212> PRT  
 <213> homo sapiens

<400> 416

Gly Arg Arg Asn Asp Gln Leu Asn Leu His Ile Pro Gln Ala Gly Pro  
 1 5 10 15  
 Phe Ala Gly Pro Tyr Arg Leu Gly Trp Pro Leu Leu Ser Ser Gly Ile  
 20 25 30  
 Arg Leu Pro Asp Trp Leu Val Leu His Val Ser Ile Lys Leu Lys Val  
 35 40 45  
 Ile Pro Trp Pro Pro Pro Gly Glu Asn Gln Pro His Pro Ala Ser Trp  
 50 55 60  
 Gly Gln Trp Gly Arg Asp Phe Gly Leu Ser Glu Gln Leu Leu Glu Ala  
 65 70 75 80  
 Ala His Asp

<210> 417  
 <211> 93  
 <212> PRT  
 <213> homo sapiens

<400> 417

Arg Arg Lys Ala Ser Ile Ile Ala Phe Lys Gly Ile Leu Leu Thr Leu  
 1 5 10 15  
 Thr Gln Gly Val Gln Ser Ala Arg Glu Pro Ile Leu Ile Ser Ser Ser  
 20 25 30  
 Lys Met Phe Leu Glu Glu Asn Pro Trp Asn Val Leu Lys Asp Val Ser  
 35 40 45  
 Gly Val Arg Ser Ser Met Trp Leu Ala Lys Gly His Leu Tyr Leu Phe  
 50 55 60  
 Gln Leu Glu Phe Ile Asn Ser Cys Ser Leu Val Ser Leu Gly Ala Glu  
 65 70 75 80  
 Val Trp His Ile Phe Lys Pro Val His Ser Arg Ile Gln  
 85 90

<210> 418  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 418

Thr Leu Asn Pro His Lys Thr Leu Ser Ala Lys Lys Ala Arg Val Ile

00673305.722700

1				5				10				15			
Phe	Phe	Cys	Ile	Gln	Asp	Ser	Thr	Ala	Asn	Leu	Val	Phe	Cys	Tyr	Lys
			20					25					30		
Asn	Leu	Val	Ser	His	Phe	Leu	Leu	Lys	Arg	Thr	Arg	Ile	Thr	Gly	Thr
		35					40					45			
His	Pro	Gln	Leu	His	Glu	Thr	Pro	Ser	Phe	Leu	Asn	Glu	His	Glu	Ser
	50					55					60				
Ile	Tyr	Val	His	Pro	Ser	Thr	His	Met	Lys	Met	Leu	Cys	Ser	Ser	Thr
65					70					75					80
Gly	Met	Asp	Gly	Ile	Arg	Ile	Lys	Pro	Ile	Trp	Lys	Leu	Lys	Tyr	Phe
				85					90					95	

<210> 419  
 <211> 68  
 <212> PRT  
 <213> homo sapiens

<400> 419

Tyr	Ser	Phe	Phe	Phe	Phe	Leu	Tyr	Gln	Asn	Asn	His	Leu	Pro	Leu	Phe
1				5					10					15	
Phe	Leu	Glu	Arg	Glu	Glu	Glu	Ser	Gly	Glu	Glu	Gly	Lys	Asn	Ala	Lys
			20					25				30			
Cys	His	Phe	Glu	Leu	Leu	Val	His	His	Thr	Arg	Gly	Ser	Pro	Leu	Met
		35					40					45			
Ser	Ala	Ala	Ser	Val	His	Arg	Pro	Gln	Val	Lys	Glu	Arg	Met	Arg	Ser
	50					55					60				
Ser	Trp	Thr	Ser												
65															

<210> 420  
 <211> 60  
 <212> PRT  
 <213> homo sapiens

<400> 420

Lys	Pro	Ser	Ile	His	Phe	Phe	Phe	Ser	Cys	Thr	Lys	Thr	Ile	Ile	Phe
1				5					10				15		
Leu	Tyr	Phe	Ser	Trp	Ser	Gly	Lys	Arg	Arg	Val	Glu	Lys	Lys	Gly	Arg
			20					25				30			
Met	Gln	Ser	Val	Thr	Leu	Asn	Phe	Ser	Phe	Thr	Thr	His	Val	Gly	Val
		35					40					45			
His	Ser	Cys	Gln	Gln	Pro	Pro	Cys	Thr	Gly	Pro	Arg				
	50					55					60				

<210> 421  
 <211> 52  
 <212> PRT  
 <213> homo sapiens

00673395.122700

<400> 421

Asp 1	Ala	Gly	Cys	Arg 5	Phe	Val	Ala	Pro	Ala 10	Leu	Ser	Gly	Ser	Pro 15	Glu
Ile	Thr	Pro	Gln 20	Arg	Gln	Leu	Pro	Phe 25	Val	Asn	Thr	Arg	Gln 30	Ala	Val
Leu	Ala	Gly 35	Pro	Thr	Arg	Pro	His 40	Ser	Phe	Phe	His	Leu 45	Gly	Pro	Val
His	Gly 50	Gly	Cys												

<210> 422

<211> 52

<212> PRT

<213> homo sapiens

<400> 422

Val 1	Leu	Gly	Lys	Ser 5	Ser	Met	Ser	Ile	Thr 10	Ile	Val	Trp	Lys	Ala 15	Asn
Leu	His	Pro	Lys 20	Gln	Ile	Glu	Val	Ser 25	Gln	Val	Lys	Pro	His 30	Arg	Met
Ala	Asn	Arg 35	Cys	Leu	Gly	Cys	Arg 40	Met	Gln	Val	Arg	Gly 45	Pro	Gly	Pro
Val	Trp 50	Leu	Pro												

<210> 423

<211> 59

<212> PRT

<213> homo sapiens

<400> 423

Tyr 1	Arg	Tyr	Val	Phe 5	Pro	Thr	Thr	His	Tyr 10	Gly	Tyr	Asn	Gly	Val 15	Glu
Leu	Gln	Thr	Val 20	Lys	Phe	Cys	Phe	Gly 25	Leu	Val	Ser	Pro	Asp 30	Pro	Pro
Arg	Gln	Glu 35	Leu	Pro	Leu	Pro	Pro 40	Tyr	Leu	Pro	Ala	Leu 45	Lys	Leu	Cys
Pro	Ile 50	Lys	Leu	Asp	Thr	Asn 55	Leu	Thr	Gly	Phe					

<210> 424

<211> 79

<212> PRT

<213> homo sapiens

<400> 424

Val 1	Thr	Cys	Leu	Ser 5	Leu	Tyr	Val	Glu	Thr 10	Asn	Phe	Thr	Met	Ile 15	Thr
Asp	Leu	Cys	Asn	Ile	Ser	Ser	Leu	Asn	Phe	His	Thr	Ile	Leu	Lys	Cys

09673305.122700



<210> 427  
 <211> 62  
 <212> PRT  
 <213> homo sapiens

<400> 427

Gly	Arg	Ala	Ser	Ala	Leu	Ala	Cys	His	Arg	Tyr	Arg	Ser	Asp	Trp	Ala
1				5					10					15	
Ser	Gly	Leu	Tyr	Ile	Leu	Ala	Ala	Leu	Ser	Thr	Ser	Ser	Ser	Ile	Gly
			20					25					30		
Ser	Ser	Gly	Gly	Arg	Gly	Asn	Trp	Gln	Gln	Val	Gly	Asn	Tyr	Val	Lys
		35					40					45			
Glu	Ser	Pro	Asp	Val	Ile	Ile	Ser	Gly	Cys	His	Arg	Asn	Ile		
	50					55					60				

<210> 428  
 <211> 100  
 <212> PRT  
 <213> homo sapiens

<400> 428

Arg	Glu	His	Gln	Leu	Leu	Ser	Gly	Asn	Asp	Phe	Gln	Gly	Thr	Ser	Gly
1				5					10					15	
Val	Ala	Trp	Leu	Val	Thr	Ser	Pro	Ser	His	Tyr	Arg	Gln	His	Trp	Ser
			20					25					30		
Ser	Ala	Gln	Val	Pro	Ala	Gln	Leu	Lys	Asn	Leu	Leu	Leu	Pro	Leu	Glu
		35					40					45			
Thr	Ser	Leu	Ala	Gly	Phe	Gln	Ile	Glu	Lys	Ala	Tyr	Phe	Thr	Glu	Asn
	50					55					60				
Gln	Lys	Arg	Leu	Ser	Leu	Ile	Pro	Val	Glu	Val	Asn	Lys	Ser	Met	Leu
	65				70					75					80
Ser	Thr	Gly	Leu	Ser	Thr	Glu	Gly	Trp	Asn	Cys	Gln	Arg	Asn	Asp	Asp
				85					90					95	
Gln	Met	Phe	Arg												
			100												

<210> 429  
 <211> 40  
 <212> PRT  
 <213> homo sapiens

<400> 429

Asn	Ser	His	Leu	Asn	Val	Thr	Leu	Ile	Ile	Ile	Met	Leu	Ile	Phe	Ser
1				5					10					15	
Ile	Ser	Tyr	Arg	Asn	Gln	Ser	Leu	Leu	Lys	Leu	His	Arg	Gly	Leu	Lys
			20					25					30		
Asn	Val	Tyr	His	Ser	Ile	Phe	Ile								
		35					40								

00573305-122700

<210> 430  
 <211> 31  
 <212> PRT  
 <213> homo sapiens

<400> 430

Gly	Gly	Ile	Gly	Tyr	Lys	Gly	Arg	Tyr	Leu	Asn	Ser	Ser	Asn	Asn	Gly
1				5					10					15	
Tyr	Asn	Pro	Phe	Phe	His	Asn	His	Leu	Gly	Cys	Phe	Lys	Ala	Ile	
			20					25					30		

<210> 431  
 <211> 53  
 <212> PRT  
 <213> homo sapiens

<400> 431

Thr	Leu	Ile	Pro	Ile	Arg	Asp	Ala	Lys	Asn	Gln	His	Asn	Tyr	Tyr	Gln
1				5					10					15	
Cys	His	Ile	Gln	Val	Gly	Ile	Leu	Pro	Asn	Thr	Thr	Ile	Lys	Gly	Arg
			20					25					30		
Ile	Lys	Leu	Asp	Asn	Lys	Ile	Lys	Lys	Tyr	Lys	Ala	Phe	Lys	Asn	Leu
		35					40					45			
Thr	His	His	Leu	Lys											
	50														

<210> 432  
 <211> 31  
 <212> PRT  
 <213> homo sapiens

<400> 432

Ile	Ala	Leu	Lys	His	Pro	Lys	Trp	Leu	Trp	Lys	Lys	Gly	Leu	Tyr	Pro
1				5					10					15	
Leu	Phe	Glu	Leu	Phe	Arg	Tyr	Leu	Pro	Leu	Tyr	Pro	Ile	Pro	Pro	
			20					25					30		

<210> 433  
 <211> 85  
 <212> PRT  
 <213> homo sapiens

<400> 433

Cys	Asn	Ile	Phe	Gln	Trp	Gly	Pro	Ser	Glu	His	Thr	Cys	Trp	Thr	Val
1				5					10					15	
Gln	Thr	Ile	Ser	Ser	Pro	Glu	Gly	Lys	Tyr	Phe	Cys	Ile	Arg	Gly	Asn
			20					25					30		
Ser	Val	Leu	Glu	Arg	Asn	Met	Phe	Phe	Ile	Ser	Gln	Ile	Lys	Thr	Leu
		35					40					45			
Ser	Asn	Gly	Lys	Leu	Ala	Ser	Asn	Phe	Phe	Lys	Tyr	Ser	Ile	Phe	Phe
	50					55					60				

00673305.122700

Ser 65 Pro Leu Val Val Thr 70 Gly Phe Tyr Arg Ser 75 Ser Tyr Thr Val Cys 80

Phe Asn Ser Gly Pro 85

<210> 434

<211> 81

<212> PRT

<213> homo sapiens

<400> 434

Leu 1 Leu Ile Arg Glu 5 Ile Asn Gln Val Phe 10 Pro Leu Ile Tyr Asp 15 Ala

Ile Tyr Phe Ser 20 Gly Gly Leu Gln Ser 25 Thr Pro Val Gly Arg 30 Cys Lys

Pro Tyr Leu 35 Leu Gln Lys Ala Asn 40 Thr Phe Val Ser Glu 45 Glu Thr Gln

Phe Trp 50 Arg Gly Ile Cys Ser 55 Leu Tyr Leu Lys Ser 60 Lys Leu Ser Leu

Met 65 Val Asn Trp Leu Leu 70 Ile Phe Leu Ser Thr 75 Val Phe Phe Phe Pro 80

Leu

<210> 435

<211> 95

<212> PRT

<213> homo sapiens

<400> 435

Tyr 1 Lys Ser Ile Cys 5 Leu Leu Glu Lys Ile 10 Trp Phe Ala Pro Ser 15 Asn

Arg Cys Ala Leu 20 Lys Ala Pro Thr Glu 25 Ile Tyr Cys Ile Ile 30 Asp Glu

Gly Lys Asp 35 Leu Val Asn Phe Ser 40 Tyr Gln Lys Leu Val 45 Phe Arg Thr

Ser Cys 50 Pro Thr Trp Leu Pro 55 Gly Ala Gln Gly Phe 60 Phe Ser Glu Ile

Val 65 Leu Arg Asp Pro Gln 70 Thr Cys Ser Pro Ser 75 Pro Gly Ala Thr Cys 80

Ala Ser Ser Pro Arg 85 Arg Gln Ala Val Arg 90 Ser Met Arg Leu Ser 95

<210> 436

<211> 81

<212> PRT

<213> homo sapiens

<400> 436

00673305.122700

Ser 1	Cys	Ala	Phe	Leu 5	Leu	Leu	Trp	Gly	His 10	Ser	Gly	Pro	Thr	Trp 15	Ala
Ser	Met	Asp	Pro 20	Gly	Leu	Glu	Gln	Ala 25	His	Leu	His	Leu	Phe 30	His	Leu
Arg	Gln	Cys 35	Gly	Ser	Arg	Cys	Gln 40	Glu	Gly	Leu	Thr	Ser 45	Gly	Pro	Ser
Arg	Phe 50	Leu	Cys	Ala	Arg	Asn 55	Glu	Arg	Pro	Gly	Pro 60	Ile	Leu	Pro	Pro
Arg 65	Leu	Asp	Pro	Glu	Val 70	Arg	Ala	Gly	Gln	Pro 75	Ser	Arg	Lys	His	Thr 80

Val

<210> 437  
 <211> 94  
 <212> PRT  
 <213> homo sapiens

<400> 437

Ser 1	Arg	Trp	Asn	Asp 5	Ser	His	Pro	Leu	Leu 10	Ile	Ser	Pro	Leu	Thr 15	Ser
Leu	Lys	Leu	Leu 20	Ser	Ser	Ser	Lys	Ser 25	His	Cys	Gln	Leu	Pro 30	Tyr	Val
Val	Leu	Gly 35	Pro	Arg	Glu	Pro	Trp 40	Asn	Leu	Ala	Pro	Trp 45	Gly	Gly	Leu
Ile	Pro 50	Ala	Arg	Glu	His	Ser 55	Cys	Phe	Ser	Arg	Asp 60	Thr	Val	Ala	Cys
Met 65	Gly	Gln	His	Gly	Pro 70	Trp	Ala	Asp	His	Val 75	His	Ser	Cys	Phe	Ser 80
Gly	Asp	Thr	Val	Gly 85	Pro	His	Gly	Pro	Ala 90	Trp	Thr	Leu	Gly		

<210> 438  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 438

His 1	Leu	Glu	Pro	His 5	Cys	Leu	Arg	Trp	Lys 10	Arg	Trp	Arg	Cys	Ala 15	Cys
Ser	Ser	Pro	Gly 20	Ser	Met	Leu	Ala	His 25	Val	Gly	Pro	Leu	Cys 30	Pro	Gln
Arg	Ser	Arg 35	Asn	Ala	His	Asp	Gln 40	Pro	Arg	Val	His	Ala 45	Gly	Pro	Cys
Arg	Pro 50	Leu	Cys	Pro	Leu	Arg 55	Ser	Arg	Asn	Ala	Leu 60	Val	Pro	Glu	Leu
Asn 65	His	Pro	Arg	Val	Pro 70	Gly	Ser	Lys	Ala	Pro 75	Trp	Asp	Pro	Glu	Pro 80

00673395.122700



His Thr Glu Val Gly Asn Gly Ser Leu Met Ser  
85 90

<210> 439  
<211> 456  
<212> PRT  
<213> homo sapiens

<400> 439

Ile	Thr	Lys	Thr	His	Lys	Val	Asp	Leu	Gly	Leu	Pro	Glu	Lys	Lys	
1				5					10				15		
Lys	Lys	Lys	Val	Val	Lys	Glu	Pro	Glu	Thr	Arg	Tyr	Ser	Val	Leu	Asn
			20					25					30		
Asn	Asp	Asp	Tyr	Phe	Ala	Asp	Val	Ser	Pro	Leu	Arg	Ala	Thr	Ser	Pro
		35					40					45			
Ser	Lys	Ser	Val	Ala	His	Gly	Gln	Ala	Pro	Glu	Met	Pro	Leu	Val	Lys
	50					55					60				
Lys	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Val	Ser	Thr	Leu	Cys	Glu	Glu	His
	65					70				75					80
Val	Glu	Pro	Glu	Thr	Thr	Leu	Pro	Ala	Arg	Arg	Thr	Glu	Lys	Ser	Pro
				85					90					95	
Ser	Leu	Arg	Lys	Gln	Val	Phe	Gly	His	Leu	Glu	Phe	Leu	Ser	Gly	Glu
			100					105					110		
Lys	Lys	Asn	Lys	Lys	Ser	Pro	Leu	Ala	Met	Ser	His	Ala	Ser	Gly	Val
		115					120					125			
Lys	Thr	Ser	Pro	Asp	Pro	Arg	Gln	Gly	Glu	Glu	Glu	Thr	Arg	Val	Gly
	130					135					140				
Lys	Lys	Leu	Lys	Lys	His	Lys	Lys	Glu	Lys	Lys	Gly	Ala	Gln	Asp	Pro
	145				150					155					160
Thr	Ala	Phe	Ser	Val	Gln	Asp	Pro	Trp	Phe	Cys	Glu	Ala	Arg	Glu	Ala
				165					170					175	
Arg	Asp	Val	Gly	Asp	Thr	Cys	Ser	Val	Gly	Lys	Lys	Asp	Glu	Glu	Gln
			180					185					190		
Ala	Ala	Leu	Gly	Gln	Lys	Arg	Lys	Arg	Lys	Ser	Pro	Arg	Glu	His	Asn
		195					200					205			
Gly	Lys	Val	Lys	Lys	Lys	Lys	Lys	Ile	His	Gln	Glu	Gly	Asp	Ala	Leu
	210					215					220				
Pro	Gly	His	Ser	Lys	Pro	Ser	Arg	Ser	Met	Glu	Ser	Ser	Pro	Arg	Lys
	225				230					235					240
Gly	Ser	Lys	Lys	Lys	Pro	Val	Lys	Val	Glu	Ala	Pro	Glu	Tyr	Ile	Pro
				245					250					255	
Ile	Ser	Asp	Asp	Pro	Lys	Ala	Ser	Ala	Lys	Lys	Lys	Met	Lys	Ser	Lys
			260					265					270		
Lys	Lys	Val	Glu	Gln	Pro	Val	Ile	Glu	Glu	Pro	Ala	Leu	Lys	Arg	Lys

00673305.122700

275					280					285					
Lys	Lys	Lys	Glu	Arg	Glu	Ser	Gly	Val	Ala	Gly	Asp	Pro	Trp	Lys	Glu
	290					295					300				
Glu	Thr	Asp	Thr	Asp	Leu	Glu	Val	Val	Leu	Glu	Lys	Lys	Gly	Asn	Met
305					310					315					320
Asp	Glu	Ala	His	Ile	Asp	Gln	Val	Arg	Arg	Lys	Ala	Leu	Gln	Glu	Glu
				325					330					335	
Ile	Asp	Arg	Glu	Ser	Gly	Lys	Thr	Glu	Ala	Ser	Glu	Thr	Arg	Lys	Trp
			340					345					350		
Thr	Gly	Thr	Gln	Phe	Gly	Gln	Trp	Asp	Thr	Ala	Gly	Phe	Glu	Asn	Glu
		355					360					365			
Asp	Gln	Lys	Leu	Lys	Phe	Leu	Arg	Leu	Met	Gly	Gly	Phe	Lys	Asn	Leu
	370					375					380				
Ser	Pro	Ser	Phe	Ser	Arg	Pro	Ala	Ser	Thr	Ile	Ala	Arg	Pro	Asn	Met
385					390					395					400
Ala	Leu	Gly	Lys	Lys	Ala	Ala	Asp	Ser	Leu	Gln	Gln	Asn	Leu	Gln	Arg
				405					410					415	
Asp	Tyr	Asp	Arg	Ala	Met	Ser	Trp	Lys	Tyr	Ser	Arg	Gly	Ala	Gly	Leu
			420					425					430		
Gly	Phe	Ser	Thr	Ala	Pro	Asn	Lys	Ile	Phe	Tyr	Ile	Asp	Arg	Asn	Ala
		435					440					445			
Ser	Lys	Ser	Val	Lys	Leu	Glu	Asp								
	450					455									
<210> 440															
<211> 125															
<212> PRT															
<213> homo sapiens															
<400> 440															
Val	Arg	Val	Cys	Phe	Leu	Leu	Pro	Arg	Val	Ser	Cys	Tyr	Pro	Thr	Leu
1				5					10					15	
Ser	Leu	Leu	Leu	Phe	Leu	Pro	Phe	Gln	Ser	Trp	Leu	Leu	Asp	Asp	Trp
			20					25					30		
Leu	Leu	Tyr	Leu	Leu	Phe	Gly	Leu	His	Leu	Phe	Leu	Cys	Gly	Gly	Leu
		35					40					45			
Arg	Val	Ile	Thr	Tyr	Gly	Asp	Val	Phe	Arg	Ser	Leu	Asn	Phe	Asp	Trp
	50					55					60				
Leu	Leu	Phe	Thr	Ser	Phe	Pro	Arg	Ala	Ala	Leu	His	Gly	Pro	Gly	Gly
65					70					75					80
Leu	Gly	Val	Ala	Trp	Glu	Gly	Ile	Ser	Leu	Leu	Val	Asp	Phe	Phe	Phe
				85					90					95	
Leu	Leu	His	Leu	Pro	Ile	Val	Phe	Ser	Gly	Ala	Leu	Pro	Leu	Pro	Phe
			100					105					110		

Leu Pro Gln Gly Cys Leu Phe Leu Ile Leu Leu Pro His  
115 120 125

<210> 441  
<211> 381  
<212> PRT  
<213> homo sapiens

<400> 441

Ser 1	Arg	Cys	Arg	Phe 5	Cys	Cys	Arg	Leu	Ser 10	Ala	Ala	Phe	Leu	Pro 15	Arg
Ala	Met	Leu	Gly 20	Leu	Ala	Ile	Val	Leu 25	Ala	Gly	Arg	Leu	Asn 30	Glu	Gly
Asp	Arg	Phe 35	Leu	Lys	Pro	Pro	Ile 40	Ser	Leu	Arg	Asn	Phe 45	Ser	Phe	Trp
Ser	Ser 50	Phe	Ser	Lys	Pro	Ala 55	Val	Ser	His	Trp	Pro 60	Asn	Trp	Val	Pro
Val 65	His	Phe	Leu	Val	Ser 70	Glu	Ala	Ser	Val	Leu 75	Pro	Asp	Ser	Arg	Ser 80
Ile	Ser	Ser	Cys	Lys 85	Ala	Phe	Arg	Leu	Thr 90	Trp	Ser	Met	Cys	Ala 95	Ser
Ser	Met	Leu	Pro 100	Phe	Phe	Ser	Asn	Thr 105	Thr	Ser	Lys	Ser	Val 110	Ser	Val
Ser	Ser	Phe 115	Gln	Gly	Ser	Pro	Ala 120	Thr	Pro	Leu	Ser	Leu 125	Ser	Phe	Phe
Phe	Phe 130	Leu	Phe	Arg	Ala	Gly 135	Ser	Ser	Met	Thr	Gly 140	Cys	Ser	Thr	Phe
Phe 145	Leu	Asp	Phe	Ile	Phe 150	Phe	Phe	Ala	Glu	Ala 155	Leu	Gly	Ser	Ser	Leu 160
Met	Gly	Met	Tyr	Ser 165	Gly	Ala	Ser	Thr	Leu 170	Thr	Gly	Phe	Phe	Leu 175	Leu
Pro	Phe	Leu	Gly 180	Leu	Leu	Ser	Met	Asp 185	Leu	Glu	Gly	Leu	Glu 190	Trp	Pro
Gly	Arg	Ala 195	Ser	Pro	Ser	Trp	Trp 200	Ile	Phe	Phe	Phe	Phe 205	Phe	Thr	Phe
Pro	Leu 210	Cys	Ser	Leu	Gly	Leu 215	Phe	Arg	Phe	Arg	Phe 220	Cys	Pro	Lys	Ala
Ala 225	Cys	Ser	Ser	Ser	Phe 230	Phe	Pro	Thr	Glu	Gln 235	Val	Ser	Pro	Thr	Ser 240
Leu	Ala	Ser	Leu	Ala 245	Ser	Gln	Asn	Gln	Gly 250	Ser	Trp	Thr	Glu	Lys 255	Ala
Val	Gly	Ser	Trp 260	Ala	Pro	Phe	Phe	Ser 265	Phe	Leu	Cys	Phe	Leu 270	Ser	Phe
Leu	Pro	Thr 275	Leu	Val	Ser	Ser	Ser 280	Pro	Cys	Leu	Gly	Ser 285	Gly	Glu	Val

00673395-122700

Phe	Thr	Pro	Glu	Ala	Trp	Asp	Met	Ala	Arg	Gly	Asp	Phe	Leu	Phe	Phe
290						295					300				
Phe	Ser	Pro	Leu	Arg	Asn	Ser	Lys	Trp	Pro	Asn	Thr	Cys	Phe	Leu	Arg
305					310					315					320
Leu	Gly	Asp	Phe	Ser	Val	Arg	Leu	Ala	Gly	Ser	Val	Val	Ser	Gly	Ser
				325					330					335	
Thr	Cys	Ser	Ser	Gln	Arg	Val	Leu	Thr	Pro	Phe	Phe	Phe	Phe	Phe	Phe
			340					345					350		
Phe	Phe	Thr	Arg	Gly	Ile	Ser	Gly	Ala	Cys	Pro	Trp	Ala	Thr	Leu	Leu
		355					360					365			
Glu	Gly	Asp	Val	Ala	Leu	Lys	Gly	Glu	Thr	Ser	Ala	Lys			
	370					375					380				

<210> 442

<211> 43

<212> PRT

<213> homo sapiens

<400> 442

Asp	His	His	Asn	Lys	Leu	Ser	Leu	Gln	Ser	Gln	Thr	Tyr	Tyr	Ile	Leu
1				5					10					15	
Leu	Ser	Val	Asn	Gly	Glu	Lys	Ile	Ser	Pro	Tyr	Val	Leu	Trp	Val	Lys
			20					25					30		
Cys	Cys	Asn	Arg	Leu	Gly	Leu	Ser	Asn	Leu	Pro					
		35					40								

<210> 443

<211> 45

<212> PRT

<213> homo sapiens

<400> 443

Met	Val	Ile	Ser	Ile	Phe	Pro	Pro	Leu	Leu	Tyr	Lys	Leu	Ile	Phe	Thr
1				5					10					15	
His	Leu	Leu	Leu	Tyr	Lys	Leu	Thr	Phe	Ile	Asn	Thr	Asn	Lys	Arg	Leu
			20					25					30		
Val	Leu	Ser	Gln	Phe	Ile	Cys	His	Glu	Pro	Arg	Asn	Asn			
		35					40					45			

<210> 444

<211> 40

<212> PRT

<213> homo sapiens

<400> 444

Gly	Lys	Pro	Lys	Asn	Cys	Cys	Asp	Phe	Phe	Gln	Gly	Lys	Leu	Asp	Asn
1				5					10					15	
Pro	Asn	Leu	Leu	Gln	His	Phe	Thr	His	Lys	Thr	Tyr	Gly	Leu	Ile	Phe
			20					25					30		

00673395-12700

Ser Pro Leu Thr Asp Ser Ser Ile  
35 40

<210> 445  
<211> 78  
<212> PRT  
<213> homo sapiens

<400> 445

Gly 1	Val	Gly	Gly	Gly 5	Ala	Leu	Arg	Ser	Ala 10	Ala	Leu	Pro	Trp	Arg 15	Thr
Leu	Pro	Leu	Thr 20	Ser	Thr	Cys	Ser	Arg 25	Cys	Thr	Lys	Pro	Ser 30	Thr	Ala
Glu	Met	Glu 35	His	Leu	Val	Gln	Ser 40	Trp	Cys	Leu	Leu	Asn 45	Ile	Leu	Met
Leu	Gln 50	Thr	His	Asp	Phe	Lys 55	Trp	Pro	Leu	Gln	Arg 60	Arg	Ser	Val	Asn
Lys 65	Ser	Trp	Asn	Pro	Leu 70	Met	Met	Lys	Cys	Leu 75	Gln	Leu	Ile		

<210> 446  
<211> 125  
<212> PRT  
<213> homo sapiens

<400> 446

Arg 1	Leu	Arg	Arg	Arg 5	Gly	Trp	Arg	Ser	Pro 10	Phe	Gly	Gly	Ala	Pro 15	Met
Ala	His	Ile	Thr 20	Ile	Asn	Gln	Tyr	Leu 25	Gln	Gln	Val	Tyr	Glu 30	Ala	Ile
Asp	Ser	Arg 35	Asp	Gly	Ala	Ser	Cys 40	Ala	Glu	Leu	Val	Ser 45	Phe	Lys	His
Pro	His 50	Val	Ala	Asn	Pro	Arg 55	Leu	Gln	Met	Ala	Ser 60	Pro	Glu	Glu	Lys
Cys 65	Gln	Gln	Val	Leu	Glu 70	Pro	Pro	Tyr	Asp	Glu 75	Met	Phe	Ala	Ala	His 80
Leu	Arg	Cys	Thr	Tyr 85	Ala	Val	Gly	Asn	His 90	Asp	Phe	Ile	Glu	Ala 95	Tyr
Lys	Cys	Gln	Thr 100	Val	Ile	Val	Gln	Ser 105	Phe	Leu	Arg	Ala	Phe 110	Gln	Ala
His	Lys	Glu 115	Glu	Asn	Trp	Ala	Leu 120	Leu	Ser	Cys	Met	Gln 125			

<210> 447  
<211> 80  
<212> PRT  
<213> homo sapiens

<400> 447

00673305-122700

Met 1	Ser	Cys	Lys	His 5	Phe	Ile	Ile	Arg	Gly 10	Phe	Gln	Asp	Leu	Leu 15	Thr
Leu	Leu	Leu	Trp 20	Arg	Gly	His	Leu	Lys 25	Ser	Trp	Val	Cys	Asn 30	Met	Arg
Met	Phe	Lys 35	Arg	His	Gln	Leu	Cys 40	Thr	Arg	Cys	Ser	Ile 45	Ser	Ala	Val
Asp	Gly 50	Phe	Val	His	Leu	Leu 55	Gln	Val	Leu	Val	Asn 60	Gly	Asn	Val	Arg
His 65	Gly	Ser	Ala	Ala	Glu 70	Arg	Arg	Ala	Pro	Pro 75	Pro	Thr	Pro	Gln	Ala 80

<210> 448  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 448

Arg 1	Ser	Arg	Gly	Phe 5	Ser	Cys	Val	Gln	Thr 10	Pro	Cys	His	Phe	Arg 15	Glu
Val	Thr	Gln	Ala 20	Cys	Val	Ile	Ser	Leu 25	Trp	Gln	Gln	Val	Gly 30	Gly	Leu
Pro	Gln	Gly 35	Arg	Arg	Trp	Pro	Glu 40	Met	Cys	Phe	Arg	Ser 45	Leu	Thr	His
His	Ser 50	Leu	His	Thr	Arg	Arg 55	Glu	His	His	Ser	Trp 60	Ser	Ile	Leu	Arg
Met 65	Glu	Ile													

<210> 449  
 <211> 60  
 <212> PRT  
 <213> homo sapiens

<400> 449

Pro 1	Ile	Thr	Pro	Tyr 5	Thr	His	Asp	Val	Asn 10	Thr	Thr	Pro	Gly	Ala 15	Phe
Ser	Glu	Trp	Arg 20	Phe	Glu	Phe	His	Val 25	Ala	Ala	Ser	His	Thr 30	Gln	Thr
Cys	His	His 35	Ser	Pro	His	Thr	His 40	Ser	Arg	His	Ser	Thr 45	Ala	Met	Ser
Gln	Lys 50	Lys	Phe	Leu	Val	Ser 55	Asp	Leu	Lys	Val	Leu 60				

<210> 450  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 450

00673395.122700

Arg 1	Ala	Thr	Ser	Gly 5	Arg	Ser	Gly	Phe	Ile 10	Lys	Pro	Ser	Asn	Leu 15	Lys
Gln	Gly	Thr	Ser 20	Phe	Gly	Ser	Trp	Leu 25	Leu	Asn	Val	Val	Ser 30	Gly	Cys
Val	Gly	Asn 35	Asp	Gly	Arg	Phe	Val 40	Cys	Glu	Lys	Leu	Pro 45	His	Gly	Ile
Gln	Ile 50	Ser	Ile	Leu	Arg	Met 55	Leu	Gln	Glu	Trp	Cys 60	Ser	Arg	Arg	Val
Cys 65	Arg	Glu													

<210> 451  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 451

Ser 1	Ala	Ser	His	Pro 5	Glu	Ser	Arg	Leu	Cys 10	Arg	Gly	Gly	Ala	Asp 15	Met
Gln	Ala	Pro	Arg 20	Gly	Thr	Leu	Val	Phe 25	Ala	Leu	Val	Ile	Ala 30	Leu	Val
Pro	Val	Gly 35	Arg	Glu	Pro	Ser	Ser 40	Gln	Gly	Ser	Gln	Ser 45	Ala	Leu	Gln
Thr	Tyr 50	Glu	Leu	Gly	Ser	Glu 55	Asn	Val	Lys	Val	Pro 60	Ile	Phe	Glu	Glu
Asp 65	Thr	Pro	Ser	Val	Met 70	Glu	Ile	Glu	Met	Glu 75	Glu	Leu	Asp	Lys	Trp 80
Met	Asn	Ser	Met	Asn 85	Arg	Asn	Ala	Asp	Phe 90	Glu	Cys	Leu	Pro	Thr 95	Leu
Lys	Glu	Glu	Lys 100	Glu	Ser	Asn	His	Asn 105	Pro	Ser	Asp	Ser	Glu 110	Ser	

<210> 452  
 <211> 51  
 <212> PRT  
 <213> homo sapiens

<400> 452

Glu 1	Glu	Trp	Ala	Leu 5	Glu	Glu	Thr	Ala	Lys 10	Gly	Ser	Cys	Val	Tyr 15	Val
Asp	Leu	Lys	Leu 20	Ile	Lys	Phe	Val	Ser 25	Ser	Ser	Ser	Ser	Val 30	Gly	Ser
Leu	Ser	Arg 35	Leu	Pro	Gln	Gly	Leu 40	Leu	Leu	Leu	Glu	Asn 45	Met	Ser	Ala
Ile	Gln 50	Val													

00673305-122700

<210> 453  
 <211> 59  
 <212> PRT  
 <213> homo sapiens

<400> 453

Phe	Asp	Ser	Phe	Ser	Ser	Phe	Lys	Val	Gly	Lys	His	Ser	Lys	Ser	Ala
1				5					10					15	
Phe	Leu	Phe	Met	Leu	Phe	Ile	His	Leu	Ser	Ser	Ser	Ser	Ile	Ser	Ile
			20					25					30		
Ser	Ile	Thr	Glu	Gly	Val	Ser	Ser	Ser	Lys	Ile	Gly	Thr	Phe	Thr	Phe
		35					40					45			
Ser	Leu	Pro	Ser	Ser	Tyr	Val	Cys	Lys	Ala	Leu					
	50					55									

<210> 454  
 <211> 107  
 <212> PRT  
 <213> homo sapiens

<400> 454

Pro	Ile	Thr	Thr	Cys	Ser	Leu	Gly	Asp	Pro	Gly	Lys	Asp	Lys	Tyr	Thr
1				5					10					15	
Cys	Thr	His	Arg	Gly	Arg	Glu	Arg	Cys	Val	Gln	Arg	Ile	Cys	Ile	Asn
			20					25					30		
Ile	Leu	Phe	Ser	His	Pro	Asp	Met	Arg	Ser	Gln	Cys	Cys	Met	Met	Lys
		35					40					45			
Arg	Trp	Tyr	Asp	Ser	Thr	Tyr	Val	Pro	Ile	Val	Leu	Leu	Phe	Leu	Tyr
	50					55					60				
Phe	Leu	Phe	Arg	Ser	Phe	Thr	Ile	Gly	Arg	Phe	Gln	Lys	His	Ser	Phe
	65				70					75					80
His	His	His	Leu	Glu	Met	Val	Cys	Leu	Asn	Gly	Asp	Asn	Ser	Arg	Ser
				85					90					95	
Cys	Ser	Ile	Ser	Ser	Arg	His	Gly	Leu	Leu	Ile					
			100					105							

<210> 455  
 <211> 73  
 <212> PRT  
 <213> homo sapiens

<400> 455

Arg	Arg	Gly	Val	Ser	Phe	Leu	Leu	Ser	Arg	Gln	Lys	Trp	Tyr	His	Tyr
1				5					10					15	
Val	Ala	Ala	Leu	Gln	Ser	Pro	Arg	Ala	Arg	Ser	Leu	Glu	Asn	His	Leu
			20					25					30		
Leu	Ser	Arg	Phe	Phe	Phe	Phe	Leu	Arg	Val	Gly	Val	Ser	Leu	Cys	Cys
		35					40					45			

00573395.122700



Pro Lys Thr Arg Pro Gly Asn Cys Trp Gly Ala Lys Gly Ile Ala Pro  
 50 60  
 Val Pro Gln Ala Ser Arg Val Gly Arg  
 65 70

<210> 456  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 456

Ser Trp Gly Asn Ile Val Arg Leu Leu Pro Ser Lys Lys Lys Lys Asn  
 1 5 10 15  
 Ala Lys Glu Gly Asp Ser Leu Glu Ser Glu Leu Trp Glu Ile Gly Glu  
 20 25 30  
 Arg Gln His Asn Asp Thr Ile Ser Ala Tyr Leu Glu Gly Lys Lys Leu  
 35 40 45  
 Leu Ser Phe Ser Cys Met Val Thr Val Ile Ser Ser Arg Lys Asp Ile  
 50 55 60  
 Ser Lys Glu  
 65

<210> 457  
 <211> 81  
 <212> PRT  
 <213> homo sapiens

<400> 457

Asp Gln Pro Ser Leu Pro Phe Ile Arg His Lys Thr Leu Asn Leu Thr  
 1 5 10 15  
 Ser Met Ala Thr Lys Ile Ile Gly Ser Pro Glu Thr Lys Trp Ile Asp  
 20 25 30  
 Ala Thr Ser Gly Ile Tyr Asn Ser Glu Lys Ser Ser Asn Leu Ser Val  
 35 40 45  
 Thr Thr Asp Phe Ser Glu Ser Leu Gln Ser Ser Asn Ile Glu Ser Lys  
 50 55 60  
 Glu Ile Asn Gly Ile His Asp Glu Ser Asn Ala Phe Glu Ser Lys Ala  
 65 70 75 80  
 Ser

<210> 458  
 <211> 41  
 <212> PRT  
 <213> homo sapiens

<400> 458

Gln Leu Ile Ser Pro Lys Ala Phe Arg Val Leu Ile Leu Asn Pro Lys  
 1 5 10 15  
 Lys Ser Met Glu Phe Met Met Lys Ala Met Leu Leu Asn Gln Lys His

00573395.122700

20 25 30  
 Leu Glu Ser 35 Ile Phe Phe Glu Lys 40 Pro  
 <210> 459  
 <211> 36  
 <212> PRT  
 <213> homo sapiens  
 <400> 459  
 Ile Pro Glu Val Ala Ser Ile His Phe Val Ser Gly Glu Pro Ile Ile  
 1 5 10 15  
 Leu Val Ala Ile Leu Val Arg Leu Arg Val Leu Cys Arg Ile Asn Gly  
 20 25 30  
 Arg Glu Gly Trp  
 35  
 <210> 460  
 <211> 36  
 <212> PRT  
 <213> homo sapiens  
 <400> 460  
 Asn Ser Glu Gly Phe Arg Arg Asn Gln Leu Leu Gln Ile Asp Leu Lys  
 1 5 10 15  
 Ile Phe Leu Ser Cys Lys Phe Gln Lys Leu His Gln Ser Thr Leu Phe  
 20 25 30  
 Gln Val Asn Leu  
 35  
 <210> 461  
 <211> 83  
 <212> PRT  
 <213> homo sapiens  
 <400> 461  
 Gly Arg Arg Asn Asp Gln Leu Asn Leu His Ile Pro Gln Ala Gly Pro  
 1 5 10 15  
 Phe Ala Gly Pro Tyr Arg Leu Gly Trp Pro Leu Leu Ser Ser Gly Ile  
 20 25 30  
 Arg Leu Pro Asp Trp Leu Val Leu His Val Ser Ile Lys Leu Lys Val  
 35 40 45  
 Ile Pro Trp Pro Pro Pro Gly Glu Asn Gln Pro His Pro Ala Ser Trp  
 50 55 60  
 Gly Gln Trp Gly Arg Asp Phe Gly Leu Ser Glu Gln Leu Leu Glu Ala  
 65 70 75 80  
 Ala His Asp  
 <210> 462  
 <211> 93

<212> PRT  
<213> homo sapiens

<400> 462

Arg	Arg	Lys	Ala	Ser	Ile	Ile	Ala	Phe	Lys	Gly	Ile	Leu	Leu	Thr	Leu
1				5					10					15	
Thr	Gln	Gly	Val	Gln	Ser	Ala	Arg	Glu	Pro	Ile	Leu	Ile	Ser	Ser	Ser
			20					25					30		
Lys	Met	Phe	Leu	Glu	Glu	Asn	Pro	Trp	Asn	Val	Leu	Lys	Asp	Val	Ser
		35					40					45			
Gly	Val	Arg	Ser	Ser	Met	Trp	Leu	Ala	Lys	Gly	His	Leu	Tyr	Leu	Phe
	50					55					60				
Gln	Leu	Glu	Phe	Ile	Asn	Ser	Cys	Ser	Leu	Val	Ser	Leu	Gly	Ala	Glu
65					70					75					80
Val	Trp	His	Ile	Phe	Lys	Pro	Val	His	Ser	Arg	Ile	Gln			
				85					90						

<210> 463  
<211> 96  
<212> PRT  
<213> homo sapiens

<400> 463

Thr	Leu	Asn	Pro	His	Lys	Thr	Leu	Ser	Ala	Lys	Lys	Ala	Arg	Val	Ile
1				5					10					15	
Phe	Phe	Cys	Ile	Gln	Asp	Ser	Thr	Ala	Asn	Leu	Val	Phe	Cys	Tyr	Lys
			20					25					30		
Asn	Leu	Val	Ser	His	Phe	Leu	Leu	Lys	Arg	Thr	Arg	Ile	Thr	Gly	Thr
		35					40					45			
His	Pro	Gln	Leu	His	Glu	Thr	Pro	Ser	Phe	Leu	Asn	Glu	His	Glu	Ser
	50					55					60				
Ile	Tyr	Val	His	Pro	Ser	Thr	His	Met	Lys	Met	Leu	Cys	Ser	Ser	Thr
65					70					75					80
Gly	Met	Asp	Gly	Ile	Arg	Ile	Lys	Pro	Ile	Trp	Lys	Leu	Lys	Tyr	Phe
				85					90					95	

<210> 464  
<211> 76  
<212> PRT  
<213> homo sapiens

<400> 464

Asn	Leu	Phe	Thr	Met	Lys	Phe	Leu	Pro	Glu	Phe	Ser	Pro	Phe	Asp	Thr
1				5					10					15	
Asn	Ser	Met	His	Val	Ser	Thr	Phe	Glu	Thr	Gln	Pro	Asn	Val	Ile	Ser
			20					25					30		
Val	Lys	Ser	Ser	Leu	Ser	Leu	Pro	Ser	Ser	Asn	Leu	Pro	Ser	Pro	Arg
		35					40					45			

00673305.122700

Val	Tyr	Leu	Pro	Phe	Cys	Ala	His	Leu	Ser	Tyr	Ser	Ser	Met	Leu	Phe
	50					55					60				
Tyr	Asn	Cys	Asp	Ser	Pro	Gly	Ser	Leu	Gly	Ala	Ile				
65					70					75					

<210> 465  
 <211> 59  
 <212> PRT  
 <213> homo sapiens

<400> 465

Asn	Gln	Arg	Met	Ile	Glu	Ile	Tyr	Ser	Asn	Thr	Lys	Thr	Glu	Arg	Lys
1				5					10					15	
Cys	His	Ser	Thr	Leu	Lys	Ala	Ala	Asn	Thr	Ile	Asp	His	Phe	Ile	Trp
			20					25					30		
Leu	Pro	Asp	Ser	Gln	Glu	Ser	His	Asn	Cys	Lys	Ile	Thr	Cys	Tyr	Cys
		35					40					45			
Asn	Ser	Asn	Val	His	Lys	Met	Ala	Gly	Lys	Leu					
	50					55									

<210> 466  
 <211> 40  
 <212> PRT  
 <213> homo sapiens

<400> 466

His	Ala	Thr	Val	Thr	Gln	Met	Cys	Thr	Lys	Trp	Gln	Val	Asn	Ser	Arg
1				5					10					15	
Arg	Arg	Gln	Ile	Thr	Ala	Trp	Lys	Thr	Gln	Gly	Arg	Phe	Tyr	Arg	Asn
			20					25					30		
Asp	Ile	Trp	Leu	Ser	Leu	Glu	Gly								
		35					40								

<210> 467  
 <211> 41  
 <212> PRT  
 <213> homo sapiens

<400> 467

Ile	Pro	Leu	Gln	Arg	Phe	Ser	Leu	Leu	Thr	Ser	Leu	Phe	Phe	Val	Leu
1				5					10					15	
Lys	Leu	Asp	Phe	Leu	Val	Val	His	Ala	Ser	Leu	Ser	Leu	Val	Thr	Val
			20					25					30		
Asn	Asn	Leu	Pro	Thr	Ser	Ser	Asn	Gln							
		35					40								

<210> 468  
 <211> 65  
 <212> PRT  
 <213> homo sapiens

00673305 122700

<400> 468

Leu 1	Ser	Lys	Ala	Ile 5	Tyr	Phe	Cys	Lys	Lys 10	Ala	Ala	Ala	Cys	Ile 15	Asn
His	Asp	His	Ser 20	Ser	Thr	Leu	Asn	Lys 25	Glu	Arg	Lys	Arg	Phe 30	Leu	Ser
Leu	Thr	Gln 35	Ser	Leu	Pro	Leu	Cys 40	His	Ser	Pro	Arg	Gly 45	Trp	Gly	Trp
Thr	Ala 50	His	Ser	Lys	Leu	Thr 55	Arg	Leu	Ala	Ile	Cys 60	Glu	Tyr	Phe	Ser
Lys 65															

<210> 469

<211> 56

<212> PRT

<213> homo sapiens

<400> 469

Pro 1	Asp	Trp	Leu	Phe 5	Val	Asn	Thr	Phe	Pro 10	Asn	Lys	Glu	Gly	Lys 15	Gly
Asp	Val	Ser	Tyr 20	Ser	Gly	Gly	Lys	Cys 25	Ser	Phe	Ser	Gly	Lys 30	Asn	Gly
Cys	Arg	Val 35	Gly	Asn	Gln	Gly	Ser 40	Arg	Cys	Glu	Leu	Leu 45	Ile	Arg	Thr
Gly	Gly 50	Lys	Val	Val	His	Ser 55	Asn								

<210> 470

<211> 109

<212> PRT

<213> homo sapiens

<400> 470

Ala 1	Arg	Pro	Ala	Pro 5	Ala	Gly	Arg	Glu	Gly 10	Arg	Gly	Glu	Gly	Glu 15	Ala
Thr	Ser	Arg	Arg 20	Cys	Gly	Val	Gly	His 25	Arg	Ala	Gly	Pro	Arg 30	Glu	Pro
Ala	Pro	His 35	Gly	Ala	Ala	Ala	Val 40	Arg	Pro	Thr	Pro	Gly 45	Pro	His	His
His	Cys 50	Ala	Ala	Leu	Ser	Gly 55	Ala	Glu	Asn	Tyr	Arg 60	Ser	Arg	His	Ala
Met 65	Lys	Leu	Ala	Ser	Ala 70	Leu	Arg	Arg	Gly	Pro 75	Ala	Leu	His	Pro	Leu 80
Pro	Pro	Arg	Ala	Asn 85	Arg	Gly	Arg	Glu	Pro 90	Trp	Arg	Arg	Arg	His 95	Arg
Pro	Arg	Gly	Trp 100	Ala	Ala	Ala	Ser	Arg 105	Thr	Trp	Arg	Ser			

00673395.122700

<210> 471  
 <211> 399  
 <212> PRT  
 <213> homo sapiens

<400> 471

Ala	Ala	Gly	Ala	Cys	Gly	Ala	Arg	Gly	Ser	Gly	Arg	Arg	Gly	Ser	Tyr
1				5					10					15	
Val	Pro	Glu	Val	Arg	Cys	Gly	Ala	Pro	Gly	Gly	Ala	Ala	Gly	Thr	Gly
			20					25					30		
Ala	Pro	Arg	Ser	Cys	Cys	Cys	Gln	Thr	Asn	Pro	Gly	Pro	Pro	Ser	Ser
		35					40					45			
Leu	Arg	Arg	Ala	Phe	Arg	Arg	Arg	Glu	Leu	Pro	Phe	Pro	Ala	Cys	His
	50					55					60				
Glu	Ile	Gly	Leu	Gly	Ala	Glu	Ala	Gly	Ser	Gly	Pro	Pro	Pro	Ala	Pro
	65				70					75					80
Ala	Ala	Arg	Glu	Ser	Arg	Ser	Arg	Ala	Met	Glu	Glu	Glu	Ala	Ser	Ser
				85					90					95	
Pro	Gly	Leu	Gly	Cys	Ser	Lys	Pro	His	Leu	Glu	Lys	Leu	Thr	Leu	Gly
			100					105					110		
Ile	Thr	Arg	Ile	Leu	Glu	Ser	Ser	Pro	Gly	Val	Thr	Glu	Val	Thr	Ile
		115					120					125			
Ile	Glu	Lys	Pro	Pro	Ala	Glu	Arg	His	Met	Ile	Ser	Ser	Trp	Glu	Gln
	130					135					140				
Lys	Asn	Asn	Cys	Val	Met	Pro	Glu	Asp	Val	Lys	Asn	Phe	Tyr	Leu	Met
	145				150					155					160
Thr	Asn	Gly	Phe	His	Met	Thr	Trp	Ser	Val	Lys	Leu	Asp	Glu	His	Ile
				165					170					175	
Ile	Pro	Leu	Gly	Ser	Met	Ala	Ile	Asn	Ser	Ile	Ser	Lys	Leu	Thr	Gln
			180					185					190		
Leu	Thr	Gln	Ser	Ser	Met	Tyr	Ser	Leu	Pro	Asn	Ala	Pro	Thr	Leu	Ala
		195					200					205			
Asp	Leu	Glu	Asp	Asp	Thr	His	Glu	Ala	Ser	Asp	Asp	Gln	Pro	Glu	Lys
	210					215					220				
Pro	His	Phe	Asp	Ser	Arg	Ser	Val	Ile	Phe	Glu	Leu	Asp	Ser	Cys	Asn
	225				230				235						240
Gly	Ser	Gly	Lys	Val	Cys	Leu	Val	Tyr	Lys	Ser	Gly	Lys	Pro	Ala	Leu
				245					250					255	
Ala	Glu	Asp	Thr	Glu	Ile	Trp	Phe	Leu	Asp	Arg	Ala	Leu	Tyr	Trp	His
			260					265					270		
Phe	Leu	Thr	Asp	Thr	Phe	Thr	Ala	Tyr	Tyr	Arg	Leu	Leu	Ile	Thr	His
		275					280					285			
Leu	Gly	Leu	Pro	Gln	Trp	Gln	Tyr	Ala	Phe	Thr	Ser	Tyr	Gly	Ile	Ser

09673395.122700

300

<400> 472

```
<210> 473
<211> 56
<212> PRT
<213> homo sapiens
```

<400> 473

Lys 1	Tyr	Val	Ser	His 5	Ala	Asn	Ile	Ser	Ile 10	Tyr	Lys	Trp	Arg	Thr 15	Leu
Thr	Leu	Leu	Leu 20	Phe	Ser	Tyr	Lys	Ile 25	Pro	Asn	Phe	Val	Ile 30	Ile	Leu
Ser	Gly	Ile 35	Thr	Leu	Tyr	Cys	Lys 40	Asn	Ala	Ser	Tyr	Phe 45	Thr	Phe	Lys
Phe	Asp 50	Asn	Val	Cys	Asp	Glu 55	Leu								

**DECEMBER 2007**

<210> 474  
 <211> 37  
 <212> PRT  
 <213> homo sapiens

<400> 474

Trp	Ile	Phe	Arg	Val	Cys	Cys	Ile	Ser	Arg	Glu	Ile	His	Phe	Tyr	Ile
1				5					10					15	
Leu	Phe	Tyr	Tyr	Lys	His	Leu	Asp	Lys	Gly	His	Leu	Thr	His	Phe	Lys
			20					25					30		
Lys	His	Lys	Cys	Ile											
		35													

<210> 475  
 <211> 33  
 <212> PRT  
 <213> homo sapiens

<400> 475

Pro	Lys	Gly	Leu	Ser	Ile	Lys	Val	Arg	Arg	Asn	Leu	Asp	Thr	Arg	Arg
1				5					10					15	
Lys	Arg	Cys	Arg	Leu	Leu	Asn	Phe	Ile	Ile	His	His	Ile	His	Cys	Gln
			20					25					30		
Ile															

<210> 476  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 476

His	Ile	Lys	Ile	Glu	Phe	Phe	Gly	Gln	Asn	Phe	Trp	Glu	Ala	Met	His
1				5					10					15	
Pro	Thr	Trp	Ala	Asp	Ile	Gln	Pro	Glu	Leu	Phe	Ser	Arg	Gly	Glu	Trp
			20					25					30		
Tyr	Trp	Gln	Phe	Met	Ala	Glu	Ile	His	Ser	Asp	Trp	Leu	Glu	Ser	Met
		35					40					45			
Leu	Tyr	Gln	Leu	Leu	Asn	Ile	Leu	Ser	Ile	Thr	Leu	Ala	Tyr	Cys	Tyr
	50					55					60				
Tyr	Tyr	Ile	Ser	Ser	Ile	Tyr	Arg	Gln	Lys	Gly	His	Phe	Arg	Asn	Ile
65					70					75					80

<210> 477  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 477

Ser	Ser	Leu	Gly	Lys	Thr	Phe	Gly	Lys	Gln	Cys	Ile	Leu	His	Gly	Leu
1				5					10					15	

00/227.462700



Ile	Phe	Ser	Leu 20	Ser	Cys	Ser	Gln	Glu 25	Glu	Ser	Gly	Thr	Gly 30	Ser	Leu
Trp	Leu	Lys 35	Ser	Ile	Leu	Ile	Gly 40	Trp	Ser	Leu	Cys	Tyr 45	Thr	Ser	Cys

<210> 478  
 <211> 70  
 <212> PRT  
 <213> homo sapiens

<400> 478

Glu 1	Gln	Leu	Arg	Leu 5	Asn	Ile	Ser	Pro	Cys 10	Arg	Met	His	Cys	Phe 15	Pro
Lys	Val	Leu	Pro 20	Lys	Glu	Leu	Tyr	Phe 25	Tyr	Val	Leu	Ser	His 30	Arg	Thr
Gly	Glu	Lys 35	Cys	Ser	Gly	His	Cys 40	Trp	Asp	Leu	Ile	Phe 45	Leu	Gly	Met
Gly	Ser 50	Gly	Leu	Met	Ile	Leu 55	Ala	Thr	Gly	Val	Gln 60	Glu	Asn	Gly	Ser
Pro 65	Gly	Ser	Asp	Ser	Trp 70										

<210> 479  
 <211> 400  
 <212> PRT  
 <213> homo sapiens

<400> 479

Pro 1	Gln	Gln	Thr	Pro 5	Trp	Ala	Val	Ala	Gly 10	Arg	Trp	Cys	Asn	Gly 15	Pro
Ser	Leu	His	Arg 20	Asn	Arg	Ala	Gly	Leu 25	Asp	Leu	Pro	Thr	Ile 30	Asp	Thr
Gly	Tyr	Asp 35	Ser	Gln	Pro	Gln	Asp 40	Val	Leu	Gly	Ile	Arg 45	Gln	Leu	Glu
Arg	Pro 50	Leu	Pro	Leu	Thr	Ser 55	Val	Cys	Tyr	Pro	Gln 60	Asp	Leu	Pro	Arg
Pro 65	Leu	Arg	Ser	Arg	Glu 70	Phe	Pro	Gln	Phe 75	Glu	Pro	Gln	Arg	Tyr	Pro 80
Ala	Cys	Ala	Gln	Met 85	Leu	Pro	Pro	Asn	Leu 90	Ser	Pro	His	Ala	Pro 95	Trp
Asn	Tyr	His	Tyr 100	His	Cys	Pro	Gly	Ser 105	Pro	Asp	His	Gln	Val 110	Pro	Tyr
Gly	His	Asp 115	Tyr	Pro	Arg	Ala	Ala 120	Tyr	Gln	Gln	Val	Ile 125	Gln	Pro	Ala
Leu	Pro 130	Gly	Gln	Pro	Leu	Pro 135	Gly	Ala	Ser	Val	Arg 140	Gly	Leu	His	Pro

09673395.122700

Val 145	Gln	Lys	Val	Ile	Leu 150	Asn	Tyr	Pro	Ser	Pro 155	Trp	Asp	Gln	Glu	Glu 160
Arg	Pro	Ala	Gln	Arg 165	Asp	Cys	Ser	Phe	Pro 170	Gly	Leu	Pro	Arg	His 175	Gln
Asp	Gln	Pro	His 180	His	Gln	Pro	Pro	Asn 185	Arg	Ala	Gly	Ala	Pro 190	Gly	Glu
Ser	Leu	Glu 195	Cys	Pro	Ala	Glu	Leu 200	Arg	Pro	Gln	Val	Pro 205	Gln	Pro	Pro
Ser	Pro 210	Ala	Ala	Val	Pro	Arg 215	Pro	Pro	Ser	Asn	Pro 220	Pro	Ala	Arg	Gly
Thr 225	Leu	Lys	Thr	Ser	Asn 230	Leu	Pro	Glu	Glu	Leu 235	Arg	Lys	Val	Phe	Ile 240
Thr	Tyr	Ser	Met	Asp 245	Thr	Ala	Met	Glu	Val 250	Val	Lys	Phe	Val	Asn 255	Phe
Leu	Leu	Val	Asn 260	Gly	Phe	Gln	Thr	Ala 265	Ile	Asp	Ile	Phe	Glu 270	Asp	Arg
Ile	Arg	Gly 275	Ile	Asp	Ile	Ile	Lys 280	Trp	Met	Glu	Arg	Tyr 285	Leu	Arg	Asp
Lys	Thr 290	Val	Met	Ile	Ile	Val 295	Ala	Ile	Ser	Pro	Lys 300	Tyr	Lys	Gln	Asp
Val 305	Glu	Gly	Ala	Glu	Ser 310	Gln	Leu	Asp	Glu	Asp 315	Glu	His	Gly	Leu	His 320
Thr	Lys	Tyr	Ile	His 325	Arg	Met	Met	Gln	Ile 330	Glu	Phe	Ile	Lys	Gln 335	Gly
Ser	Met	Asn	Phe 340	Arg	Phe	Ile	Pro	Val 345	Leu	Phe	Pro	Asn	Ala 350	Lys	Lys
Glu	His	Val 355	Pro	Thr	Trp	Leu	Gln 360	Asn	Thr	His	Val	Tyr 365	Ser	Trp	Pro
Lys	Asn 370	Lys	Lys	Asn	Ile	Leu 375	Leu	Arg	Leu	Leu	Arg 380	Glu	Glu	Glu	Tyr
Val 385	Ala	Pro	Pro	Arg	Gly 390	Pro	Leu	Pro	Thr	Leu 395	Gln	Val	Val	Pro	Leu 400

&lt;210&gt; 480

&lt;211&gt; 225

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 480

Ser 1	Ser	Ser	Gly	Trp 5	Arg	Val	Ala	Arg	Gly 10	Ser	Arg	His	Ser	Ser	Trp
Gly	Arg	Arg	Leu 20	Gly	Asn	Leu	Trp	Ser 25	Gln	Leu	Cys	Arg	Ala 30	Leu	Gln
Gly	Leu	Pro 35	Arg	Ser	Thr	Ser	Ser 40	Ile	Arg	Trp	Leu	Val 45	Met	Trp	Leu

Val	Leu	Val	Pro	Trp	Lys	Pro	Arg	Lys	Gly	Ala	Val	Ser	Leu	Cys	Gly
50						55					60				
Pro	Leu	Phe	Leu	Val	Pro	Gly	Ala	Gly	Ile	Ile	Gln	Asp	Asn	Leu	Leu
65					70					75					80
His	Arg	Val	Gln	Ala	Ser	His	Thr	Gly	Ser	Arg	Gln	Gly	Leu	Pro	Arg
			85						90					95	
Gln	Ser	Arg	Leu	Asp	His	Leu	Leu	Val	Gly	Cys	Ser	Arg	Val	Val	Met
			100					105					110		
Ala	Ile	Trp	His	Leu	Val	Ile	Gly	Thr	Ser	Arg	Thr	Met	Val	Met	Ile
		115					120					125			
Val	Pro	Trp	Ser	Met	Trp	Gly	Lys	Ile	Gly	Arg	Gln	His	Leu	Cys	Thr
	130					135					140				
Cys	Trp	Ile	Pro	Leu	Arg	Phe	Lys	Leu	Arg	Glu	Leu	Pro	Gly	Pro	Glu
145					150					155					160
Arg	Ser	Gly	Glu	Val	Leu	Gly	Val	Thr	His	Gly	Gly	Glu	Gly	Gln	Gly
				165					170					175	
Pro	Phe	Gln	Leu	Pro	Asp	Ala	Gln	Asp	Ile	Leu	Gly	Leu	Gly	Ile	Ile
			180					185					190		
Ser	Arg	Val	Tyr	Gly	Trp	Gln	Ile	Gln	Ala	Cys	Ser	Val	Pro	Val	Gln
		195					200					205			
Ala	Gly	Ala	Val	Ala	Pro	Ser	Pro	Cys	Tyr	Arg	Pro	Arg	Ser	Leu	Leu
	210					215					220				
Arg															
225															

&lt;210&gt; 481

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 481

Lys	Gln	Arg	Met	Gln	Ser	Ser	His	Arg	Leu	His	Phe	Lys	Ala	Arg	Val
1				5					10					15	
Cys	Gly	Gly	Leu	Arg	Gly	Arg	Ala	Leu	His	Asn	Arg	Phe	Pro	Gly	Gly
			20					25					30		
Gln	Arg	Ala	Ser	Arg	Gly	Gly	Thr	Glu	Lys	Asn	Gln	Pro	Gly	Val	Leu
		35					40					45			
Pro	Thr	Ser	Leu	Ser	Gln	Asn	Ala	Val	Arg	Thr	Arg	Pro	Gln	Thr	Trp
	50					55					60				
Pro	Gly	Leu	Ser	Asp	Leu	Gly	Met	Asn	Gly	Val	Thr	Arg	Glu	Pro	Pro
65					70					75					80
Glu	Gly	Trp	Ala	Glu	Ala	Pro	Val	Glu	Glu	Pro	His	Thr	Leu	Pro	Leu
				85					90					95	
Ser	Ala	Ala	Ala	Ala	Gly	Cys	Phe	Phe	Tyr	Ser	Trp	Ala	Ser	Cys	Arg

100										105				110				
His	Glu	Cys	Ser	Glu	Ala	Arg	Trp	Ala	His	Ala	Pro	Ser						
		115					120					125						
<210> 482																		
<211> 96																		
<212> PRT																		
<213> homo sapiens																		
<400> 482																		
Val	Ala	Met	Thr	Ala	Lys	Asp	Cys	Ser	Ile	Met	Ile	Ala	Leu	Ser	Pro			
1				5					10					15				
Cys	Leu	Gln	Asp	Ala	Ser	Ser	Asp	Gln	Arg	Pro	Val	Val	Pro	Ser	Ser			
			20					25					30					
Arg	Ser	Arg	Phe	Ala	Phe	Ser	Val	Ser	Val	Leu	Asp	Leu	Asp	Leu	Lys			
		35					40					45						
Pro	Tyr	Glu	Ser	Ile	Pro	His	Gln	Tyr	Lys	Leu	Asp	Gly	Lys	Ile	Val			
	50					55					60							
Asn	Tyr	Tyr	Ser	Lys	Thr	Val	Arg	Ala	Lys	Asp	Asn	Ala	Val	Met	Ser			
65					70					75				80				
Thr	Arg	Phe	Lys	Glu	Ser	Glu	Asp	Cys	Thr	Leu	Val	Leu	His	Lys	Val			
				85					90					95				
<210> 483																		
<211> 66																		
<212> PRT																		
<213> homo sapiens																		
<400> 483																		
Leu	His	Cys	Leu	Pro	Val	Cys	Arg	Met	Pro	Ala	Leu	Ile	Lys	Gly	Leu			
1				5					10					15				
Trp	Ser	Leu	His	Arg	Gly	Pro	Gly	Leu	Pro	Phe	Pro	Cys	Leu	Cys	Trp			
			20					25					30					
Thr	Leu	Thr	Ser	Ser	Pro	Thr	Arg	Ala	Phe	Pro	Ile	Ser	Ile	Asn	Trp			
		35					40					45						
Thr	Ala	Arg	Ser	Ser	Thr	Ile	Ile	Gln	Arg	Leu	Tyr	Val	Pro	Lys	Thr			
	50					55					60							
Thr	Pro																	
65																		
<210> 484																		
<211> 109																		
<212> PRT																		
<213> homo sapiens																		
<400> 484																		
Asn	Lys	Ala	Phe	Arg	Ile	Arg	Glu	Ser	Asp	Met	Ser	Pro	Gly	Trp	Glu			
1				5					10					15				
Arg	Arg	Thr	Ile	Gln	Asn	Val	Phe	Pro	Gly	Leu	Asn	Gly	His	Phe	His			

			20						25					30			
Phe	Lys	Ser	Val	Ser	Ser	Phe	Leu	Gly	His	Ser	Thr	His	Phe	Leu	His		
		35					40					45					
Ser	Leu	Ser	Arg	Lys	Leu	Phe	Leu	Val	Leu	Phe	Asn	Ser	Met	Ser	Pro		
	50					55					60						
Arg	Gly	Asn	Pro	Thr	Ser	Lys	Gly	Val	Lys	Ser	Lys	Asn	Ile	His	Asn		
65					70					75					80		
Gln	Arg	Ser	Pro	Asn	Thr	Thr	Glu	Asn	Ile	Ser	Ile	Ile	Gln	Pro	Ser		
				85					90					95			
His	Tyr	Val	Gln	Val	Ser	Lys	Thr	Leu	Gln	Gly	Lys	Ser					
			100					105									

<210> 485  
 <211> 66  
 <212> PRT  
 <213> homo sapiens

<400> 485

Cys	Ser	Ser	Ile	Pro	Cys	Leu	Gln	Glu	Ala	Ile	Pro	Pro	Gln	Lys	Gly
1				5					10					15	
Leu	Lys	Ala	Lys	Thr	Phe	Thr	Thr	Lys	Gly	His	Pro	Thr	Gln	Gln	Lys
			20					25					30		
Ile	Ser	Leu	Ser	Phe	Ser	Leu	His	Ile	Met	Phe	Lys	Phe	Gln	Arg	His
		35					40					45			
Cys	Arg	Glu	Arg	Val	Arg	Pro	Cys	Gly	Glu	Leu	Met	Cys	Asn	Leu	Arg
	50					55					60				
Phe	Pro														
65															

<210> 486  
 <211> 109  
 <212> PRT  
 <213> homo sapiens

<400> 486

Ala	Arg	Pro	Ala	Pro	Ala	Gly	Arg	Glu	Gly	Arg	Gly	Glu	Gly	Glu	Ala
1				5					10					15	
Thr	Ser	Arg	Arg	Cys	Gly	Val	Gly	His	Arg	Ala	Gly	Pro	Arg	Glu	Pro
			20					25					30		
Ala	Pro	His	Gly	Ala	Ala	Ala	Val	Arg	Pro	Thr	Pro	Gly	Pro	His	His
		35					40					45			
His	Cys	Ala	Ala	Leu	Ser	Gly	Ala	Glu	Asn	Tyr	Arg	Ser	Arg	His	Ala
	50					55					60				
Met	Lys	Leu	Ala	Ser	Ala	Leu	Arg	Arg	Gly	Pro	Ala	Leu	His	Pro	Leu
65					70					75				80	
Pro	Pro	Arg	Ala	Asn	Arg	Gly	Arg	Glu	Pro	Trp	Arg	Arg	Arg	His	Arg
				85					90					95	

00573335.122700

Pro Arg Gly Trp Ala Ala Ala Ser Arg Thr Trp Arg Ser  
100 105

<210> 487  
<211> 389  
<212> PRT  
<213> homo sapiens

<400> 487

Ala 1	Ala	Gly	Ala	Cys 5	Gly	Ala	Arg	Gly	Ser 10	Gly	Arg	Arg	Gly	Ser 15	Tyr
Val	Pro	Glu	Val 20	Arg	Cys	Gly	Ala	Pro 25	Gly	Gly	Ala	Ala	Gly 30	Thr	Gly
Ala	Pro	Arg 35	Ser	Cys	Cys	Cys	Gln 40	Thr	Asn	Pro	Gly	Pro 45	Pro	Ser	Ser
Leu	Arg 50	Arg	Ala	Phe	Arg	Arg 55	Arg	Glu	Leu	Pro	Phe 60	Pro	Ala	Cys	His
Glu 65	Ile	Gly	Leu	Gly	Ala 70	Glu	Ala	Gly	Ser	Gly 75	Pro	Pro	Pro	Ala	Pro 80
Ala	Ala	Arg	Glu	Ser 85	Arg	Ser	Arg	Ala	Met 90	Glu	Glu	Glu	Ala	Ser 95	Ser
Pro	Gly	Leu	Gly 100	Cys	Ser	Lys	Pro	His 105	Leu	Glu	Lys	Leu	Thr 110	Leu	Gly
Ile	Thr	Arg 115	Ile	Leu	Glu	Ser	Ser 120	Pro	Gly	Val	Thr	Glu 125	Val	Thr	Ile
Ile	Glu 130	Lys	Pro	Pro	Ala	Glu 135	Arg	His	Met	Ile	Ser 140	Ser	Trp	Glu	Gln
Lys 145	Asn	Asn	Cys	Val	Met 150	Pro	Glu	Asp	Val	Lys 155	Asn	Phe	Tyr	Leu	Met 160
Thr	Asn	Gly	Phe	His 165	Met	Thr	Trp	Ser	Val 170	Lys	Leu	Asp	Glu	His 175	Ile
Ile	Pro	Leu	Gly 180	Ser	Met	Ala	Ile	Asn 185	Ser	Ile	Ser	Lys	Leu 190	Thr	Gln
Leu	Thr	Gln 195	Ser	Ser	Met	Tyr	Ser 200	Leu	Pro	Asn	Ala	Pro 205	Thr	Leu	Ala
Asp	Leu 210	Glu	Asp	Asp	Thr	His 215	Glu	Ala	Ser	Asp	Asp 220	Gln	Pro	Glu	Lys
Pro 225	His	Phe	Asp	Ser	Arg 230	Ser	Val	Ile	Phe	Glu 235	Leu	Asp	Ser	Cys	Asn 240
Gly	Ser	Gly	Lys	Val 245	Cys	Leu	Val	Tyr	Lys 250	Ser	Gly	Lys	Pro	Ala 255	Leu
Ala	Glu	Asp	Thr 260	Glu	Ile	Trp	Phe	Leu 265	Asp	Arg	Ala	Leu	Tyr 270	Trp	His
Phe	Leu	Thr	Asp	Thr	Phe	Thr	Ala	Tyr	Tyr	Arg	Leu	Leu	Ile	Thr	His

00673355-122700

275					280					285					
Leu	Gly	Leu	Pro	Gln	Trp	Gln	Tyr	Ala	Phe	Thr	Ser	Tyr	Gly	Ile	Ser
	290					295					300				
Pro	Gln	Ala	Lys	Gln	Trp	Phe	Ser	Met	Tyr	Lys	Pro	Ile	Thr	Tyr	Asn
305				310					315						320
Thr	Asn	Leu	Leu	Thr	Glu	Glu	Thr	Asp	Ser	Phe	Val	Asn	Lys	Leu	Asp
				325					330					335	
Pro	Ser	Lys	Val	Phe	Lys	Ser	Lys	Asn	Lys	Ile	Val	Ile	Pro	Lys	Lys
			340					345					350		
Lys	Gly	Pro	Val	Gln	Pro	Ala	Gly	Gly	Gln	Lys	Gly	Pro	Ser	Gly	Pro
		355					360					365			
Ser	Gly	Pro	Ser	Thr	Ser	Ser	Thr	Ser	Lys	Ser	Ser	Ser	Gly	Ser	Gly
	370					375					380				
Asn	Pro	Thr	Arg	Lys											
385															
<210> 488															
<211> 96															
<212> PRT															
<213> homo sapiens															
<400> 488															
Arg	Ser	Ala	Gly	Gly	Phe	Ser	Met	Met	Val	Thr	Ser	Val	Thr	Pro	Gly
1				5					10					15	
Glu	Asp	Ser	Arg	Met	Arg	Val	Met	Pro	Arg	Val	Ser	Phe	Ser	Arg	Cys
			20					25					30		
Gly	Leu	Leu	Gln	Pro	Ser	Pro	Gly	Asp	Asp	Ala	Ser	Ser	Ser	Met	Ala
		35					40					45			
Arg	Asp	Arg	Asp	Ser	Arg	Ala	Ala	Gly	Ala	Gly	Gly	Gly	Pro	Asp	Pro
	50					55					60				
Ala	Ser	Ala	Pro	Arg	Pro	Ile	Ser	Trp	His	Ala	Gly	Asn	Gly	Ser	Ser
65						70					75				80
Arg	Arg	Leu	Lys	Ala	Arg	Arg	Ser	Asp	Asp	Gly	Gly	Pro	Gly	Leu	Val
				85					90					95	
<210> 489															
<211> 152															
<212> PRT															
<213> homo sapiens															
<400> 489															
Leu	Ala	Ala	Gly	Arg	Gly	Lys	Glu	Glu	Glu	Met	Gly	Phe	Glu	Asp	His
1				5					10					15	
Gly	Leu	Pro	Phe	Leu	Pro	Leu	Thr	His	His	Thr	Pro	Phe	Pro	Pro	Leu
			20					25					30		
Ser	Leu	Ser	Pro	Leu	Pro	Lys	Lys	Lys	Lys	Lys	Glu	Thr	Phe	Ile	Met
		35					40					45			

Asn	Gln	Gln	Gly	Phe	Ser	Pro	Tyr	Gln	Arg	Glu	Met	Trp	Lys	Glu	Leu
	50					55					60				
Lys	Lys	Pro	Pro	Phe	Val	Pro	Asn	Ser	Thr	Leu	Pro	Ile	Phe	Tyr	Ala
65					70					75					80
Thr	Gln	Thr	Leu	Ser	Phe	Trp	Val	Pro	Phe	Leu	Gln	Met	Asp	Leu	Leu
				85					90					95	
Arg	Arg	Ile	Ile	Val	Phe	His	Val	Phe	Ser	Pro	Gln	Val	Thr	Lys	Ile
			100					105					110		
Asn	Ile	Cys	Ile	Tyr	Asn	Leu	Tyr	Tyr	Cys	Tyr	Ile	Phe	Val	Asp	Asn
		115					120					125			
Thr	Phe	Arg	Trp	Cys	Trp	Val	Ile	Tyr	Tyr	Asn	Leu	Asn	Leu	Gly	Ile
	130					135					140				
Ser	Phe	Gly	Leu	Pro	Gln	Ser	Cys								
145					150										

<210> 490  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 490

Gly	Pro	Trp	Leu	Thr	Phe	Pro	Ala	Phe	Asp	Pro	Ser	His	Pro	Ile	Ser
1				5					10					15	
Ser	Ser	Phe	Pro	Leu	Pro	Ala	Ala	Lys	Lys	Lys	Lys	Lys	Gly	Asn	Val
			20					25					30		
Tyr	His	Glu	Ser	Thr	Gly	Phe	Gln	Ser	Leu	Ser	Lys	Arg	Asp	Val	Glu
		35					40					45			
Arg	Ala	Lys	Glu	Thr	Thr	Leu	Cys	Ser	Gln	Leu	His	Phe	Thr	His	Ile
	50					55					60				
Leu	Cys	Asn	Thr	Asn	Thr	Val	Leu	Leu	Gly	Pro	Phe	Leu	Thr	Asp	Gly
65					70					75					80
Pro	Leu	Glu	Lys	Asn	Tyr	Arg	Ile	Pro	Arg	Phe					
				85					90						

<210> 491  
 <211> 64  
 <212> PRT  
 <213> homo sapiens

<400> 491

Lys	Trp	Gly	Thr	Gln	Arg	Ala	Gly	Asn	Phe	His	Tyr	Pro	Ile	Leu	Gly
1				5					10					15	
Leu	Asn	Leu	Lys	Glu	Tyr	Ile	His	Tyr	Gln	Glu	Leu	Ser	Thr	Lys	Ala
			20					25					30		
Gly	Val	Lys	Leu	His	Tyr	Thr	Trp	Leu	Phe	Thr	Ile	Pro	Gly	Ser	Pro
		35					40					45			

00573305-122700



Pro Gln His Asp Cys Gly Arg Pro Lys Asp Ile Pro Arg Phe Arg Leu  
50 55 60

<210> 492  
<211> 79  
<212> PRT  
<213> homo sapiens

<400> 492

Arg Phe Thr Ala Ser Arg Val Gly Asn Glu Pro Asp Ile Asn Thr Pro  
1 5 10 15  
Ser Ser Met Pro Cys Pro Pro Ser Gly Pro Val Pro Val Lys Ala Gly  
20 25 30  
Ser His Phe Ser His Pro Gln Ala Val Pro Lys Ala Leu Glu Glu Pro  
35 40 45  
Lys Glu Arg Gln Glu Pro Ser Trp Glu Leu Thr Leu Met Thr Arg Gly  
50 55 60  
Gln Leu Ala Gln Phe Pro Leu Phe Ser Trp Gly Glu Gly Thr Leu  
65 70 75

<210> 493  
<211> 100  
<212> PRT  
<213> homo sapiens

<400> 493

Lys Ser Ser Pro Asp Pro Ala Arg His Tyr Gly Ser Pro Pro Glu Gly  
1 5 15  
Glu Arg Arg Gly Lys Arg Ser Val Pro Lys Val Asn Pro Arg Ser Leu  
20 25 30  
Gly Pro Thr Ser Leu Pro Thr Ala Thr Ser His Gln Pro His Ala Arg  
35 40 45  
Ala Arg Pro Phe Pro Leu Gln Leu Thr Ala Gln Gln Met Leu Gly Gln  
50 55 60  
Asn Ala Ser Pro His Leu Thr Lys Gly Leu Gln Pro Ala Gly Trp Glu  
65 70 75 80  
Met Asn Gln Ile Leu Thr Pro Pro Pro Pro Cys Pro Ala His Leu Leu  
85 90 95  
Gly Gln Tyr Gln  
100

<210> 494  
<211> 83  
<212> PRT  
<213> homo sapiens

<400> 494

Lys Gly Ser Leu Pro Pro Thr Lys Gln Gly Lys Leu Gly Gln Leu Ala  
1 5 10 15

00673395-12700

Pro Gly His Gln Gly Gln Leu Pro Thr Trp Leu Leu Pro Phe Leu Gly  
 20 25 30  
 Phe Phe Gln Gly Phe Gly Asn Ser Leu Gly Val Gly Glu Val Ala Ser  
 35 40 45  
 Cys Leu His Trp Tyr Trp Pro Arg Arg Trp Ala Gly His Gly Gly Gly  
 50 55 60  
 Gly Val Asn Ile Trp Phe Ile Ser His Pro Ala Gly Cys Lys Pro Leu  
 65 70 75 80

Val Lys

<210> 495  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 495

Arg Val Pro Ser Pro Gln Leu Asn Lys Gly Asn Trp Ala Asn Trp Pro  
 1 5 10 15  
 Leu Val Ile Lys Val Asn Ser Gln Leu Gly Ser Cys Leu Ser Leu Gly  
 20 25 30  
 Ser Ser Arg Ala Leu Gly Thr Ala Trp Gly Trp Glu Lys Trp Leu Pro  
 35 40 45  
 Ala Phe Thr Gly Thr Gly Pro Glu Gly Gly Gln Gly Met Glu Glu Gly  
 50 55 60  
 Val Leu Ile Ser Gly Ser Phe Pro Thr Leu Leu Ala Val Asn Leu  
 65 70 75

<210> 496  
 <211> 88  
 <212> PRT  
 <213> homo sapiens

<400> 496

Ile Gln Lys Val Gln Tyr Tyr Thr Ser Pro Ala Ala Phe Val Asn Gly  
 1 5 10 15  
 Ser Leu His Ser His Trp Gly Thr Thr Val Cys Met Gly Arg Asn Ser  
 20 25 30  
 Lys Cys Pro His Cys Gly His Trp Val Gly Ser Ala Phe Cys Gln Gly  
 35 40 45  
 Val Cys Arg Asn Trp Leu Ile Ser Val Cys Gln Ser Asp Gln His Thr  
 50 55 60  
 Lys Val Ser Ala Ile Lys Asn Val Ala Ser Leu His Pro Pro Ser Cys  
 65 70 75 80

Tyr Ser Gly Pro Ser Asn Leu Met  
 85

<210> 497  
 <211> 98

00673695-122700

<212> PRT  
<213> homo sapiens

<400> 497

Ser	His	Thr	Ser	Glu	Lys	Arg	Arg	Gly	Thr	Arg	Glu	Glu	Val	Thr	Pro
1				5					10					15	
Ala	Ser	Arg	Ser	Ile	Ser	Gly	Val	Lys	Arg	Gly	Thr	Val	Ala	Leu	
			20				25					30			
Pro	Ser	Trp	Leu	Arg	Met	Arg	Lys	Ser	Phe	Leu	Gln	Trp	Glu	Glu	Ile
		35					40					45			
His	Phe	Ser	Ile	Pro	Val	Gln	Ser	Asp	Phe	Met	Gly	Pro	Val	Leu	Asn
	50					55					60				
Ser	Asp	Cys	Ile	Ile	Asn	Thr	Ile	Lys	Arg	Asp	Ser	Glu	Met	Gly	Ser
65					70					75					80
Arg	Ile	His	Trp	Asp	Asn	Ser	Lys	Ala	Tyr	Asn	Thr	Ala	Leu	Met	Asp
				85					90					95	

Pro Thr

<210> 498  
<211> 83  
<212> PRT  
<213> homo sapiens

<400> 498

Ala	Gly	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Ile	Arg	Gln	Leu	His	Gln	Ile
1				5					10					15	
Thr	Gly	Pro	Arg	Val	Thr	Gly	Trp	Arg	Met	Gln	Gly	Ser	His	Ile	Leu
			20					25					30		
Tyr	Gly	Arg	Asp	Phe	Gly	Val	Leu	Ile	Thr	Leu	Ala	Tyr	Arg	Asn	Lys
		35					40					45			
Pro	Ile	Pro	Ala	Asp	Ser	Leu	Thr	Lys	Gly	Thr	Pro	His	Pro	Met	Thr
	50					55					60				
Thr	Met	Arg	Ala	Leu	Ala	Val	Ser	Ala	His	Ala	His	Ser	Cys	Thr	Pro
65					70					75					80

Met Ala Val

<210> 499  
<211> 85  
<212> PRT  
<213> homo sapiens

<400> 499

Gly	Lys	Ile	Cys	Glu	Tyr	Val	Asn	Phe	Leu	Ser	Leu	Arg	Asp	Asp	Arg
1				5					10					15	
Met	Phe	Pro	Tyr	Phe	Ser	Cys	Lys	Glu	Asn	Asn	Ile	Leu	Thr	Tyr	Thr
			20					25					30		
Ser	Cys	Arg	Lys	Tyr	His	Leu	Phe	Pro	Leu	Tyr	Tyr	Ser	Thr	Met	Phe

00673395-122700

			35					40						45					
Thr	Leu			Tyr	Cys	Gln	Ala	Glu	Ser	Ile	Lys	Asn	Val	His	Ile	His			
	50						55					60							
Phe	Glu	Leu		Cys	Ile	Leu	Phe	Leu	Lys	Lys	Gly	Ala	Gly	Leu	Trp	His			
65					70						75					80			
Trp	Ala	Gly		His	Asp														
					85														

<210> 500  
 <211> 98  
 <212> PRT  
 <213> homo sapiens

<400> 500

Ser	Tyr	Arg	Leu	Lys	Gly	Ile	Gly	Lys	Cys	Val	Phe	Ser	Arg	Asp	His				
1				5					10					15					
Val	Glu	Ser	Glu	Gln	Cys	Trp	Gln	Thr	Leu	Pro	Arg	Lys	Ser	Cys	Phe				
			20					25					30						
Ser	Arg	Cys	Pro	Cys	Phe	Gly	Ile	Ser	Phe	Leu	Gly	Arg	Lys	Lys	Lys				
		35					40					45							
Ser	Ser	Leu	Thr	Ile	Val	Asn	Ser	Ile	Ser	Tyr	Phe	Ser	Phe	Cys	Cys				
	50					55					60								
Ser	Asn	Gly	Phe	Pro	Pro	Thr	Ile	Ile	Pro	Ser	Ile	Tyr	Val	Leu	Leu				
65					70					75				80					
Tyr	Ser	Pro	Leu	Ser	Pro	Val	Thr	Phe	Leu	Ser	Asn	Thr	Pro	Phe	Pro				
				85					90					95					
Lys	Phe																		

<210> 501  
 <211> 87  
 <212> PRT  
 <213> homo sapiens

<400> 501

Val	Ser	Ser	Cys	Thr	Ser	Asn	His	Gly	Val	Arg	Ser	Ser	Leu	Ser	Ser				
1				5					10				15						
Gly	Glu	His	Lys	Cys	Thr	Glu	Arg	Asp	Val	Leu	Arg	Val	Thr	Thr	Lys				
			20					25					30						
Glu	Leu	Pro	Ser	Leu	Ser	Leu	Thr	Gln	Ala	Met	Cys	Thr	Cys	Asp	Ala				
		35					40					45							
Ala	Glu	Cys	Ala	Gly	Val	Gly	Gly	Gly	His	Val	Ala	Pro	Pro	Glu	His				
	50					55					60								
Phe	Leu	Thr	Gly	Lys	Leu	Gly	Asp	Pro	Leu	Leu	Val	Asn	Phe	Val	Glu				
65					70					75					80				
Ile	Arg	Thr	Val	Ser	Phe	Thr													
				85															

00673395.122700

<210> 502  
 <211> 53  
 <212> PRT  
 <213> homo sapiens

<400> 502

Thr	Pro	Lys	Thr	Leu	Gly	Cys	Leu	Leu	Val	Ser	Arg	Val	Glu	Gln	Ala
1				5					10					15	
Gln	Arg	Glu	Ser	Leu	Gly	Pro	Glu	Leu	Lys	Glu	Phe	Ile	Glu	Pro	Trp
			20					25					30		
Gln	Thr	Gly	Ser	Lys	Gln	Pro	Ile	Leu	Ala	Ala	Val	Leu	Arg	Arg	Glu
		35					40					45			
Cys	Gly	Gly	Gln	Ile											
	50														

<210> 503  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 503

Pro	Ser	Gly	Pro	Phe	Ser	Ser	Leu	Glu	Ser	Thr	Leu	Leu	Leu	Gln	Gln
1				5					10					15	
Val	Gln	Ala	Ala	Ile	Ala	Ser	Phe	Leu	Ser	Asp	Cys	Asn	Ser	Pro	Ile
			20					25					30		
Arg	Phe	Pro	Cys	Phe	Tyr	Ile	Cys	Pro	Pro	His	Ser	Leu	Leu	Asn	Thr
		35					40					45			
Ala	Ala	Arg	Met	Gly	Cys	Leu	Leu	Pro	Val	Cys	His	Gly	Ser	Ile	Asn
	50					55					60				
Ser	Leu	Ser	Ser	Gly	Pro	Lys	Asp	Ser	Arg	Trp	Ala	Cys	Ser	Thr	Arg
	65				70					75					80
Asp	Thr	Ser	Arg	Gln	Pro	Ser	Val	Leu	Gly	Val					
				85					90						

<210> 504  
 <211> 59  
 <212> PRT  
 <213> homo sapiens

<400> 504

Val	Phe	Ile	Tyr	Asp	Ser	Leu	Ile	Ile	Pro	Thr	Ser	Ile	Ser	Ser	Val
1				5					10					15	
His	Thr	Val	Cys	Gln	Met	Phe	His	Ala	Glu	Pro	Val	Ser	Arg	Ile	Leu
			20					25					30		
Leu	Ser	Asp	Tyr	Gly	Gly	Phe	Thr	Thr	Arg	Pro	Gly	Ser	Asn	Ser	Leu
		35					40					45			
Gly	Ser	Lys	Val	Gly	His	Ser	Ser	Met	His	Arg					
	50					55									

00673395-122700

<210> 505  
 <211> 72  
 <212> PRT  
 <213> homo sapiens

<400> 505

Asp 1	Arg	Lys	Phe	Trp 5	Asn	Gln	Lys	Ile	Asp 10	Pro	Val	Phe	Ser	Tyr 15	Ile
Gln	Ser	Ser	Thr 20	Ser	Glu	Phe	Leu	Phe 25	Leu	Asn	Ile	Gly	Val 30	Leu	Ala
Leu	Phe	Leu 35	Lys	Asp	Ala	Leu	Tyr 40	Leu	Lys	Arg	Lys	Leu 45	Asp	Phe	Arg
Thr	Gly 50	Cys	Gly	Ala	Val	Lys 55	Tyr	Phe	Arg	Pro	Arg 60	Ser	Val	Tyr	Thr
Phe 65	Tyr	Arg	Arg	Asn	Glu 70	Val	Leu								

<210> 506  
 <211> 102  
 <212> PRT  
 <213> homo sapiens

<400> 506

Ser 1	Ile	Leu	Gly	Pro 5	Gly	Leu	Cys	Thr	His 10	Phe	Ile	Glu	Glu	Met 15	Lys
Tyr	Ser	Glu	Val 20	Phe	Trp	Leu	Pro	Phe 25	His	Phe	Asn	Cys	Val 30	Leu	Asn
Leu	Ser	Asp 35	His	Thr	Tyr	Ile	Val 40	Leu	Leu	Gly	Ala	Val 45	Val	Ser	Phe
Ile	Lys 50	Pro	Leu	Ala	Cys	Val 55	Gln	Lys	Phe	Leu	Lys 60	Gly	Asn	Thr	Ser
Asn 65	Ala	Tyr	Pro	Leu	Leu 70	Ala	Cys	Tyr	Ala	Ala 75	Cys	Phe	Thr	Ala	Ile 80
Ala	Val	Cys	Phe	Thr 85	Val	Phe	Val	Lys	Ile 90	Pro	Leu	Ser	Pro	Phe 95	Leu
Val	Thr	Gly	Lys 100	Ala	Cys										

<210> 507  
 <211> 68  
 <212> PRT  
 <213> homo sapiens

<400> 507

Asn 1	Asn	Glu	His	Lys 5	Met	Leu	Phe	Ile	Ile 10	Thr	Ser	Ile	Cys	Glu 15	Ile
Ser	Tyr	Cys	Lys 20	Thr	Thr	Thr	Gly	Leu 25	Leu	Leu	Asn	Ser	Leu 30	Val	Ile

00673305-122700

Val	Phe	Arg 35	Leu	Glu	Met	Pro	Pro 40	Thr	Leu	Val	Ile	Asn 45	Ile	Thr	Lys
Tyr	Asn 50	Val	Phe	Leu	Gly	Arg 55	His	Phe	Ile	Lys	Cys 60	Ile	Met	Pro	Trp
Leu 65	Leu	Leu	Arg												

<210> 508  
 <211> 65  
 <212> PRT  
 <213> homo sapiens

<400> 508

Leu 1	Lys	Phe	Leu	Gln 5	Val	Leu	Lys	Phe	Phe 10	Phe	Tyr	Ser	Leu	His 15	Trp
Ile	Tyr	Val	Phe 20	Leu	Ile	Pro	Asn	Met 25	Phe	Asn	Trp	Asp	Val 30	Cys	His
Ser	Arg	Ala 35	Ala	Arg	Gln	Thr	Phe 40	Lys	Ser	Asn	Ser	His 45	Thr	Ala	Glu
Leu 50	Ala	Phe	Leu	Leu	Thr	Gln 55	Lys	Phe	Arg	Lys	Leu 60	Thr	Val	Thr	Val
Thr 65															

<210> 509  
 <211> 78  
 <212> PRT  
 <213> homo sapiens

<400> 509

Gly 1	Pro	Arg	Ala	His 5	Trp	Pro	Leu	Pro	Asn 10	Thr	Met	Leu	Glu	Pro 15	Lys
Arg	Ala	Asn	Met 20	Gly	Pro	Glu	Tyr	Asn 25	Gly	Asp	Ile	Phe	Met 30	Phe	Gln
Pro	Phe	Asn 35	Leu	Thr	Cys	Leu	Leu 40	Leu	Ser	Phe	Pro	Pro 45	Ile	Ser	Ser
Asn 50	Leu	Phe	Cys	Leu	Thr	Ile 55	Tyr	Tyr	Leu	Leu	Gly 60	Ile	Thr	Ser	Ser
Tyr 65	Arg	Ile	Pro	Ser	Ser 70	Leu	Met	Ser	Cys	Pro 75	Lys	Gln	Tyr		

<210> 510  
 <211> 63  
 <212> PRT  
 <213> homo sapiens

<400> 510

Ser 1	Leu	Lys	Leu	Leu 5	Gly	Phe	Leu	Asp	Val 10	Glu	Asn	Thr	Pro	Cys 15	Ala
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

00673395.122700

Arg	His	Ser	Ile	Leu	Tyr	Gly	Ser	Leu	Gly	Ser	Val	Val	Ala	Gly	Phe
			20					25					30		
Gly	His	Phe	Leu	Phe	Thr	Ser	Glu	Tyr	Leu	Tyr	Phe	Leu	Phe	Leu	Tyr
		35					40					45			
Val	Leu	Lys	Lys	Ala	Phe	Leu	Tyr	Ile	Met	Asn	Tyr	Phe	Phe	Phe	
	50					55					60				

<210> 511  
 <211> 53  
 <212> PRT  
 <213> homo sapiens

<400> 511

Ser	Phe	Val	Lys	Trp	Ser	Pro	Asn	Leu	Lys	Leu	Gly	Asn	Tyr	Glu	Glu
1				5					10					15	
Glu	Lys	Ile	Ala	Arg	Tyr	Leu	Leu	Arg	Ser	Ala	Cys	Arg	Ser	Ala	Val
			20					25					30		
Gly	Leu	Val	Thr	Ile	Gly	Ser	Lys	Val	Leu	Leu	Gln	Trp	Gln	Ile	Leu
		35					40					45			
Trp	Pro	Leu	Ser	Gly											
	50														

<210> 512  
 <211> 43  
 <212> PRT  
 <213> homo sapiens

<400> 512

Ile	Cys	Cys	Arg	Ala	Cys	His	His	Trp	Lys	Gln	Gly	Pro	Thr	Ser	Val
1				5					10					15	
Ala	Asp	Leu	Val	Ala	Phe	Glu	Trp	Leu	Lys	Thr	Thr	Thr	Leu	His	Arg
			20					25					30		
Ala	Gly	Ala	Met	His	Arg	His	Pro	Ser	Leu	Pro					
		35					40								

<210> 513  
 <211> 37  
 <212> PRT  
 <213> homo sapiens

<400> 513

Gln	Ala	Leu	Gln	Gln	Ile	Tyr	Arg	Gln	Thr	Leu	Thr	Asp	Thr	Gly	Gln
1				5					10					15	
Phe	Ser	Leu	Leu	Arg	Asn	Phe	Leu	Val	Leu	Ser	Trp	Val	Thr	Ile	Leu
			20					25					30		
Gln	Asn	Phe	Thr	Thr											
		35													

<210> 514  
 <211> 228  
 <212> PRT

09673395.122700



<213> homo sapiens

<400> 514

Thr 1	Gly	Gly	Ala	Arg 5	Ala	Arg	Arg	Pro	Leu 10	Ser	Ala	Val	Ala	Arg 15	Pro
Ala	Arg	Ser	Ser 20	Asp	Pro	Leu	Arg	Ser 25	Ala	Pro	Leu	Gly	Pro 30	Ala	Pro
Pro	Val	Asn 35	Met	Ile	Arg	Cys	Gly 40	Leu	Ala	Cys	Glu	Arg 45	Cys	Arg	Trp
Ile	Leu 50	Pro	Leu	Leu	Leu 55	Ser	Ala	Ile	Ala	Phe 60	Asp	Ile	Ile	Ala	
Leu 65	Ala	Gly	Arg	Gly	Trp 70	Leu	Gln	Ser	Ser	Asp 75	His	Gly	Gln	Thr	Ser 80
Ser	Leu	Trp	Trp	Lys 85	Cys	Ser	Gln	Glu	Gly 90	Gly	Gly	Ser	Gly	Ser 95	Tyr
Glu	Glu	Gly	Cys 100	Gln	Ser	Leu	Met	Glu 105	Tyr	Ala	Trp	Gly	Arg 110	Ala	Ala
Ala	Ala	Met 115	Leu	Phe	Cys	Gly	Phe 120	Ile	Ile	Leu	Val	Ile 125	Cys	Phe	Ile
Leu	Ser 130	Phe	Phe	Ala	Leu	Cys 135	Gly	Pro	Gln	Met	Leu 140	Val	Phe	Leu	Arg
Val 145	Ile	Gly	Gly	Leu	Leu 150	Ala	Leu	Ala	Ala	Val 155	Phe	Gln	Ile	Ile	Ser 160
Leu	Val	Ile	Tyr	Pro 165	Val	Lys	Tyr	Thr	Gln 170	Thr	Phe	Thr	Leu	His 175	Ala
Asn	Arg	Ala	Val 180	Thr	Tyr	Ile	Tyr	Asn 185	Trp	Ala	Tyr	Gly	Phe 190	Gly	Trp
Ala	Ala	Thr 195	Ile	Ile	Leu	Ile	Gly 200	Cys	Ala	Phe	Phe	Phe 205	Cys	Cys	Leu
Pro	Asn 210	Tyr	Glu	Asp	Asp	Leu 215	Leu	Gly	Asn	Ala	Lys 220	Pro	Arg	Tyr	Phe
Tyr 225	Thr	Ser	Ala												

<210> 515

<211> 94

<212> PRT

<213> homo sapiens

<400> 515

Asp 1	Pro	Leu	Pro	Pro 5	Pro	Ser	Trp	Glu	His 10	Phe	His	His	Ser	Glu 15	Asp
Val	Trp	Pro	Trp 20	Ser	Leu	Asp	Cys	Asn 25	Gln	Pro	Arg	Pro	Ala 30	Ser	Ala
Met	Met	Ser	Lys	Ala	Met	Ala	Leu	Ser	Arg	Ser	Arg	Gly	Arg	Ile	Gln

00673305-122700

35						40						45					
Arg	Gln	Arg	Ser	Gln	Ala	Arg	Pro	Gln	Arg	Ile	Met	Leu	Thr	Gly	Gly		
	50					55					60						
Ala	Gly	Pro	Ser	Gly	Ala	Glu	Arg	Ser	Gly	Ser	Glu	Glu	Arg	Ala	Gly		
65					70					75					80		
Arg	Ala	Thr	Ala	Glu	Ser	Gly	Leu	Arg	Ala	Arg	Ala	Pro	Pro				
				85					90								

<210> 516  
 <211> 208  
 <212> PRT  
 <213> homo sapiens

<400> 516

Thr	Leu	Pro	Lys	Asn	Gly	Phe	Lys	Val	Ala	Trp	Arg	Asn	Ser	Phe	Phe
1				5					10					15	
Phe	Trp	Ser	Pro	Ser	Gln	Gln	Gln	Arg	Phe	Ser	Pro	Thr	Phe	Ile	Pro
			20					25					30		
Lys	Leu	Gly	Arg	Cys	Val	Glu	Val	Pro	Gly	Leu	Gly	Ile	Ala	Gln	Lys
		35					40					45			
Val	Ile	Phe	Val	Val	Gly	Glu	Ala	Ala	Glu	Glu	Glu	Gly	Thr	Ala	Asp
	50					55					60				
Gln	Asp	Asn	Arg	Gly	Cys	Pro	Pro	Lys	Ala	Val	Gly	Pro	Val	Ile	Asp
65					70					75					80
Val	Ser	Asp	Ser	Thr	Val	Gly	Met	Lys	Gly	Glu	Gly	Leu	Gly	Val	Leu
				85					90					95	
His	Gly	Val	Asn	Tyr	Gln	Gly	Asp	Asp	Leu	Glu	His	Ser	Ser	Gln	Gly
			100					105					110		
Lys	Glu	Thr	Ser	Asn	His	Ser	Gln	Glu	Asp	Lys	His	Leu	Gly	Ser	Thr
		115					120					125			
Glu	Gly	Glu	Glu	Gly	Glu	Asp	Glu	Thr	Asp	His	Gln	Asp	Asp	Glu	Ala
	130					135					140				
Thr	Glu	Glu	His	Gly	Ser	Arg	Cys	Ser	Thr	Pro	Arg	Val	Leu	His	Glu
145					150					155					160
Ala	Leu	Thr	Ala	Leu	Leu	Val	Gly	Pro	Ala	Ala	Ala	Ala	Leu	Leu	Gly
				165					170					175	
Ala	Phe	Pro	Pro	Gln	Arg	Gly	Arg	Leu	Ala	Val	Val	Ala	Arg	Leu	Gln
			180					185					190		
Pro	Ala	Ala	Ala	Gly	Gln	Arg	Asp	Asp	Val	Glu	Gly	Asp	Gly	Ala	Glu
		195					200					205			

<210> 517  
 <211> 204  
 <212> PRT  
 <213> homo sapiens

<400> 517

00673305.122700

Pro 1	Ser	Cys	Pro	Pro 5	Glu	Met	Lys	Lys	Glu 10	Leu	Pro	Val	Asp	Ser 15	Cys
Leu	Pro	Arg	Ser 20	Leu	Glu	Leu	His	Pro 25	Gln	Lys	Met	Asp	Pro 30	Lys	Arg
Gln	His	Ile 35	Gln	Leu	Leu	Ser	Ser 40	Leu	Thr	Glu	Cys	Leu 45	Thr	Val	Asp
Pro	Leu 50	Ser	Ala	Ser	Val	Trp 55	Arg	Gln	Leu	Tyr	Pro 60	Lys	His	Leu	Ser
Gln 65	Ser	Ser	Leu	Leu	Leu 70	Glu	His	Leu	Leu	Ser 75	Ser	Trp	Glu	Gln	Ile 80
Pro	Lys	Lys	Val	Gln 85	Lys	Ser	Leu	Gln	Glu 90	Thr	Ile	Gln	Ser	Leu 95	Lys
Leu	Thr	Asn	Gln 100	Glu	Leu	Leu	Arg	Lys 105	Gly	Ser	Ser	Asn	Asn 110	Gln	Asp
Val	Val	Thr 115	Cys	Asp	Met	Ala	Cys 120	Lys	Gly	Leu	Leu	Gln 125	Gln	Val	Gln
Gly	Pro 130	Arg	Leu	Pro	Trp	Thr 135	Arg	Leu	Leu	Leu	Leu 140	Leu	Leu	Val	Phe
Ala 145	Val	Gly	Phe	Leu	Cys 150	His	Asp	Leu	Arg	Ser 155	His	Ser	Ser	Phe	Gln 160
Ala	Ser	Leu	Thr	Gly 165	Arg	Leu	Leu	Arg	Ser 170	Ser	Gly	Phe	Leu	Pro 175	Ala
Ser	Gln	Gln	Ala 180	Cys	Ser	Lys	Phe	Thr 185	Pro	Thr	Val	Cys	Lys 190	Val	Thr
Gly	Trp	Leu 195	Gly	Glu	Lys	Cys	Arg 200	Phe	Gly	Val	Pro				

<210> 518  
 <211> 90  
 <212> PRT  
 <213> homo sapiens

<400> 518

Pro 1	Glu	Val	Met	Ala 5	Gln	Glu	Ala	Tyr	Ser 10	Glu	Asp	Gln	Gln	Gln 15	Gln
Glu	Glu	Pro	Arg 20	Pro	Gly	Gln	Pro	Arg 25	Thr	Leu	Asn	Leu	Leu 30	Gln	Gln
Ala	Leu	Ala 35	Gly	His	Val	Thr	Gly 40	Asp	Asp	Ile	Leu	Val 45	Val	Thr	Ala
Thr	Leu 50	Pro	Gln	Gln	Leu	Leu 55	Val	Gly	Lys	Leu	Glu 60	Gly	Leu	Asn	Gly
Phe 65	Leu	Gln	Arg	Leu	Leu 70	Tyr	Leu	Leu	Gly	Asn 75	Leu	Leu	Pro	Gly	Ala 80
Glu	Gln	Val	Leu	Gln	Gln	Lys	Ala	Gly	Leu						

00673305-122700

<210> 519  
 <211> 76  
 <212> PRT  
 <213> homo sapiens

<400> 519

Gly	Thr	Pro	Lys	Arg	His	Phe	Ser	Pro	Asn	Gln	Pro	Val	Thr	Leu	Gln
1				5					10					15	
Thr	Val	Gly	Val	Asn	Leu	Glu	His	Ala	Cys	Trp	Leu	Ala	Gly	Lys	Lys
			20					25					30		
Pro	Asp	Asp	Arg	Ser	Asn	Arg	Pro	Val	Arg	Glu	Ala	Trp	Lys	Glu	Leu
		35					40					45			
Cys	Asp	Arg	Arg	Ser	Trp	His	Arg	Lys	Pro	Thr	Ala	Lys	Thr	Ser	Ser
	50					55					60				
Asn	Arg	Arg	Ser	Arg	Val	Gln	Gly	Ser	Arg	Gly	Pro				
65					70					75					

<210> 520  
 <211> 355  
 <212> PRT  
 <213> homo sapiens

<400> 520

Phe	Arg	His	Ser	Met	Asn	Gly	Cys	Glu	Lys	Asp	Ser	Ser	Ser	Thr	Asp
1				5					10					15	
Ser	Ala	Asn	Glu	Lys	Pro	Ala	Leu	Ile	Pro	Arg	Glu	Lys	Lys	Ile	Ser
			20					25					30		
Ile	Leu	Glu	Glu	Pro	Ser	Lys	Ala	Leu	Arg	Gly	Val	Thr	Gly	Pro	Asn
		35					40					45			
Ile	Glu	Lys	Ser	Val	Lys	Asp	Leu	Gln	Arg	Cys	Thr	Val	Ser	Leu	Thr
	50					55					60				
Arg	Tyr	Arg	Val	Met	Ile	Lys	Glu	Glu	Val	Asp	Ser	Ser	Val	Lys	Lys
65				70						75				80	
Ile	Lys	Ala	Ala	Phe	Ala	Glu	Leu	His	Asn	Cys	Ile	Ile	Asp	Lys	Glu
				85					90					95	
Val	Ser	Leu	Met	Ala	Glu	Met	Asp	Lys	Val	Lys	Glu	Glu	Ala	Met	Glu
			100					105					110		
Ile	Leu	Thr	Ala	Arg	Gln	Lys	Lys	Ala	Glu	Glu	Leu	Lys	Arg	Leu	Thr
		115					120					125			
Asp	Leu	Ala	Ser	Gln	Met	Ala	Glu	Met	Gln	Leu	Ala	Glu	Leu	Arg	Ala
	130					135					140				
Glu	Ile	Lys	His	Phe	Val	Ser	Glu	Arg	Lys	Tyr	Asp	Glu	Glu	Leu	Gly
	145				150					155				160	
Lys	Ala	Ala	Arg	Phe	Ser	Cys	Asp	Ile	Glu	Gln	Leu	Lys	Ala	Gln	Ile
				165					170					175	

09573395-122700

00673305-122700

Met	Leu	Cys	Gly 180	Glu	Ile	Thr	His	Pro 185	Lys	Asn	Asn	Tyr	Ser 190	Ser	Arg
Thr	Pro	Cys 195	Ser	Ser	Leu	Leu	Pro 200	Leu	Leu	Asn	Ala	His 205	Ala	Ala	Thr
Ser	Gly 210	Lys	Gln	Ser	Asn	Phe 215	Ser	Arg	Lys	Ser	Ser 220	Thr	His	Asn	Lys
Pro 225	Ser	Glu	Gly	Lys	Ala 230	Ala	Asn	Pro	Lys	Met 235	Val	Ser	Ser	Leu	Pro 240
Ser	Thr	Ala	Asp	Pro 245	Ser	His	Gln	Thr	Met 250	Pro	Ala	Asn	Lys	Gln 255	Asn
Gly	Ser	Ser	Asn 260	Gln	Arg	Arg	Arg	Phe 265	Asn	Pro	Gln	Tyr	His 270	Asn	Asn
Arg	Leu	Asn 275	Gly	Pro	Ala	Lys	Ser 280	Gln	Gly	Ser	Gly	Asn 285	Glu	Ala	Glu
Pro	Leu 290	Gly	Lys	Gly	Asn	Ser 295	Arg	His	Glu	His	Arg 300	Arg	Gln	Pro	His
Asn 305	Gly	Phe	Arg	Pro	Lys 310	Asn	Lys	Gly	Gly	Ala 315	Lys	Asn	Gln	Glu	Ala 320
Ser	Leu	Gly	Met	Lys 325	Thr	Pro	Glu	Ala	Pro 330	Ala	His	Ser	Glu	Lys 335	Pro
Arg	Arg	Arg	Gln 340	Ala	Arg	Cys	Arg	Thr 345	Pro	Arg	Glu	Gly	Gln 350	Gly	Pro
Phe	Arg	Gly 355													

<210> 521  
 <211> 120  
 <212> PRT  
 <213> homo sapiens

<400> 521

Asn 1	Gln	Asn	Val	Lys 5	Asn	Arg	Gly	Thr	Gln 10	Lys	Lys	Cys	Leu	Pro 15	Ser
Val	Glu	Lys	Leu 20	Pro	Asn	Pro	Pro	Trp 25	Gly	Gln	Lys	Asn	Ala 30	Thr	Val
Lys	Thr	Pro 35	Asn	Arg	Lys	Leu	Thr 40	Pro	Glu	Arg	Pro	Leu 45	Ala	Leu	Pro
Arg	Cys 50	Pro	Ala	Ala	Cys	Leu 55	Pro	Ser	Pro	Gly	Leu 60	Phe	Arg	Met	Gly
Arg 65	Gly	Leu	Gly	Gly	Leu 70	His	Pro	Gln	Gly	Ser 75	Leu	Leu	Ile	Phe	Gly 80
Thr	Ala	Phe	Val	Phe 85	Gly	Pro	Glu	Ala	Val 90	Val	Arg	Leu	Ser	Ser 95	Val
Phe	Val	Ala	Ala	Val	Ala	Leu	Ser	Gln	Trp	Leu	Gly	Phe	Ile	Pro	Thr

100										105					110				
Ala	Leu	Arg	Leu	Gly	Arg	Pro	Ile												
		115					120												
<210> 522																			
<211> 116																			
<212> PRT																			
<213> homo sapiens																			
<400> 522																			
Arg	Ala	Val	Arg	Ile	Ser	Met	Ala	Ser	Ser	Leu	Thr	Leu	Ser	Ile	Ser				
1				5					10					15					
Ala	Ile	Asn	Glu	Thr	Ser	Leu	Ser	Met	Met	Gln	Leu	Cys	Asn	Ser	Ala				
			20					25					30						
Lys	Ala	Ala	Leu	Ile	Phe	Phe	Thr	Glu	Leu	Ser	Thr	Ser	Ser	Leu	Ile				
		35					40					45							
Met	Thr	Arg	Tyr	Leu	Val	Arg	Glu	Thr	Val	Gln	Arg	Cys	Lys	Ser	Phe				
	50					55					60								
Thr	Asp	Phe	Ser	Ile	Phe	Gly	Pro	Val	Thr	Pro	Arg	Ser	Ala	Phe	Glu				
	65				70					75					80				
Gly	Ser	Ser	Ser	Ile	Glu	Ile	Phe	Phe	Ser	Arg	Gly	Ile	Arg	Ala	Gly				
				85					90					95					
Phe	Ser	Leu	Ala	Glu	Ser	Val	Asp	Glu	Leu	Ser	Phe	Ser	Gln	Pro	Phe				
			100					105					110						
Met	Leu	Cys	Arg																
		115																	
<210> 523																			
<211> 130																			
<212> PRT																			
<213> homo sapiens																			
<400> 523																			
Arg	Arg	Gln	Arg	Lys	Ala	Glu	Pro	Gly	Ala	Cys	Ala	Leu	Gly	Arg	Val				
1				5					10					15					
Gly	Ser	Glu	Cys	Ile	Pro	Glu	Pro	Gly	Ala	Arg	Arg	Thr	Ala	Gln	Ala				
			20					25					30						
Ala	Gly	Leu	Arg	Ser	Val	Ser	Gly	Ala	Ala	Asn	Thr	Lys	Val	Arg	Glu				
		35					40					45							
Leu	Lys	His	Phe	Arg	Phe	Leu	Gly	Leu	Leu	Arg	Ser	Cys	Arg	Ser	Glu				
	50					55					60								
Met	Glu	Val	Asp	Ala	Pro	Gly	Val	Asp	Gly	Arg	Asp	Gly	Leu	Arg	Glu				
	65				70				75						80				
Arg	Arg	Gly	Phe	Ser	Glu	Gly	Gly	Arg	Gln	Asn	Phe	Asp	Val	Arg	Pro				
				85					90					95					
Gln	Ser	Gly	Ala	Asn	Gly	Leu	Pro	Lys	His	Ser	Tyr	Trp	Leu	Asp	Leu				
			100					105					110						

Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe Leu Phe Val Tyr Phe  
115 120 125

Leu Pro  
130

<210> 524  
<211> 78  
<212> PRT  
<213> homo sapiens

<400> 524

Ile 1	Ser	Ala	Asn 5	Lys 5	Ser	Trp	Gln	Lys	Ile 10	His	Lys	Glu	Lys	His 15	His
His	Ile	Glu	Lys 20	Asp	Glu	Lys	Pro	Glu 25	Val	Gln	Pro	Val	Gly 30	Val	Phe
Gly	Lys	Pro 35	Ile	Cys	Pro	Arg	Leu 40	Arg	Pro	His	Ile	Glu 45	Val	Leu	Pro
Pro	Ser 50	Leu	Ala	Lys	Ala	Ser 55	Pro	Leu	Pro	Glu	Thr 60	Ile	Ser	Thr	Ile
Asn 65	Thr	Arg	Cys	Val	His 70	Leu	His	Leu	Ala	Pro 75	Ala	Ala	Ser		

<210> 525  
<211> 95  
<212> PRT  
<213> homo sapiens

<400> 525

Gly 1	Leu	Thr	Ser	Lys 5	Phe	Cys	Leu	Pro	Pro 10	Ser	Leu	Lys	Pro	Arg 15	Arg
Ser	Arg	Arg	Pro 20	Ser	Arg	Pro	Ser	Thr 25	Pro	Gly	Ala	Ser	Thr 30	Ser	Ile
Ser	Leu	Leu 35	Gln	Leu	Arg	Asn	Asn 40	Pro	Arg	Asn	Arg	Lys 45	Cys	Leu	Ser
Ser	Arg 50	Thr	Leu	Val	Phe	Ala 55	Ala	Pro	Glu	Thr	Glu 60	Arg	Ser	Pro	Ala
Ala 65	Cys	Ala	Val	Arg	Arg 70	Ala	Pro	Gly	Ser	Gly 75	Met	His	Ser	Glu	Pro 80
Thr	Leu	Pro	Ser	Ala 85	Gln	Ala	Pro	Gly	Ser 90	Ala	Phe	Arg	Cys	Leu 95	

<210> 526  
<211> 112  
<212> PRT  
<213> homo sapiens

<400> 526

Ser 1	Leu	Asn	Ser	Thr 5	Phe	Ser	Val	Leu	Pro 10	Gln	Lys	Phe	Pro	Gln 15	Phe
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

00673305.122700

Gln	Gln	His	Arg	Ala	Val	Tyr	Asn	Ser	Phe	Ser	Phe	Pro	Gly	Gln	Ala
			20					25					30		
Ala	Arg	Tyr	Pro	Trp	Met	Ala	Phe	Pro	Arg	Asn	Ser	Ile	Met	His	Leu
		35					40					45			
Asn	His	Thr	Ala	Asn	Pro	Thr	Ser	Asn	Ser	Asn	Phe	Leu	Asp	Leu	Asn
	50					55					60				
Leu	Pro	Pro	Gln	His	Asn	Thr	Gly	Leu	Gly	Gly	Ile	Pro	Val	Ala	Gly
65					70					75					80
Glu	Glu	Glu	Val	Lys	Val	Ser	Thr	Met	Pro	Leu	Ser	Thr	Ser	Ser	His
				85					90					95	
Ser	Leu	Gln	Gln	Gly	Gln	Gln	Pro	Thr	Ser	Leu	His	Thr	Thr	Val	Ala
			100					105					110		

<210> 527  
 <211> 72  
 <212> PRT  
 <213> homo sapiens

<400> 527

Arg	Phe	Arg	Pro	Cys	His	Cys	Gln	Pro	Leu	Pro	Ile	His	Tyr	Asn	Lys
1				5					10					15	
Asp	Ser	Ser	Leu	Gln	Val	Ser	Thr	Leu	Leu	Trp	Pro	Asp	Asn	Arg	Thr
			20					25					30		
Glu	Arg	Arg	Gly	Leu	Asp	Ser	Gly	Val	Leu	Ala	Trp	Ala	Thr	Gly	Phe
		35					40					45			
Leu	His	Asp	Ser	Phe	Met	Ile	Leu	Leu	Leu	Met	Tyr	Thr	Pro	Arg	Arg
	50					55					60				
Ala	Asn	Ile	Asn	Val	Pro	His	Ala								
65					70										

<210> 528  
 <211> 102  
 <212> PRT  
 <213> homo sapiens

<400> 528

Arg	Asn	His	Ala	Lys	Ile	Gln	Leu	Pro	Met	Gln	Ala	Pro	Gln	Ser	Leu
1				5					10					15	
Ile	Leu	Ser	Ser	Gln	Phe	Cys	Cys	Gln	Ala	Thr	Val	Val	Trp	Arg	Leu
			20					25					30		
Val	Gly	Cys	Cys	Pro	Cys	Cys	Asn	Glu	Trp	Glu	Glu	Val	Asp	Ser	Gly
		35					40					45			
Met	Val	Glu	Thr	Phe	Thr	Ser	Ser	Pro	Ala	Thr	Gly	Ile	Pro	Pro	
	50					55				60					
Arg	Pro	Val	Leu	Cys	Cys	Gly	Gly	Arg	Phe	Lys	Ser	Lys	Lys	Leu	Leu
65					70					75					80

0067305-122700



Phe Glu Val Gly Phe Ala Val Trp Phe Lys Cys Met Met Leu Leu Arg  
85 90 95

Gly Lys Ala Ile Gln Gly  
100

<210> 529

<400> 529

000

<210> 530

<400> 530

000

<210> 531

<211> 1708

<212> DNA

<213> homo sapiens

<400> 531

```

cctggaaca agatccaac ccaagtgacc ccgccgaaa gtgacccagt caggtttaaa 60
aatccaaca aacgcagctg aacaaataga ccgaccaacc aaatatcaa tccgtcaaaa 120
tacattcaat tccactacga aacccaaca aaggggtgta atgcccgcac aggagagacg 180
gttttggttt catcaagtgt gtggatcggt atgttcgtat gttcttccac tcagtgaaa 240
ttctggatgg gaaccagctc catattgcag atgaagtaga gtttactgtg gttcctgata 300
tgctctctgc tcaagaataa catgctatta ggattaaaaa acttcccaag ggcacgggtt 360
catttcattc ccattcagat caccgttttc tgggcacggt agaaaaagaa gccacttttt 420
ccaatcctaa aaccactagc ccaataaag gcaaaagaaa ggaggctgag gatggcata 480
tgcttatga tgactgtggg gtgaaactga ctattgcttt tcaagccaag gatgtggaag 540
gatctacttc tcttcaaata ggagataaagg ttgaatttag tattagtgc aaacagaggc 600
ctggacagca ggttgcaact tgtgtgcgac ttttaggtcg taattctaac tccaagaggc 660
tcttgggtta tgtgtgcaact ctgaaggata attttggatt tattgaaaca gccaatcatg 720
ataaggaaat ctttttccat tacagttagt tctctgggtga tgttgatagc ctggaactgg 780
gggacatggg cgagtatagc ttgtccaaag gcaaaaggcaa caaagtcagt gcagaaaaag 840
tgaacaaaaa acactcagtg aatggcatta ctgaggaagc tgatcccaac atttactctg 900
gcaaaagtaat tgcggccctg aggagtgttg atccaacaca gactgagtac caaggaatga 960
ttgagattgt ggaggagggg gatatgaaag gtgagggtcta tccatttggc atcgttggga 1020
tgggccaaca aggggattgc ctgcagaaag gggagagcgt caagtgtccaa tgggtgtcc 1080
tggggcaaaa tgcacaaact atggcttaca acatcacacc cctgcgcagg gccacagtg 1140
aatgtgtgaa agatcagttt ggcttcatta actatgaagt agggatagtc aagaagctc 1200
ttttccatgt gaaagaagtt caggatggca ttgagctaca ggcaggagat gaggtggagt 1260
tctcagtgat tcttaactcag cgcactggca agtgcagcgc ctgtaaatgt tggcgagtct 1320
gtgagggccc caagcgtctg gcagctcctc gacctgatcg gttggtcaat cgcttgaaga 1380
atatacactt ggatgatgac agtgcctctc gctaatggt tcttcgtcac caaaggggaa 1440
cagataaact aatgggggtt ggtgcagaaa gaaagatccg tcaagctggt gtcattgact 1500
aacacatcac acaagcaca ccattaatcc actatgatca agttgggggg aatctggtga 1560
agggttctga atctctcctt cttcctccct ccgaaatctt ggaatactta tcttattgag 1620
ctattacacc agttttaaca ctttctcgtt gttatgttta aaaaaataaa taaatttaag 1680
aaaaccattt taaataatga aaagttag 1708

```

<210> 532

<211> 2128

<212> DNA

<213> homo sapiens

<400> 532

```

ctgtatccta atttcttggt gaatgaactc attcttaaac agaagcaaa atttgaggaa 60
aagaggttca aatggacaca ctcagtgagt agccacaatg gccacaggtg gcagatat 120
caagatctgt tgggaaactga ccaagataac ctgtatttgg ccaatgtcaa tcttatgttg 180
gagttactag tgcagaagaa gaaacaactg gaagcagaat cacatgcagc ccaactacag 240

```

00673395.122700

```

attcttatgg aattcctcaa ggttgcaaga agaaataaga gagagcaact ggaacagatc 300
cagaaggagc taagtgtttt ggaagaggat attaagagag tgggaagaat ggtggctcta 360
tactctctgc tcaagtggga tagcacagtg cctcaatttg aagctctctc tccatcacac 420
agtagtatta ttgattccac agaatacagc caacctccag gtcttcagtg cagttctcag 480
acaaagaaac agcctttgta taatagcagc ttagcatcaa gacgaaaacg acttactgct 540
cattttgtag acttggaagc gtgttacttt tctacaagga tgtctctgat ctcagatgac 600
agtcgaactg caagccagtg ggaatgaatt caggaaatgct tgtccaagtt tactcgtatt 660
aattcagtag gaccttttag cacatttgca tatgctagtg atctctataa tgggtccagtg 720
atagctctca gttattgaatt tgaccgggat tgtgactatt ttgcgattgc tggagttaca 780
aagaagatta aagttctatga atatgacact gtcactccagg atgcagtgga tattcattac 840
cctgagaagt aaatgacctg caattcgaaa atcagctgta tcagtttggag tagttaccat 900
aagaacctgt tagctagcag tgattatgaa ggcactgtta ttttatggga tggattccac 960
ggacagaggt caaagggtcta tcaggagcat gagaagaggt gtgtggagtgt tgactttaat1020
ttgatggatc ctaaacctctt ggcttcagggt tctgatgatg caaaaagtga cgtgtggtct1080
accaacttag acaactcagt ggcaagcatt gaggcaagg cagatcactg tgtccactac1200
ttcagccctc cttccagata ccatttggct ttccgctgtg aaggacaccg taaagcagtc1260
tatgatcttc gtaacactaa acagccaatc atggtattca cctcaacaga cagtcagta1320
tcttatgcaa agttttgttag tggtaggaaa attgtctctg cctcaaggtca tatcaatgaal380
aaactctgga atgtatgggaa accatactgc ctacgttctc ctgttgggag tgaataatca1440
aaaaactctg taggctctgc ttccaatgga gattatagag taacttttaa gtttgataca1500
tctctctacc tgtactataa aggaactttct aagactttgc caaatgaatt tgttagtgct1560
gtgcaaaagt ttctgcagaa agaccgaaaa gaagatgata tgatttctgc taacagtcag1620
gtgtgtctga gggcactacc agatggggag tccaatgtgc caagtcaaat tgaacttgat1680
ggtaacaatt atgtgctaga attggtatga agggtttaac cagtgtatgt1740
ctctgtgaaa tacattgcga gctgacaatg agagaagaaa taattttttc tttttttctt1800
ctctccccaa agtcatcatg ggttttggat ttgttttgaa ccaactctcc accatcaatg1860
ttccctctct tatgaccttt gggacattgg gaataccagg tttttgtgat agggaaaaca1920
taactccatg gacatttgct ctcttgggtg tgttatctaa tattgagcca caaaaaaaa1980
attcttttga ataaaaataa ataaacaaac aataaaaagt tacgaaagt caatgtgtaa2040
aaaaaaaaaa aaaaaaaaac acaaaagaga aaaaaaaggt ccaacctctt tgggaattac2100
ctataatgta acagtgaata atttgtaag ttctgtatttc
acatacaat ataaacaaaa tataaagt

```

2128

- <210> 533  
 <211> 2640  
 <212> DNA  
 <213> homo sapiens

<400> 533

```

ctagcaagca ggttaaacgag ctttgtacaa acacacacag accaacacat ccggggatgg 60
ctgtgtgttg ttagtcagaga ggttgattaa acactcagtg tttgtgctct ctgtgccact 120
cctgggaaat aatgaattgtg gtaaggaaaca gttataaaga aaatgtgctct gctcactctg 180
gcactatata caaaagagct ggcagctcct gaaggaaaaa ggtgtgtgcc gtgcgcgttc 240
aaacttgtca gtcaactcat gccagcagcc tcagcgtctg cctcccccagc acacccctat 300
tatcatgtgt tgtctggcct gatctgtgca tctgctcggg gacgctctct acaagtccgg 360
aatttctcta tttctccact ggtgcaaaaga ggggatttct cctgtctctt ctctgtctac 420
ccccgtctct ctcccccagg aggtcctctg atttatggta gctttggagt gcttccccg 480
tctgactctg ctctgactct agaattggaag aagctgagct ggtgaaggga agactccagg 540
ccatccacaga taaaagaaaa atacagggaag aaatctcaca gaagcgtctg aaaaatagagg 600
aagacaaact aaagccacag catttgaaga aaaaaggcctt gagggagaaa cagcttctag 660
atggaattcag cagcggaaaa gaacagggaag agatgaagaa gcaaaatcaa caagaccagg 720
accagatcca ggttctagaaa caaagatctc tcaggcttga gaaagagatc caagactctg 780
aaaaagctga actgcacatc tcaacgaagg aagaggccat tttaaagaaa ctcaagtcaa 840
ttgagcggag aacagaagac attataaagt ctgtgaaagt ggaaagagca gaaagagcag 900
aagagtcaat tggagacatc tatgtcaata tccctgacct tccaaagtgc tacatacctt 960
ctaggtttaag gaaggagata aatgaagaaa aagaagatga tgaacaaatc agggaaagctt1020
tataatgcat ggaaattaaa gttgaaaaag acttgaagac ttggagaagt acagttctgt1080
cttccaatca ctctggccat cagatgactt taaaaggtag agggatgaaa gtttaagatg1140
atgggcaaaa gtcctcagtgta ttcaagtaag tgctaatgaa aagttggagg tcaatggcac1200
cgatggcctg gcaccaggtg aagtagagga acttctaaga caagcctcag agagaactct1260
taaatcccca acagagtatc atgagcctgt atatgccaat cctctttaca ggcctacaac1320

```

```

ccccagagaga gaaacgggtga cccctggacc aaactttcaa gaaaggataa agattaaaac1380
taatggactcg ggtatgtgtg taaatggaatc catacacaat atggggcaatg gtctttcaga1440
gggaaggggga aacaacttca atcacatcag tccattccg ccaatgctct atccccgatc1500
agtgtattcaa caagcagaag agaagcttca caccocgcaa aaaaggctaa tgactcctgt1560
gggaagaatcg aatgtctgc aggcacaaaga tgcacctct ccaaaagctaa ggctgagccc1620
cagagagaca atatttggga aatctgaaca ccagaattct tccccactt gtccaggagga1680
cgaggaagat gtcagatata atactgttca ttccctgctt ccagacataa atgatacaga1740
accgggtgaca atgattttca tggggatata gcaggcagaa gacagtgaag aagataaaga1800
gtttcttgaca ggatattgat ggatcatcca tgcgtgactg gttgtgattg atgatgagga1860
ggagggaggat gaaggagaag cagagaaaacc gtccatccac cccatagtca1920
ggtgtaccag ccagcccaaac caacaccact tccatagaaa agatcagaag atagtctctca1980
tgaaaaacaca aatcataaat cccccacaa aaattccata tctctgaaag agcaagaaga2040
aagcttaggc agccctgtcc accattcccc atttgtgct cagacaaact gagatgggac2100
tgaggatcca tctttaaag ctttaaggat gagaatggca aagctgggaa aaaagtgat2160
ctaagagttg tacccactat ataaccactc ttggaagaag aaactaagaa gcatttgcaa2220
atttctcttc tggatatttt gtttattttt tctgaagtcc aaaaaattat cattacagt2280
taccatatta agccattgtga ataatgtata gtcattatt gtgaaaaatt cccaaaaagc2340
tggggaaaaa aaatgtgtaa ctttccagt tacttgacac gattcagtg gggaaaaacca2400
gcatttttta ttctattgat accaaagcat ttctaataag agcttgttaa atttaagaat2460
aaagtatttt aaaaattctt gagtatagta tattaactgt cattgtaat ttgatgatac2520
aaagatgaa agatcatagg aaagcattgc cctctatcac aactctgaca2580
aataaatatg tcatcctgaa ttaataatgc cttaataaaa gtacatcctc ctgctaaaaa2640

```

<210> 534  
 <211> 1245  
 <212> DNA  
 <213> homo sapiens

<400> 534

```

tgcagcgcgt gcgtgctgcg ctactgagca gcgccatgga ggactctgaa gcactgggct 60
tcgaacacat gggcctcgat ccccggtccc ttccaggctgt caccgatctg ggctgggtgc 120
gacctacgct gatccaggag aaggccatcc cactggccctt agaagggaag gacctcctgg 180
ctcgggcccg catcgctccc ggggaagacg ccgcttatgc tattccgatg ctgcagctgt 240
tgctccatag gaagggcgaca ggtccgggtgg tagaacaggg agtgagagggc atgtgtcttg 300
ttcttaccaa ggaagctggca cggcaagcac agtccatgat tcagcagctg gctacctact 360
gtgctcgga tgtccgagtg gccaatgtct cagctgctga agactcagtc tctcagagag 420
ctgtgctgat ggagaagcca gatgtggtag tagggacccc atctcgcata ttaagccact 480
tgcagcaaga cagcctgaaa cttcgtgact cccctggagct tttggtgggt gacgaagctg 540
accttctttt ttcctttggc ttggaagaag agctcaagag agtctcttag tcaactgccc 600
cggtattacc aggcctttct catgtcagct acfittaacg aggcagctaca agcactcaag 660
gagctgatat tacataaacc ggttacctt aagttacagg agtcccagct gctctggcca 720
gaccagttac agcagtttca ggtggtctgt gagactgagg aagacaaatt cctcctgctg 780
tatgccccgt tcaagctgtc attgattcgg ggcaggtctc tgctctttgt caaacactta 840
gaacggagtt accgggtcacg cctgttcttg gaacagttca tgcctcccac ctgtgtgctc 900
aatggagagc ttccactgcg ctcagggtgc cacatcatct cacagttcaa ccaagcttcc 960
tacgactgtg tcatagcaac tgatgctgaa gtccctgggg cccocagctca acgggcaatg1020
cgaccocggc gacgagccaa aacgggggaca atggcctctc gattcctgga acgcacgggt1080
gtgcccctgg ggccactagc cttccaccat cgtgtctgca tgtgtctaac ttttgatctt1140
cccccccaac ccttgaggcc taacatccat ctagcttggc aggcagcaga cgcgctaaca1200
accagggca tagtgtctaa cttttgggtc ttccacagg aggcg

```

1245

<210> 535  
 <211> 822  
 <212> DNA  
 <213> homo sapiens

<400> 535

```

aagatcggtc tttgtcetta tccattactc tattotaatg gcagttagat gcnntttctt 60
agagggggca atgagacagc caggtgggaa ggggtcccca gagaactcc agcctgcaac120
ctgggaggag tgtgcactgg ggtgaagcca cgggaagttt gcgccatctc cagtggggaal80

```

gagccagcc	cctcctcttc	ctgggtggga	aactgogatt	caaactgcc	ggtgggaagt240
ccatggggc	gaacacggct	ctcgttttgc	taagagtcct	tggtttcccc	ttttttccct300
tatgccta	taataaattc	catttttttc	acocctcaaa	cagcctgtga	gcctaattt360
ttgtggccat	gggacagaca	aggaccccg	cttcagctga	actaaggaga	aagtccccaa420
acaatgggaa	gaagcagcgg	gagtagacat	ccaatttcct	ggcggtgatt	gtggagggg2480
accatggttc	tgaccacgat	tgtatcagga	gctgtgttgc	aggaagtctc	aggaatgaag540
ttgatagctt	ctcttcacat	acatgatgac	tgaaaagacg	aaggcatcta	atgagttaga600
gtcacaccat	ctcatgctcg	tatactatca	aacaaacttt	gggaagctag	ccttggttgg660
gaaaaacata	ttctcttaact	gaatgcctgg	atgcaagcaa	agtcctcatc	ttgatcatga720
tgaggtttac	cagtgtctct	tgacaggatc	ctgcaaacaa	accacaaatt	gctactatga780
catgcaactc	catggttaatt	tccttggata	gcaaatagct	cg	822

<210> 536  
 <211> 2703  
 <212> DNA  
 <213> homo sapiens

<400> 536

agttcgccac	agggggaggga	acctggccct	gggaggaggc	tggtgcgtgc	tcctagagaa	60
tcocgtctcg	aagggaagag	catgttttgcg	ggcgtcccca	ccatgogtga	gagctcccc	120
aaacagttaca	tgcagctctgg	aggcagggttc	ttgctgtgttc	tgatgttcat	gacctcctt	180
cacttttgagc	ccagcttctct	ttctattgtc	cagaaacatcg	tgngcagacn	gctcttgata	240
tttttnagtgg	ccatttggttt	taaaaccaa	ctggctgctt	tgactcttgt	tggtgtgctc	300
tttgccatca	acgtatattt	caacgccttc	tggaaccattc	cagctctgga	ngcccatgca	360
tgactctcct	gaaatacgac	ntctctccag	accatgtcgg	tgattggggg	cttgctcctg	420
gntggntgct	cctgggcccct	nggggggtgc	tcctatggatg	agaagaagaa	ggagtggtaa	480
cagtcacaga	tcctacacctg	ctcggcctna	agacccngtn	ggccgtcaag	gnactggntt	540
ctnggggttga	ttcaacnaaa	anctgnccag	ctttttnatgt	atcctctctc	cttccccctc	600
cgtgtgtaag	gcacagatgt	tttgagaanc	tttatttgca	gagacacctg	agaatnecat	660
ggncctcagt	tgctctggag	ccacagctctg	gcgtctgacc	cttcagtngc	aggccnagcc	720
gtgcanctg	gnaagcctc	cccnacgcc	gaggctttng	gnagtgaanc	agncccgctt	780
nggncgtg	catctcagt	ccntattttt	gagttttttt	gtgggggtan	ncaggagggg	840
gccttcaagc	tgactgtga	ngcagacgca	nttggtatta	tcattcaaa	cagctcccc	900
cttnatttgt	aagtttnaca	tttttnnagc	ggaaactact	aaattatttt	gggntgggtc	960
agccaaacct	caaaaacagt	aatctccctt	ggntttnaaa	atcacacacg	tggnctttng	1020
atgttgtttc	tgcccgcgat	tngtatttta	taggnnaata	gtgaaaacat	ttagggnaca	1080
cccaanagaa	tgatnccagt	attaaagggg	tggtagaagc	tgctgtttat	gataaaagt	1140
atcggtcaga	aaatcagctt	ggattnggtg	ccaagtgnnn	ttttatggg	taacacctgt	1200
ggagttttag	tagcttggag	caaggtggag	gggcaagaag	tccttgggga	agctcgtggt	1260
ctgggtttgt	ngctggccct	caagctggca	gtgggaaggg	ctagtngaga	ccacacangg	1320
ggtagcccm	agcagcagca	ccctgcaang	ccagcctngg	ccnagctnng	ctcnagacca	1380
gcnttngcag	angccgcagn	ccgctgttng	ggcangggg	tgtnngcagg	agctcccnag	1440
caetngnag	accacggagc	ntcaacccag	tnaacctcac	atggggccnt	ttctntgagc	1500
aaggtctncg	aaagcgcagg	ccgcccctgg	ctgagcagca	ccgccccttc	ccagctgcac	1560
tgccctgtgt	gacagcccg	acacacccan	ttctctngag	gctgtcgtc	actcagattg	1620
tcctgttctg	atgcggatgt	cagccaaaaa	ttccttttta	caatttgtga	tgccctaacg	1680
atttgatctt	aatcctgtat	ttaaagtttt	cttaacactgn	nccttaaaat	gtgtttctct	1740
ttttggggga	gcttaactgc	ttgttgctcc	ctgtcgtctn	gcacatcagt	aaatgccaca	1800
agggtagtgc	aacacactct	tgcccctcag	acctatctg	ggcagcagct	ctcagmctg	1860
ctcnccangg	gctgctggcg	cccagccccc	agcctgcctc	ccctctggnc	ctctcatcca	1920
ttggnctct	caggcgangg	ggtgaggcag	gtttctngcn	ctataagtc	tttnggaag	1980
tcacctacct	ttttaaacaca	gccgaactan	gtcccaacgc	gntttgcaaa	tattccccctn	2040
ggtagctcac	ctnccctanc	ccccgaanta	ttggttaagt	cgagcaatgg	nncttcagga	2100
ncatnnggtt	ctctttctct	gtgatcattn	caagtgtcca	ctcgnatnga	angactnggc	2160
ttgnctntca	atgttttcaa	ccctnaccag	ggcctgtctc	ttggtccacn	acctcgctcc	2220
ctgttagtgc	acgttagaac	cccccatcn	aaatgacgt	ggccnaaagt	ccanngtttc	2280
ctctggtgtn	aaggttggtt	ggctgattgg	tggaaanctn	aggggtngac	cnaaangagg	2340
gnccagctga	ngcagntcna	gcacanngt	tnctgcngtc	agcagcngcc	ctcgtnccta	2400
gtgggtgttn	cctngttttn	tnccctggccc	ntgggtnggg	ctnagggncc	tgattcgggg	2460
aangatgctt	ttgncanggg	aggggaggan	taagtgggat	ctacnaant	tnagattctgg	2520

09573395.122700

caaaaacaant ttctaagant ttttttgctt tatgtgggna aacagatcta aatctcattt2580  
 tatgctgtat tttatatcnt tnatgttgtg ttgaaacng tttntgattt ttggaaacac2640  
 atcaaaaataa ataattggcgt ttgttgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa2700  
 aaa 2703

<210> 537  
 <211> 2664  
 <212> DNA  
 <213> homo sapiens

<400> 537

ctcccaggga gtgctgagta gtgatggtgt ctggagggtc aaatccattc ccaatggcaa 60  
 aggttctcca ccaactccca ccgctacaac tccaaaaacca cttatcccta cagaggccag 120  
 catcagggtc tggggcaacga ggggcacgag ccatctccat ccccgaggca tctgtatgat 180  
 tcagaagtac aaccacgatg ggggaagcagg tgggctggag gcttttagcc aagggggaaa 240  
 ggtcctaaga gaacccaagt accaggaaga gctggaggac aggtctgcat ctacgttggg 300  
 ggaatgtgac tacttgacag gcttccagat cctgtgtgac ctgcacagat gcttctcttg 360  
 ctgaggcgcg aaggcgccag agctgtcaca agatgaatat tcaggggcggg gaataataac 420  
 cggggccctg ctacctgtgc cctaccatcg tggggaggcc ctgcatctgg ctgacatgct 480  
 attaaacaca gcttttggtc tctgtcacct gactgctcac agctctcttg tctgcccctt 540  
 gtcccttgggt gggagcctgg gectgcgacc cgagccacct gtcagcttcc ctaccctgca 600  
 ttatgatgcc actctgccc tccactgcag tgcactcctg gctacagccc tggacacagt 660  
 cactgttctt tatcgcctgt gttcctctcc agtttccatg gttcatctgg ctgacatgct 720  
 gaggcttctgt gggaaaaagg ttgtgacagc aggagcaatc atccctttcc ccttggctcc 780  
 aggcagcttc cttcctgatt ccttgatgca gtttggagg gcccacccat ggaaccccat 840  
 gctctcatgt ggggagcctt ctggaacacg ttgctttgcc cagtcagctgg tgcctgaggg 900  
 gctatagacag agcatgccc acaagccaca gaaccaaagg gacacctcca cctctgtccc 960  
 ttcactgatg tccacttggg gaagaaatct tggctcagta tttaacaacg caggcactgt1020  
 gactcatgag ttcttcccat ctgctgtgta ctccctgcag ggtggtctct ccttaacccc1080  
 acctctcttc aagctgcagt ccaccgggta tggttctgga tggttccccc aaggggagcag1140  
 tctcctctgt ttccctctccc ttccacagca gtggagagca tccacagtct tggggcactg1200  
 gtctctcttt cgtccctgca ccagaccctg gaagccttgg ccagagacct caccacact1260  
 gacttgccgc cgtgggcccag cttcatggat gctggagctg agccagatga cgtagcagag1320  
 ctgctgcagag agctacaagg cctggcccag tgcctaccag gtgtgtgacg cctcgtggac1380  
 taaagtctcc agtgtgggag aaaggagcta gtttgaata aaaacagctg gatgcaggag1440  
 cccagctgct tcatgcagag gagctcaatg tcgggggact agctacacca acatatgac1500  
 tttttacatt tagaaacact gtgattagac cacagaacaa taaatatgtg ccatcagacc1560  
 aaaaaaaagt agagaaagga gctgaactcc actctcgatg ctatttacc aggcacatctg1620  
 taaagtcttc ataaaagacc ttgaatgatg cttaggatgg cagagccccc gggctcact1680  
 ccatctcca gcccttggcc ttgtctctgg cctctgctct ccagatctgt aaactgggct1740  
 caaggactgt acaagcagag tacaactacc cctcccccgt tgcaggggcg cctgttgggt1800  
 ttggctcctgt gtatgatgatt cccagagctc tctgcatcct ctgcatcctc ctcatcctca1920  
 tccccatggt cagacagctg gtctgcattg ttgcactgat ctogaaaacg gtgggaaacc1980  
 gagctggcgt caccggcagt gtggaagagc ttgcatgatt tgaaggctct tggctgtgc2040  
 tcagcagggt tcttatttcc cagctgtctg gagatgatgt cggtagcttt caggacaacc2100  
 ccttgcctcc ggcacatggt gaggatcaca cgttagcttt ccgtagcttc tgcggcctt2160  
 ttttccccc ttgagctgac cttgctgttg ttggcacaca tgtcttttag caaaccccc2220  
 ggcctgtctg cccctctctg acccttggcc tggcttccac tgcattttagc cctcttagtg2280  
 ctaggggctt ttgggaagat cctctgagtg tcaattctct atggagattc atggacagg2340  
 cactgtcctg ctcttctctt caccctagct ctgcttgagg cgagccatct cctcttagtg2340  
 tctggtttcc cggacacatg tcttctctcc gcatctctgg tcttttgaga aacagcact2400  
 aggaaggaag cagggggttc caccgtacca ggcattttct ggcatttttc cagttttcga tgcattcccag2460  
 accagcatca aagcctctga ctcactcact ggccttttgg cctccctctc tttctgaagt2520  
 ctgggggatg ctttggggga ggagcgaacc tccagcccaa cctggtttct cttaacagt2580  
 tacagtacag cctcagttgt ggggggaaat ttgaggagct ctggtggaatg aggtggtggg2640  
 ccatccagga ggagccgttc tgta 2664

<210> 538  
 <211> 3888  
 <212> DNA

09673395-122700

gaattccgc	cgggaactgac	ggagcccaat	cggtgctggg	cggtgctggg	ggcacggagg	60
accggggcag	cgagcgccaag	cgaccccgag	cgagagcccg	gagccatggc	cctgagcgag	120
ctggcctggg	tcgcgtggct	cgaggagagc	cgccgctcgc	ggaagctcat	cgtgttcatc	180
gtgttctctg	cgetgctgct	ggacaacatg	ctgctcactg	tcgtggctcc	catcatccca	240
agttatctgt	acagcattaa	gcatagaga	aagtctacag	aaatccagac	ggccaggcca	300
gtgcacactg	cctccatctc	agacagcttc	cagagcatct	ttctctatta	tgataactcg	360
actatggtca	ccgggaatcg	taccagagac	ctgacacttc	atcagacccg	cacacagcac	420
atggtgacca	acgcgtccgc	tgttctctcc	gactgtccca	gtgaagacaa	agacctctcg	480
aatgaaaacg	tgcagtttgg	ttctgttttt	gcctcgaaag	ccaccgtcca	gctcatcacc	540
aacctttcca	taggactact	gaccaacaga	attggctatc	caattcccat	atttgcggga	600
ttctgcatca	tgtttgtctc	aacaattatg	tttgctctct	ccagcagcta	tgcttctctg	660
ctgattgcca	ggtcgtcgca	gggcacatggc	tcgtctctgt	cctctgtggc	tggaatgggc	720
atgcttgcca	gtgtctacac	agatgatgaa	gagagaggca	acgtcatggg	aatcgcttgg	780
ggaggctcgg	ccatgggggt	cttagtgggc	ccccctctcg	ggagtgtgct	ctatgagttt	840
gtggggaaga	cggtctcggt	cctggtgctg	gcgcctcctg	tactcttgga	tggaactatt	900
cagctctctg	tgtctccagc	gtcccgggtg	cagccagaga	gtcagaaggg	gacaccccca	960
accacgtctg	tgaagagacc	gtacatctct	attgctgcag	gctccatctc	ctttgcaaac	1020
atgggcatcg	ccatgcttga	gccagccctg	cccatctgga	tgtgtgagac	catgtgttcc	1080
cgaaaggagg	tgcgtggcgt	tgctctcttg	ccagctagta	ttctctatct	catctgggaa	1140
aatatttttg	ggatcatctg	acacaaaaat	gggaggtggc	tttctgctct	cttgggaatg	1200
ataattgtgt	gagtcagcat	tttatgtatt	coatttccaa	aaaacatttta	tggaactcata	1260
gctccgaact	ttggagttgg	ttttgcaaat	ggaatggtgg	attcgtcaat	gatgcctatc	1320
atgggctacc	tcgtgacact	ggggcacgtg	tcctgtctat	ggagtgtgta	cgccatctgg	1380
gatgtggcat	tttgtatggg	gtatgctata	ggtcctctct	ctgggtgggtg	tattgcaaaag	1440
gcaattggat	ttccatggct	catgacaaat	attgggataa	ttgatattct	ttttgcccct	1500
ctctggtttt	ttcttcgaag	tcacactgcc	aaagaagaaa	ctctggctct	ttctatggat	1560
cacaactgcc	ctattaaaac	aaaaatgtac	actcagaata	atatccagtc	atatccgata	1620
ggtagaagtg	aagaattctg	aagtgaactg	gatgagatcc	tcaaaaatca	tcaaaagtgt	1680
taattgtata	aaacagctgt	tcagtgacac	caactcatcc	agaaactgtc	tagcctacc	1740
atcatccctc	ggtagaagag	taaaaccaaa	ggttattatt	tccttcccat	ggttatggct	1800
gattgccaac	agccttataa	agaaaaagaa	gctttcttag	gggtttgtat	aaatagttgt	1860
gaaactttat	tttatgtatt	tcattttatt	aaatatcata	caatatattt	tgatgaaata	1920
ggatattgtg	aaatctataa	atacttgaat	ccaaaccaaa	tataattttt	taactttacat	1980
taacaaacat	ttggggcaaaa	atcatattgg	taatgagttg	ttaaaaattaa	agcacacatt	2040
atctctgaga	ctcttcccaac	aaagagaaac	tagaatgaag	ctcgaaaaac	agaatcaagt	2100
aaagacagca	gttatatagt	gacactgaat	gttatttaac	ttgtagttac	ctcatataata	2160
tttatcgctt	aaacagctag	ttctctcaag	tgtagaggac	aaagaactct	gtcagttatc	2220
ttttgaatcc	ataaactctta	gctggcattat	gttttctatg	taatcacctc	ctcagagaga	2280
gttgtaatac	atatgtttaac	atgtttatctg	gttggcagca	aacactaaag	ccaataaagg	2340
aaaaacagta	aatgttccga	aagcagagaa	aagcaaccac	acatatgtgt	atgaaactaaa	2400
agctttccct	ttaagatgca	tacttgtctt	actggatgaa	gaaaatttga	ggtagactgt	2460
ccttataact	tcaaggttgt	ttaaaacatg	taaggttaat	cgccactctac	ttcaagtttt	2520
agaaaaaggaa	acaagaagct	aaaaacagct	gctctgactt	taatatctga	ctatatcttt	2580
gactgttttg	caggtctcat	aagtgttttc	tgagaaatata	tttatttttg	gttgtctgaa	2640
actactaatt	tttagactcc	tgaagtgtgt	tcacatcaat	gtgaagacaa	atttttaagt	2700
aaaaatgaga	atgataaatt	gtcttgaatc	atataattag	aagtaaaaat	ataagtgtat	2760
aggcagaaaa	gaaaaatgga	acatctaaaa	atgtatgtgc	taactatata	atccagttgt	2820
cagtggttgt	tatttttcta	agcatgacaa	catgtatgtg	ctctttcagt	gtaaacagcaa	2880
atactgttag	tgaacattgt	caattttatg	cattttgtta	agagataatg	ctggagttgt	2940
cagtggtgaa	tgctctaatg	actacttgag	aatctctcag	ttctataatc	ataaacaaaa	3000
attacttagt	ttcgttaagc	taagatttgt	tttgtgttaa	cttcgacatc	aaggagcaaa	3060
gaactttaga	acagactcct	caatcttgtg	actttcttat	ttctctaggaa	agtaaacatt	3120
cgcttctaga	agctttttctg	tggggcttctg	attattttcaa	gtctgttttc	taagtgcagt	3180
gtgtttgaag	caaacgaact	tccaactcac	ttatttggca	ttggggcaact	tgggccaagt	3240
tgctacttgt	gaagatggct	ctggaggaaa	ctctcatata	gctcaaaaag	caggatgatt	3300
cttactttct	acaggggttag	agccttaaaa	aagaaactgc	tacaaaattg	ttctctttga	3360
gggtttcttg	ttctccctgc	ccccaatacc	atatacttta	ttgcaatttt	ttttttgcct	3420
ttacggctct	gtgtctttct	gcaagaagcg	ctggcaaaag	tatgcctctg	gttggctccc	3480
cgggataaga	taaaaatata	ataaaacctt	cagaaactgt	ctggagacaa	agatagcttg	3540

tacttgggga	aaaaaatctt	aagttctttt	atatgactaa	tattcttggg	tagcaagact3600
ggaagagggt	gtttttttta	aatgtacata	ccagaacaaa	gaacatacag	ctctctgaac3660
atttattttt	tgaaacagag	tggtttttat	gtttggacct	ggtaatacag	atacaaaaac3720
tttaattgag	tagcaaatgaa	tattcaactg	tttgactgct	aagtgtattc	gtccatattt3780
tagcaagttt	acttaataaaa	tcttctgaac	catgttttgg	gctgtgttgc	attcctttat3840
aaaccaaattg	ttgttgggaat	aaaatacata	aggtatcatt	ttgacctgt	3888

<210> 539  
 <211> 3304  
 <212> DNA  
 <213> homo sapiens

<400> 539

aaacccctct	ggctgtctgc	tgccacagga	gtcgccactc	ccttcattat	agccttgcct	60
agagtgcagc	ggcagggcct	gggtagggct	cgggagaggg	accacagagc	accagctcgc	120
atggaacttc	cttctccact	cagcttccca	cgttgccagc	tgggacagag	gagatggagt	180
aattttgcgt	tgaaagaact	tcacgtcttg	cggaatgaaa	gtcccgctgt	tctgtccagc	240
tgatgcccgt	gcagctgtct	gagcaccogg	aatggaatga	gtctatgcac	tcctctccga	300
tcagtgtggg	gggccttctc	gtcgtggcgt	ccatgaccaa	ggccggggac	ccccgtctcc	360
gcccccgctg	gaaggtgatc	ctgacgttct	ttgtgggtgc	tgccatcctc	tggtgtctct	420
gtcccccacg	cccgccccc	ggcagggccc	ccaccacaaa	tgccacacac	tgaggctctg	480
gccagcgccc	cgcccaactg	tacaatgaca	cctaccccc	gtctccccc	caaaggacac	540
cggctgggat	tcgggtatcg	atcgacgtta	tcgcagacct	ggacacagag	ccaaccgccc	600
aagacgaaaa	cacctggcgc	agcgacctga	aaaagggcta	cctgacctgt	tcagacagtg	660
gggacaaggt	ggccgtggaa	tgggacaaag	accatggggg	cctggagtcc	caactggcgg	720
agaaggggag	aggcatggag	ctatccgacc	tgattgtttt	caatgggaaa	ctctactccg	780
ttgatgaccg	gacgggggtc	gtctaccaga	tcgaaggcag	caaagccgtg	ccctgggtga	840
tctgttcgca	cggcgacggc	accgtggaga	aaggcttcaa	ggccgaatgg	ctggcagtga	900
aggacagagc	tctgtacgtg	ggcggcctgg	gcaaggagtg	gacgacacct	acgggtgatg	960
tggtgaacga	gaacccggag	tggtgaaggg	tggtgggcta	caaggcgagc	gtggaccacg	1020
agaactgggt	gtcccaactc	aacgcctcgc	gggtgtgtgc	cggtatccag	ctccgcagct	1080
acctcatcca	tcagttctgc	tgctggagtg	acacgtgca	gcgtgcgcg	cttctgcgcg	1140
gcccgcggag	ccagggagcg	tacagcgaga	aggacgcaga	gcgcaaggcg	gccaaacctgc	1200
tcctgagcgc	ctccccctgc	ttccgggaca	tcgtgtgtag	ccagctggcg	cggtgtgtcc	1260
ggactcacgg	cttctctgtc	ttcaagtcca	ttccccaac	cgacgaccag	atcattgtgg	1320
ccctcaaatc	cgaggaggag	agcggcagag	tcgcctctca	catcatggcc	ttcacgctgg	1380
acggggcgct	cctgttgcgc	gagaccaaga	tcgggaagcg	gaatacga	ggcatcgagt	1440
ctatttaact	caaaacggaa	acactgagca	aggccatcag	gactcagctt	ttataaaaa	1500
aagagagag	cactttttgt	ttgtttttgt	ctttttggaa	gtctgcctgt	gttggaggtc	1560
tggaacaggga	gcccagctcc	gggccccata	gttgtgctgg	cactggacc	ccggggccca	1620
cggaggccgc	gggtctgaac	gctttccatg	ctgccatctg	gttgtgat	cggtcactct	1680
aggtcatgac	tcaaagggctg	cctaactggc	tggtgtgttt	cttccatcct	acctcgtttt	1740
ttttctctcc	tatgtctctt	tgttcagtga	atatccctag	ctctctccac	atatgtcagg	1800
ccctatgctc	caccttgaga	acgcagtgag	catgaggtgg	acctgtttgc	tgggaaaccc	1860
aggtcacccc	cttttcttcc	caaaactggg	gccttggaa	aatcagggtc	agccctgaag	1920
atccttgggg	aagaaaaagt	ttatgttgca	gggtattgca	tggttcacgag	tgaggggcag	1980
gccccctggg	gacacatatg	cccacagctg	cacaggccag	gggcacagcg	acatctgtgt	2040
gtctctcagg	ctcagataaa	accatctccg	catcatatgg	ccagtgaccg	cttctccctt	2100
tcaagaataat	tctgtggcgt	tgacgtacct	tgaagtttta	attatataac	tgctttaatt	2160
aaagcagttt	cctttcttat	aaagtggaa	cacaaaaatc	tatcacacag	accacagctc	2220
tgtagttacc	ccaccgcgtc	cagcagtgcc	ggagattgta	aggaagcggg	ggcgctgtgt	2280
gaagcaagtg	tcagctgtgc	gcgttcttgg	ccaatggata	caaaagataa	gaaaatgttg	2340
cctttttcta	ggaactgtca	gaaatctcca	tgcccttcaa	gaactctctg	aatgaactga	2400
attttttatt	ccctgctgac	ggctgtgtga	cgaggcctgt	gtcttctctt	gggtttcttt	2460
ctatggcctt	tatttctctc	cttccagtg	gagttttgca	ctctctcttc	tggtgaaact	2520
tcacagaggt	tggtggggcc	tcgggtctgc	tgaggtgtac	tcacaggtga	aggcagagtg	2580
ggattttgga	cccaggttag	gcacgaccca	ggctgagaag	ggacgtttcc	atcattcaac	2640
gtgcctctcc	cacagacaac	acctcaaccc	gacccccacc	ctcactccta	ccccaccgcc	2700
cgactgtcag	gtgtgcacgc	gtgggcggga	gggtgcccgc	cttggctgtc	ccctgcgggt	2760
tcctccacaa	acctctcccc	ctttgaaact	caagcacagc	tgccagagg	gcagcgagga	2820
gggacccctc	tctcatgggt	gtctctttcc	ccgcctatgt	cataggtagt	ggagggaagc	2880

067335-2270

aaggaagtga acgctgaatg tgacgcattt ctgaagagct cagctgtcac cgggcatagc2940  
 ctggaagccc caagttgtgt ctgactttgc ctggctgtct ccttgaccgc cctccttagat3000  
 catgtccctt gaagctccagg ctgggtcatt taaaatagag atgcaatcag gaaggttggg3060  
 ggacttggga ctgctgcgtga attgagacct tgctgatgta ttcattgtcag caccctgagct3120  
 acagcccagg tgcctgggaag cagcctcttc gcattggcag tgatttgcga ttactttaaa3180  
 gctcaccctt tttctccccc tctctgttcg ctgctgtcag cataatgatt gtgttccctc3240  
 cctatgggat ccattctgtt tgtaaacaat aaagcgtctg agggagtgta aaaaaacagat3300  
 ggtat 3304

<210> 540  
 <211> 863  
 <212> DNA  
 <213> homo sapiens

<400> 540

caggattgaa acaagatggc ggggttcgtg tgagaagccg tcaaggagta gaaattggta 60  
 tgcctagaag cagattctaa aagcagtttc tcttcagaac atcttttttc ataccacttg120  
 ataagcatct tgaacacacca tggctgtgac tgcagtaaaa tgggtgatgt caaagagaac180  
 tatcttgaaa catttttttc cagtcacaaa tggagcttta tattgtgttt gtcataaatc240  
 tacgtattct cctctaccag atgactataa ttgcaacgta gagcttgctc tgacttctga300  
 tggcaggaca atagatgct accacccttc tgtggacatt ccatagaac acacaaaacc360  
 tatccctcgg ccagattcctg tgcataataa tgaagaaaca atgatcaag tgcgtgaaaac420  
 cagattggaa gaaaaagtg aacaccttga ggaaggacct catgtagaac aacttagcaa480  
 aatgtttctt actactaagg accgttggtg tccctatgga cgggtatcaca gatgtcgtaa540  
 gaattctgaa cctccaaaag acagatgtag cggaggttcc tgggggaatc aaagagaaat600  
 gtgcctcatt tgcattttga gaaaatgcag tctggtgtat tcagtaatat atagttaaagt660  
 aataatgata aatatctctt tcatatatta gaattgtgtac ttttataata agtaattctg720  
 gatttgacat tctcattttg agagacctat tctttttttc gttttctatt ttagtgtttc780  
 atttatgtgc ggtctccaat ttaggacctt tccatagtcg caaagccata catattcagt840  
 agaacatcaa taaaaaaaaa aaa 863

<210> 541  
 <211> 1962  
 <212> DNA  
 <213> homo sapiens

<400> 541

accagcggcc gcccttttct gtcttttttt tttttacatt tcaaatatat tttattactt 60  
 tccactcttag aagaatatg aaacctgcatt gcaatgctaa tgggttctga catgtacata 120  
 gcataataca cagcagatca atcgccgata tactgggggg cagtggtgtg agggggcggt 180  
 ccttaagggtta tatgtacaga ggaaggggcg catggtcatc tttagctttcg aaaggagact 240  
 gcactgttta acattgaaga attacatggg gaatcacaaa tatattgtct tagtactgca 300  
 tgttctgtgt tgggtgagga aagaaacatg ctttgaaggt tttcccttgt caacagaagt 360  
 tgtgtctgtg ctgtgtgtatt gcgcattgat tcatatattt ttaagttttc tcttaaggtt 420  
 ttgtgtgaca gtgttgggaa cctcacatgc ttctgaagca ttaaatattg aacctgtgaa 480  
 cctttcagaa atctccaggt tgggaaagac cccacacctt ctttaagggt catttgtctc 540  
 gccatcacag gatcttggaa atgtttccta ggggtgttaa aaattaacca gggggggaat 600  
 aagcacattt ttctggcaca caaacttgag ttctcagag aacagatgca gagagacctg 660  
 cctctgtctg cccggctaca gggggcactg tggagtcaca ctgaggctgt gaccggccat 720  
 aagcccagga gagcccgctg cagctgtgcc gaggcgccag gacctctaag cgggaagcttc 780  
 ccaagctagg aatggagcaa cactgcaatg aaatgtgtcc accaaagctca ttgttctctc 840  
 cgggcgctta taaagctcag atgtatagtg acgtatggac aaatacaaaa aaaaaaaa 900  
 aaaaaaaaaa aaaaaaagcc tttctttctc acaggcataa gacacataat atatatgtt 960  
 atgaagcact ttttaccac ggtcagtttt tacattttat agctgcgtgc gaaaggcttc1020  
 cagatgggag gagcctctct cttgtgtccc agacttcact acaggctgtc ttttatacaa1080  
 aaggggaaaa ctgactcctt tcttttttaa aaaatgcttt ttgttatttg tccatagctc1140  
 actatacatc tgcagctttat aagcccgccg gaggaacaaat gagcttgggtg gacacatttc1200  
 attgcagtgt tgcctccatc ctgacttggg aagcttccgc tttagaggtcc tggcgccctc1260  
 gcacagctgc cagggctctc cctgggctta tggccggtca cagcctcagt gtgactccac1320



```

agtggccccc gttagcgggc aagcaggagc aggtctctct ccatctgttc tctgaggaac1380
tcaagtttgg ttgcagaaaa aatgtgcttc attccccctt ggtaattttt tacacacctt1440
aggaaacatt tccaagatcc tgtgatggcg agacaaatga tccttaaaga aggtgtgggg1500
tctttcccaa cctcaggatt tctgaagggt tcacagggtt aatatttaat gcttcagaag1560
catgtgaggt tcccacacct gtcagcaaaa accttaggag aaaacttaaa atatatgaal1620
tacatgcgca atacacagct acagacacac attctgttga caagggaaaa ccttcaaaag1680
atgtttcttt ccttcacac aacagaacat gcagtactaa agcaatatat ttgtgattcc1740
ccatgtaatt cttcaatggt aaacagtgcg gtccctcttc gaaagctaa atgaccatgc1800
gccctttctt ctgtacatat accttaaga acgccccctt cacacactgc cccccagt1860
tacgaggga ttggtagcgg ctggtgttaa aatggctatg ggacatggtc aggaaccat1920
ttaggcattg gcattgaggg ttccataatc cgtttctaag ga 1962

```

<210> 542  
 <211> 1772  
 <212> DNA  
 <213> homo sapiens

<400> 542

```

tgggcgctgt agtccggcgg gaacctgttt gcgaccccca gtcccatgac accgcttctc 60
ctcaccccc agtcgcgagt gccctctccc agcctcgggc gggcctcccg ggagccgggc 120
gtggcgcttc agctagttag cgtttctctc cctgggctcg gaggcggaag cttgaggggc 180
gcggggagga gcttcgcgtg cggggtgaac gcccgctcta cgtcctcgtt ctcttcgcca 240
cgcgtgcgcg cgagcccgct gtcgccacgg cgggcagcag ccgccggcgg ggcggctgaa 300
cgcggaaggg gcggagggag cccgcggcgg cggcagcagc tacagcgaaa tggcgagagc 360
cgtggctgac acccgcgccc tgatcaccaa gccgcagaa cgtaatgacg cctacggacc 420
ccccagaac ttctcgcaga tcgatgtgag caaccgcga acggtggggg tcggccgggg 480
cgcgttcacc acttacgaaa tcagggtcaa gacaaatctt cctattttca agctgaaaga 540
attctactgt agaagaagat acagtgactt tgaatggctg cgaagtgaat tagaaaagga 600
gagcaaggtg gtatgtcccc cgtccctgg gaaagcgttt ttgctcagt tcctttttag 660
ggagatgatg gaattattga tgacaatttt attgagaaa gaaaacaagg cgtggagcag 720
tttataaaca aggtcgcgtg tcactctctg gcacagaaac aacgttgtct tcacatgttt 780
ttacaagatg aaataataga taaaagctat actccatcta aaataagaca tgccctgaaat 840
ttggcaagaa ggggcacaaa cgtgactatt aatgattgat aagcaccagt gaagaagttc 900
taacttttag catgctgcac agaaaactggt ataacatgcc ttcagttatc taacactcat 960
atgctcagtt ttgtttttgt ttggcagttg acaagaagtt aatttgcttt agtaaaaaat1020
cctcatccca gccctttctat ataaatagct ctttcttgct gttttaaatgt ggtgcacact1080
atagcctcac aaacctgtta ttccagtgtc attctgcagt tcgtaactaa agttactggc1140
ttggtcttat ttgcacagtt tttagctctt gtttgctctt tgcattctgat taactagaat1200
atttctcttt cctcccttta atttgtgat tcaactgacc ccatttatgt taggagcact1260
tacacattgt gtttcaatac ctgcacacat aagatacata cttgtgtgca gaaagatct1320
tcctcaggcg ttcttaatac cttcacatgg aagattaatg agggaaatct ttatatctct1380
tataaaaaaa aaagcaaat ttataactaa aatcatttgt ctataaaatt asgtttgttt1440
caataaaaaa taaaatgca tttctgatat gcactgattg tgtgtccctc agctttttt1500
gtctctcatg agtgactact taagtcaact gttagagagg attatttact aattatatac1560
ttctcatctc tgtaactcca ttccctttaa acagtgttga tatcaaat atctcccatc1620
attgaatggg gtatttttaa caacaacaaa agtgatatat taataaatgt atctcttaag1680
gcttatggaa ctattttgaa gcactttgtg tatttgaaaa ctgctttata atctcattta1740
ttaaaggagc ttcaaaagt aaaacacaaa aa 1772

```

<210> 543  
 <211> 1009  
 <212> DNA  
 <213> homo sapiens

<400> 543

```

ctcgtgcggt gatgttgagc agaagataca attcaaaaga gaaacagcca gtttgaact 60
gttaccccca cagcccgcaa ttgtggagat gaagaaagga agcaattggt atgttttcta 120
tctgagggca ggctcagaac agaaaggtca aatcatcaag gacatagatt ctggaagttc 180
agcagaggag gctggtctga agaacaatga tctggtagtt gctgtcaacg gcgagtcctg 240

```

ggaaacccctg	gatcatgaca	gtgtggtaga	aatgattaga	aaggggtggag	atcagacttc	300
actgtttggg	gtagacaaag	agacgggcaa	catgtacaga	ctggctcatt	tttctccatt	360
tctctactat	caaaagtcaag	aactgcccaa	tggctctgtc	aaggaggagc	cagctctcac	420
tcccaactct	ctgggaagct	caagtcacac	agatactaca	gaggaaagtag	atcacaagcc	480
taaaacttgc	aggtctggct	aagggtgaaa	tggctatggc	tttcaactaa	atgcgatctg	540
gggtctgcc	ggctcattca	tcaaaagaggt	acagaagggc	ggctctgctg	acttggctgg	600
gctagaggat	gaggatgtca	tcattgaagt	gaatgggggt	aatgtgctag	atgaacctta	660
tgagaaggtg	gtggatagaa	tccagagcag	tgggaagaat	gtcacacctc	tagtctgtgg	720
aaagaaggcc	tatgatattt	tccaagctaa	gaaaaatccct	attgttccct	ccctggctga	780
tgccagtctg	cagccctgca	ggttctaaa	aaggaaatag	ggtagagtag	aacctgact	840
cgcacatggc	aaaagaacgg	gcggctattg	cagacgggcta	atttatgctt	aacttaggaa	900
gagataaggt	tccttgagca	ccaaagatga	ttcataactc	tgtataaggt	acagctgctt	960
ataaaagcat	cttagcagat	aagcctatta	aaattgtgct	tttgaaca		1009

<210> 544  
 <211> 2834  
 <212> DNA  
 <213> homo sapiens

<400> 544

caactgttcgg	gcggccacttt	ttccagggtg	ttaatccagc	taatggagaa	ggatagatgc	60
acgtctaact	gttttagaaaa	aaaaacaaaa	atgagcaaac	gagacgcccc	ttccgtttta	120
tgataaactaa	gctgcaggga	aataaaatcgg	ctggccctac	tgcaactctac	tgcaactcgag	180
aaacatcaca	gaaaattctt	tgatttatct	taatatgtgac	aagtgagctc	gctctgtgtca	240
attactgaag	ctataaggag	atttttttaa	aattaaactt	caacacaaatg	aggtgtgtgcc	300
acatctgcga	acttctctggg	agagttaatg	ggattcgagt	gcttcgatta	tcttttggtgg	360
tcactctcgt	attattactg	gtagctgggtg	ctttgactgc	cttactctcc	agtgtttaaag	420
aagacaagat	gctcattgtg	cgtaggggaaa	taaaatcccc	gggcaagctcc	accatggact	480
ctcttactct	cataatgcag	acgtacacaa	gaacagatct	cttattgaaa	ctttttaaact	540
attatcaggc	tgtaaccaat	ctgcacaaag	tgattgtggt	atggaaacaat	attggagaga	600
aggcaccaga	tgaggttatgg	aattctctag	ggccccacc	tatccctgtg	atcttcaaac	660
aacagacagc	aaacaggatg	agaaatcgac	tccaggctct	tcttgaactg	gaaaccaatg	720
cagttgtgat	ggtagatgat	gacacactca	tcagcacccc	agacacttgt	tttgcctttct	780
cagtttgcca	gactaattct	gatcaaattg	taggatttgt	tcttagaag	caagctctcta	840
ctctcatcag	tatctacagt	tatggaagtt	ttgaaatgca	agcaccaggg	tctggaaatg	900
gtgaccagta	ctctatgggt	ctgattggag	cctcatctct	caatagcaaa	tatcttgaat	960
tatttcagag	gcaaacctgca	gctgtccatg	ctttgataga	tgatactcaa	aactgtgatgt	1020
atattgocat	gaattttatc	attgccaaag	atattggcaa	gacttcaggg	atatttgtga	1080
agcctgtaaa	catgggcaat	ttggaaaaag	aaaccaacag	tggtctattct	ggaatgtggc	1140
atcagactga	cagcgcctcg	cagaggtctt	attgtataaa	taagctgtgt	ataatcttat	1200
atagactgoc	cttaagatac	tccaacatta	tgatttccca	gttttggttt	ccatagtcca	1260
actacaaag	aaaaataata	aagtaaaaaca	acaaaaaaca	aacctgaaaa	ctgcttgga	1320
tttgagtgc	ttctccatgc	tatgtatttt	tttaagcaac	atcatgaatt	ttctactct	1380
cagaagtctc	tacaatagaa	aaaaaagtcg	agtgcttcta	ggatataaaa	ttcacattac	1440
ttttgaaag	caagaagtgt	gtcttatcca	gttaggtctt	ctttatgaag	gttttcatcc	1500
agggatataa	ctctcttggt	agtgtattta	ttgtttacat	cttgagactg	ttctacaggt	1560
tctttgactc	ctggcatgtg	ccttaaggac	ctatagcaag	ctgtttctag	gatcagaac	1620
tcaagagagg	catcttctct	cttttccact	aaaggtcagt	tggttttaatt	tgaaacctga	1680
aatgcctctt	tagcaaaaag	ctgtgggtatg	gggtaaaagg	atgtaaggag	agaaatgtct	1740
cagtcacata	tgaagaggaa	aatttgcagc	tgccagtgct	cttctttgtg	ccctgccaa	1800
cagctcttcc	aggacgaact	cagtcacagc	tggttttgat	tgaacacatc	atgcttttat	1860
ttttgttaag	tcttttgtga	ctgggacagt	taattttagt	agctgaagaa	cgtctagtgt	1920
tttgtgtgat	atttctgaac	atttactgca	tggatcacaa	aacaataatc	ctcgtatttc	1980
ttcacagcca	cttatatgca	gcaaggagta	aatgtgttac	tagattcggg	tagtgcattt	2040
tgctcactgaa	tctgaccttg	agaattgata	ttaatcttta	tattttactt	aatgtatgtg	2100
ttgttttaaga	aatgtatata	aaacctgaaa	aaaatgagta	agaaactgga	gaagttaaaa	2160
cccttttgtat	caaaaagatc	ttattggtag	agcaactggt	atctctgtga	tacttaaaa	2220
ttgtattaca	aaagccacaa	cttgacttca	caactttaaa	aaaagactca	aggaactatt	2280
cataatgatg	aaatccaac	tacatacaag	gaggagaaaa	taagaaccca	gtcataacag	2340
aggaattcta	taggaagctg	catcaattca	ttcttaaggt	ctgtactgtg	ctgttatgtg	2400
aattagcgtc	tggttttcc	ccattgtctg	tgtttagtcc	ttgttcacca	ctaaaggca	2460
gaattcttaa	ctaggcctct	gttttacaac	ttctctttct	ctctctttcc	ctctatttcc	2520

```

tctctctctt cttctctctt atataatgct agtatattct caaaattgca aagctgtgag2580
aatatataaa taatcatggc taatgtgccca ataattgaggt ctttgtgcac ttagttccgc2640
atatgatggt ttttttttta cattaaaagag tatatgtgtc ttaattgagc cagattgtaa2700
aaaaaiaaaa caaagaiaact aagaatctta ctaaaaatcg ataattgcag ttactgttt2760
tgtccaatat tggtagtact tttttgcctc ttatgatctc tctagcagat aaataaaaga2820
aacttttgcc atcc
2834

```

```

<210> 545
<211> 2319
<212> DNA
<213> homo sapiens

```

```

<400> 545

```

```

aacgtcattg gtaacagcaa gtcccagaca ccagccccc gttccgaagt ggttttggat 60
tcaaaagagac aagttgagag agaggaaaacc aaccatgaga tccaggagggg gaaagaagag 120
ctcagaggagg acaggctgccc gcaggagacca ggcggggagg aggtngtggga agacagacct 180
gtagggtgaaa gaggtcttcgg gggagccgga gaactggggc agaccccaca ggtgcaggct 240
gcctctgtcag tggagccagg aaaatccaga gatggagggc cctgaggcag accagcttgt 300
catcccgacg ggacaggagg aggagcagga agctggccggg gaaggggagaa accagcagaa 360
actgagagga gaagatgact acacatcgga tgaatatgaa cgagaactct agacagacaa 420
gcaagcagcc ctggcaggga atgacagaaa catagatgtt tttaattgtt aagatcagaa 480
aagagaaccc ataaatttac ttgatcagcg tgaagagcgg aatcatacac tctgaattga 540
actggaatca catatttcac aacaggggccg aagagatgac tataaaatgt tcatgaggga 600
ctgaatactg aaaactgtga aatgtactaa ataaaatgta catctgaang atgatattg 660
tgnaaatctt agtagcact ttgtgttaga aaaaatggna atnngtcttt taaacagctt 720
ttggggggnt actttnggaa gtgtctnaat aanggtgtca cnaatttttg gntagtang 780
tatttctgta gnaagnnttc aacacacaaa ctnggaacat agttctctct caagtgtgtg 840
cgacangcgg nngcttctg attctggaa ataaacttgt gtaaaattaac agccaacct 900
agaagagtcc acttgcctgt aaggagagac agagaactct gggttccgct gtctcttcca 960
cgtgctgtac caatgtctgg tgcagcctg ttacctgttc tcaactgaaa gtctggctaa1020
tgtctctgtg tagtcaactc tgattctgac aatcaatcaa tcaatggnc ttagangcact1080
gactgttaac acaaaactga ctagncaaa tagncaacna gctttaaagt taaatacaaa1140
gctgttctgt gtgagaattt tttaaaaggc tacttgtata ataacctctt tcatttttaa1200
tgtacaaaac gctattaagt ggcttagaatt ttgaacattt gtgntcttt attactttgt1260
cttncgtgtg tggggcaaac aacatcttcc ctaaaatat attaccaaga aaangcaga1320
agcagattag gntttttgac nnaaaacana acaggccnna aaagggggcn tgnacctgga1380
gcagagcatt gtgnagaggc aaggcatgna gagggcaagt ttgtttgga cagactgtgt1440
cctactttat tactgtgagt aaangaaaaa aaagttncat tgatctcgna aggatata1500
cagtgcttnag aaattnnagg nactngtttn agaaaacag gaatcnnaa tgnnttgn1560
tttatcatan gtgntacaca tttagcttgt ggnataatng actcacaaaa ctgantttta1620
aaatcaagtt atgtgaatt ttgaaaatta ctacttaac ctaattcaca atacaatgg1680
cattaaggtt tgacttgagt tggttcttag tattatttat ggtaaatagg ctcttaccac1740
tgcnaaata actggnccac atcattaagt actgaactcc cnagtaang ctctctaagg1800
ggtaagtnag gaggatccac aggatttgag atgctaaagg cccagagatc gtttgatncc1860
aacctcttta ttttcnagag gggaaaatgg ggctnagna agttacanga ccatcnnag1920
cntgtggcgc tttccncccc ntggccntcn acacnagact ccngagtag ctgggancta1980
caggcacaca gtcactgaag caggcccntg ttgtcaattc actgtggcna cctnccaacn2040
ttaaacattn ctcatatgt gatgtcttta gtcacntaag gtttaanctt tnccccacca2100
gaaaaggcaa cttagataaa atcttagagt actttcatc tcttctaang tctctctcca2160
gcctcaactt gactcctcct tnggggttga tnnnaggaa ttctctctgc ttctcaata2220
aagtcctcat tcatctcatg tttaatttgt acgcatagaa ttgctgagaa ataaaaatgt2280
ctgttcaact tannnnnaaa aaaaaaana aaaaaaaa
2319

```

```

<210> 546
<211> 2456
<212> DNA
<213> homo sapiens

```

```

<400> 546

```

00673305-122700

tgcaactgtg	caccagcatt	gccagatttt	tccccattac	acccccagtg	tggcataatcc	60
ttggttcccc	gaggcacacc	ccttgatctg	tggaccccca	ggcctggaca	agagggctgct	120
accagaaaac	ccaggccccc	gttactcaaa	ttcacagcca	gtgtgggttg	gcttgactccc	180
tcgccagccc	ctggaaacac	atccacctgg	ggagggggcct	ctgtaagtga	gttctgacac	240
cgagaggggc	aggccatgcc	cttatccgca	ctgccaggtg	ctgtcgccccc	agcctggctc	300
agagggaggaa	ctgcaggagc	tgtgtgaaca	ggctgtgtga	gatgttcagg	ctcagctcca	360
accaagatgt	tgtccagat	gtgttggggc	cctaacttgg	cacagagctc	tgtctctggg	420
aaaggaaagg	accacagcaa	acaccattct	ttttgccgta	cttctcagaa	gcactgggaag	480
aggactgggt	atggtgggag	gggtgagagg	tgcctgtttc	ctgtctccag	tccagacctt	540
ctgtgcagaa	aacattctga	gtgcagcaaa	tccatgtcca	gccagggcaac	cagctgtctgc	600
ctgtggcgctg	tgtgggctgg	atcccttgaa	ggctgagttt	ttgaggcgag	aaagctagct	660
atgggttagcc	agggctttaca	aagggtgctg	tcctctccca	acccctcatc	ggttctctctc	720
accccaagcc	tcattgttcat	accagccagt	gggttcagca	gaacgcata	caecttatca	780
cctccctcct	tgggtgagct	ctgaacacca	gctttggccc	ctccacagta	aggctgctac	840
attcaggggc	aaccctgggc	tctatcattt	tccttttttg	ccaaaaggac	cagtagcata	900
gggtgagcct	gagcactaaa	aggaggggtc	ctggaagctt	tcccactata	gtgtggagtt	960
ctgtccctga	gggtgggtaca	gcagcctgtg	ttcctctggg	gggttgagaat	aagaataagt	1020
ggggagggaaa	aactcctcct	tgaagatttc	ctgtctcaga	gtcccagaga	ggtagaagg	1080
aggaatttct	gctggacttc	atctggggcag	aggaaggatg	gaatgaagg	agaaaaggc	1140
gaattacagc	tgagcgggga	caacaaaagg	ttcttctctg	ggaaaagttt	tgctcttagag	1200
caaggatgga	aaatggggac	aacaaaaggaa	aagcaaaagt	tgacctttgt	gtttggacag	1260
cccgagggcc	cagctcccca	gtataaggcca	tacaggccag	ggaccacagc	gagagtggat	1320
tagagcacaa	gtctggcctc	actgagtgga	caagagctga	tgggctctcat	cagggtgacal	1380
ttccaccagc	ggcagctcga	ccactcttgg	ccctccaggc	attatcccat	tgtgaattgt	1440
aatgtgtgtg	caaaagtggc	agagggaccc	acctgggaac	cttttccctc	cagttagtgg	1500
ggagactagc	acctaggtag	ccacatgggt	atttatattc	gaaccagaca	gaagcttgaal	1560
tcaggccta	tgttaagaaa	tatatattat	tgctaata	tttatccaca	aatgtgtgtc	1620
ggctctgtgg	ttctgtctgt	tgtgtactgt	cactcagggt	aacaaagctc	tcctctttctal	1680
catcaagaga	agtaaatatt	ttatgtttac	agaggctagg	ctccgattcca	tgaaaggata	1740
gggttagagta	gaggggcttg	caataaagaa	tgtgtttgaa	gcocctaaaa	gtgtggcttal	1800
gtgagatcag	gggaaggaga	agcatgactg	gattcttact	gtgcttcagt	caattattatt	1860
atactgttca	cttcacacat	tatcataact	cagtgactca	gaacctggggc	aaactactctg	1920
tgcctcgcct	tttcagttca	taaaatgggc	ctacttaata	gtgttggcag	gaacttaacat	1980
agataaataga	gtgtagaaaa	tatgttccaa	agtggaaggt	tttattcagt	gatagaaaac	2040
atccaaaact	gtcacagagc	ccatctgaac	acagcatggg	accgccaaca	agaaagaaagc	2100
ccgcccgga	gcagctcaat	caggaggctg	ggctggaaat	acagcgcagc	ggggccctgaa	2160
actatttata	tcccaaagct	cctctcagat	aaacacaaat	gactgtcgct	tgccctgcact	2220
cgggctattg	cgaggacaga	gagctggctg	tcactttggc	tgaagctctc	agggccagaa	2280
ggggcctttg	tgccttctc	acaaggcaca	agttcccttc	ctgcttcccc	gagaaagggt	2340
tggtaggggt	gggtgggttag	tgctataga	acaaggcatt	tcgcttctca	cagcgttgaaa	2400
tgaaaaggaa	aaaaaggaca	cctaattctc	tacaaatggt	cttttagtaaa	ggaacc	2456

&lt;210&gt; 547

&lt;211&gt; 2218

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 547

gaggaaaaaag	aacaatgaac	agcaacgcat	ttgactgtgc	aactcagaca	ttcctgcaga	60
aaagacatat	gttgctttac	aagaaggcca	agaacactatg	ggcctttccc	agcattttgc	120
tgttcatttg	atagaatgaa	ttaaatatcc	agttacttga	atgggtataaa	cgcatgaagt	180
tgtgatttta	ttaggggcac	ctgccaatcc	ttcactgtg	gttctctctc	tgaactttgc	240
tgttcatcat	ctaaggagcc	tagatctctc	gttgactctca	ccattctcca	aacctgttaag	300
ttttctcaatt	cttccaattt	ggctttggct	cttctctcaa	cttttccaat	caagagcaat	360
ctttgtctaa	gagttaagta	atgtgaagag	taccaactac	aacaattcta	cagataatta	420
tgggattttg	tgttttggg	agagtgaagg	ttctttggca	ttctgtgtct	gattaaaggt	480
tgaagtattga	gtttctagca	tattctctca	ttgtcttgac	ttctgttgc	tgactttctc	540
atgtgtcgtt	cgtgacttgg	agaacttaaa	gtaatcgagc	tatgcctaac	tggggttgga	600
acagagtact	tcccaccaca	gtgttgaaag	ggagagcaaa	gtctcttgga	taaacctctc	660
tttcttttgg	ggacacatgt	ctctcacttg	agaagctcac	ctgtgtctgaa	tgtccacatg	720
gtcataaacc	atgttatctc	taaaaccccc	gtagtcctga	gttgaaaggg	ctctctctta	780

```

ttagggttttc atgggaaacat gaggcagcaa atctattgct aagactttac caggctcaaa 840
tcactctgagg ctgatagata ttgacttgg taagacttaa gtaaggctct ggctccagg 900
ggcataagca acagtttctt gaatgtgcc tctgagaagg gagaccagg ttatgagtt 960
tcctttgaac acattggctt ttctcctaa ttctgctct gctagactct tagctctttg1020
aggacaggga ctttgcttta tcaatcacta ttatttccct gttactagtc atgggacaag1080
tacacaacac atatttgggt agtcttctaa aagactcctc tgattggggag accatatct1140
taattgggct gtgaactcatt tcttcagtg aataaagaca caacggccaca acctcaagg1200
acatatattc tactatgaac attttactgt gagactcttt attttgcctt ctacttgcgc1260
tgaatgagaa ccaaaacagg ccgttggggt ccacaagtca atatatgtg gatgaggatt1320
ctgtgtccct attgggaaact gtgagactta ttgggtatga gaagccagta ataaaccttt1380
gacctgtttt accctaagaa gatttatgaat atgttaatat gatgtaaatt gctatttaag1440
tgtaaaagca tttaaatgtt tagtatttgg gggattgggt ttattatttt ttctctcttt1500
tgaaaaatac tgagggatct ttgtataaag ttagttaatgc atgttagatt ttagttttgc1560
aagcatgttg tttttcaaat atatcaagta tagaaaaagg taaaacagtt aagaaggaa1620
gcaattatat tattcttctg tagttaagca aacactgtt gaggctctgc tatgtgcacg1680
gcatgggccc atatgtgtga ggagcttgtc taattatgta ggaagcaata gatctcggt1740
gttacgtatt gggcagatag ttactgtatg aatgaaagaa catcacagta atcacaat1800
cagagcttag ttattccccag tbtactctgc ttggggattc cagtttctgg gaacgagag1860
tagggccatt ttttttaaaa gaaactcccg gttctatga gtctctatga acctctgaa1920
cgtacaagcc ttcaacaagt taactaaatt gggattaatc ttctgttagt tatctgcata1980
cttctgtttt ttctttccat ctggctcctg ggttgacaat ttgtggaaac atccttatgt2040
ctactattta aaaaaataca gaaattcttc cctttaagct atgtttaaatt caaactattc2100
ctgctatctc tgttttgtca aagaattata tttttcaaaa atgtgttatt ttgttgag2160
gtcccaggaa acactaataa aaaccacaga gaccagcccc aaaaaaaaaa aagttttg 2218

```

&lt;210&gt; 548

&lt;211&gt; 2196

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 548

```

cggcgcgatg cgcggagacc cccgcggggg cggcgggcgc cgtgagcccc gatgagggcc 60
gagcgtcccc ggcgcgcggg cagcgccccc ggcccgatgg agacccccgc gtagggacca 120
gcccgcaacg actcgcctgc gccccacgtg acccgcgccg tgccccccca cgtgaagctt 180
ggcctcaccc tgcgtctcac cgtgtcttac gcgtgctctc tctgttctat ctacgtgcag 240
ctctgctggg tgcctgcgtta ccgcacaaag cggctcagct accagagcgt ctctctcttt 300
ctctgcctct tctgggcctc gctcctcttc ttctggctct cctcttactt caaagacttc 360
ctggcgcgca attcgcctcag cccttcgctc ttctggctct cctactctgt cctctgtgctc 420
ctgcagtttt ttaccctcac gctgatgaac ttgatctca cgcaggtgat ttccaaagcc 480
aagtcacaaat attctccaga attactcaaa taacgggtgc cctctactac ggctcccttc 540
ttcatcagcc ttgttttctc gttggtgaat ttaacctgtg ctgtgctggt aaagacggga 600
aattggggaga ggaaggttat cgtctctgtg cgagtggcca ttaatgacac gctcttcgtg 660
ctgtgtgcgc tctctctctc catctgtctc taacaaatct ctaagatcgt ctgaccaacc 720
atttacttgg agtccaaggg cctctccgtg tgtcaagtga ctgccatcgt tgtcacctgt 780
atactgcttt acacctcttg ggctcgtcac aaacctgttc tctgtctatt ttctcagaac 840
aagacgcttc attctcttga ttatgaactg tacaatgtat cagacccagg agatttgcag 900
aatcagctgg gagatgctgg atacgttata ttggagtggt tgttatttgt ttgggaactc 960
ttacttacca ccttagtctgt ttatttcttc cgaagttagaa atctctcaaa ggaccttacc1020
aaccttgaaa tgggtcccaag ccatggattc agtccagat ctatttcttt tgacaaccc1080
cgaagatgat acagtgtatg tgaccttgcc tggaaacatt gcctcaggg atctcaggga1140
ggttttgcct cagatttacta tgattgggga caacaaacta acagcttccgt ggcacaagca1200
ggaactctgc aaagactcaaa ctttggatcc tgacaaacca agccttgcgt agcatcagtt1260
aacagtttta tggacgatcc ctacagatga aagcttcaga aaagcatagt gacagctgaa1320
tttttagggc acttttccct aagaaataga acttgatttt tattttgtac aggttccaal1380
tgccccataa ggaataagca ataatgtaga ctgataaacc ctctatttag tactaaagag1440
ggagcctgtg tatttccagt ggtataattt aaacttttta aagaaaaact gtacttttat1500
aaagatgtat ttgtataat ttaataataa atgctaaagt atactagggg tttttttctt1560
tgagaatggt actgcaatca tgttttagtt tgcacagact ttatgcata attcaactta1620
aaaaatagga atatatgttc taatagtttt ttaaacagtt ttgactaaag tattccaaal1680
atcttaccct ttttagtccac tcatggtcac tccgattctg agtgcacat ttgtagactc1740
ctaaaaatac gttgacaact tagccaattg caactccagt gttgataatt aaaaatgaa1800

```

```

ggtaaacgag cagactgttaa ggtcttttaga gatttttttt ttaagggttca ggcgcgtaggt1860
tcctcaagga atctctttaag ttttgcccaa agactgtgtac ttccctttcag tagggcgctal1920
atgtatacac attaatgtata agttgataac attaaaaatg tagctgactt atccattat1980
acccctccctg ctatgtctcag agaaccoccaa taactttttt tcagcctaact gaaatctaat2040
atgcattacc tcaggggccac atcaagaata caccoccttcc gaatgttcat2100
tacattcaag gagaaaaataa gaggggtccat aaaggggcatt aataacaaat accccaagcc2160
gttgagctaa gactatgtgg aatccctaata gttttt

```

2196

<210> 549  
 <211> 701  
 <212> DNA  
 <213> homo sapiens

<400> 549

```

aattaaaaata aatagaaaaaa tacggagatt cttttatggt ggatttatta tacctccac 60
catttttggtc cctgaaaagg gaaaagatac acggtcgagt agtacaggta tgtgtttccc120
atcacacatt atggactataa tggagttgaa ttgcaaacag ttagcttattg tttggattg180
gtttccctctg atccccccag acaggagctt cctctcccac cctacctgcc tgccttaag240
ttgtgtccta ttaacttggg cacaatctc acgggctttt agtctaataa ttgaatcata300
gtcacacaca gtgacaccag aatagctact tgttttttta tgttaccagt gagtaactgt360
tttatcctgt tatgtgaaaa ctaatttcac catgtgtgta acatctctag420
tttgaatttc cacacaattt taaaatgtct actagaaaac ttacaccttt ttgtccaag480
gtgctctcta tctataaaac cgtggggata cttcagtgtt cttctgagge caaattttgt540
gggtcgttggg ggacaatttt gtattaacat acgttatttt gtaattcatt ctccaaattt600
gaagctttat taaaggattt ctattccac tggtctccct taacttgaat aaaatttact660
cccagtgccg tggctcatgc ctgctgcaat cccagccctt t

```

701

<210> 550  
 <211> 2214  
 <212> DNA  
 <213> homo sapiens

<400> 550

```

gctaaagagg aggatgctat acttttctaa atggcaagag atggggagag aaggggatta 60
agatttgacc cgcgaacctcc cgttggtattc tttgttctta ccagatctct tggccactcc 120
cctattctga agtgcctctg gctctcttga ctgctccccct attctgaagt cgtcttggtc 180
ctcttgacta ctccccatt ctgaagtcgt cttggtctct cgtactacac tatttcaagg 240
aatgatcacc aagacacaca aagtagacct tgggtcccca gagaagaaaa agaagaagaa 300
agtggtcaaa gaaccataag ctcgatactc agttttaaac aatgatgatt actttgctga 360
tgtttctctt ttaagacta catccccctc ntaagagtgt ggcccatggg caggccactg 420
agatgcctct agtgaagaaa aagaagaagg tgcagcacc ctttgcaggg 480
agcatgtaga acctgagacc acgctgcctg ctagacggac agagaagtca cccagctca 540
gggaagcaggt gtttgcccac ttggagttcc tcagtgggga aaagaaaaaa taagaagta 600
cctatagcca tgtcccatgc ctctgggggt aaaaacctcc cgtgagggc agcgaggcca 660
aggagaaac cagagtctgc aagaagctca aaaaancaca agaagggaaa aaagggggnc 720
ccaggacccc acnagccttc tcggtccagg acccttggtt ctgtgagggc agggaggcca 780
gggattgttg ggacacttgc tncagttggg aagaagatg aggaacagcg agccttgagg 840
ncagaaaacg aagncggaag agccccagag aacacaatg gaaggtgaag aagaaaaaaa 900
aaatccacca ggagggagat gccctccag gccactccaa gcctccagg tccattgaga 960
gcagccctag gaaaggaagt aaaaagaagc cagtcaaat gaggctcccg gaatacatcc1020
ccataagtga tgacctcaag tctctcgcaa agaaaaagat gaagtccaaa aagaaggtag1080
agcagccagt catcgaggag ccagctctga aaaggaagac gaggagaaga aggaagagag1140
gtgggttagc aggaagacct tggaggggag aaacagacac ggacttagag tgggtgttgg1200
aaaaaaaagg caacatggat gaggcgacac tagaccaggt gaggcgaaag gccttccaag1260
aagaatctga tcgcagatca ggcaaaaacg aagcttctga aaccaggaag tgggtggaa1320
cccagtttgg ccagttgggt actgctggtt ttgagaacga ggaccaaaaa ctaaatcttc1380
tcagacttat ggggtgccttc aaaaacctgt ccccttcgtt cagccgcccc gccagcacga1440
ttgcaaggcc caacatggcc ctcggaaga aggcggctga cagcctgcag cagaatctgc1500
agcgggacta cgaccgggcc atgagcttgg aagtacagcc ggggagccgg cttgcgggtg1560

```

tctccacgcg	ccccaaacag	atctttttaca	ttgacaggaa	cgcttccaag	tcagtcacagc1620
tggaagatta	aactcttagag	ttttgtcccc	ccaaaactgc	cacaattgct	ttgattattc1680
catttatgct	ggagattaca	aatttttttt	ggatgaacaaa	tcagatctttg	gtggggacct1740
cgagcgagtaa	gatataataa	actcccnata	agcttagncg	ttcccagtaa	tggaacacta1800
ggcataaant	gttttattnc	agttgtgcac	atgaaagcca	tctgacagtt	ggctncacat1860
tgaacacctg	tggaagattaa	ggacgaggac	aactatatgt	atgggcttgg	atgaactggg1920
gcagggcagc	tcattttttg	ggagccaggga	gaacgagtg	gtgctaaaaa	ctcctgtttt1980
ctgtgttaaa	cattccgtgc	ctgttttgaga	catcagtatg	tacagttaac	ttttgttgag2040
tgttttagca	gtactaggga	catactagtgt	ttttccctaa	tgtatttaac	cttcataatt2100
atgaatatggg	tgtctattatt	agcccatct	tatagatgag	gcaactgagg	ttcagggata2160
aagtaataaaa	attgcctggg	gtcaccacag	cactaaaaaa	aaaaa	2214

<210> 551  
 <211> 1434  
 <212> DNA  
 <213> homo sapiens

<400> 551

gcgcggccgg	cgctctcggg	gcgagagggg	cggggcgaag	gggaagctac	gtcccgagg	60
tcgcggtgtg	ggcaccgggg	ggggccgccc	gaaccggcgc	cccacggagc	tgctgtgtgc	120
agaccaaccc	cgggccccc	tcatactctg	gcgcgcgttt	caggcgccga	gaactacogt	180
tcccggcatg	ccatgaaatt	ggcctcggcg	ctgaggcggg	gtccggccct	ccaccgcctc	240
ccgcgcgcgc	cgaattcgccg	tcgcgagcca	tgaggaggga	ggcatcgtcc	ccggggctcg	300
gctgcagcaa	ggcgcacctg	gagaagctga	ccctgggcat	cacgcgcctc	ctagaattctt	360
ccccagtggt	gactgaggtg	accatcatag	aaaagccctcc	tgctgaacgt	catatgattt	420
cttctctggga	acaaaaagaat	aactgtgtga	tgcttgaaga	tgtgaagaac	ttttacctga	480
tgaccaatgt	cttccacatg	acatggagtg	tgaagctgga	tgagcacatc	atccactgtg	540
gaagcatggc	aatttaacagc	atctcaaaac	tgactcagct	caccagctgt	tcocatgatt	600
cacttctctaa	tgacccactc	ctggcagacc	tgaggagcga	tacacatgaa	gccagtgtat	660
atcagccaga	gaagcctcac	tttgactctc	gcagtggtat	atgttagctg	gattcatgca	720
atggcagtg	gaaggtttgc	cttgtctaca	aaagtgggaa	accagcatta	gcagaagaca	780
ctgagatctg	gttctctgac	agagcgttat	actggcattt	tctcacagac	acctttactg	840
cctattacgc	gtctctctac	acccaactgg	gcctgcccca	gtggcaatat	gccttaccac	900
gctatggcat	tagccacagc	gccaaagcat	gggttcagcat	gtataaacct	atcacctaca	960
acacaaacct	gctcacagaa	gagaccgact	cccttgtgaa	taagctagat	ccagcaaaag1020	
tgtttaagag	caagaacaag	atcgtaatcc	caaaaaagaa	agggcctgtg	cagcctgcag1080	
gtggccagaa	agggccctcca	ggaccctccg	gtccctccac	ttcctccact	tctaattcct1140	
ccctctggctc	tggaiaaccc	accoggaagt	gagcaccctc	ccctcccaat	ccctaccagc1200	
tcagagtggt	tggtttccat	gcacagatgg	ccctagggtg	gacctccagt	tttgcgtgtg1260	
gagccgtagc	ctctttctag	ttgaatgacc	aaattgttaa	ggcttttagt	cccaccagac1320	
ttagccagcg	tcgtatgtag	gcctccagag	caggtttgtgc	tgtccctctg	ctctggagac1380	
aatgggggat	gtggaatcaa	gacaatgcc	aaaaaattt	taatgcagct	ggtc	1434

<210> 552  
 <211> 2434  
 <212> DNA  
 <213> homo sapiens

<400> 552

cccgagaaag	gtggaggagg	acgagaagcc	gccgagagcc	gactaccctc	cgggcccgagt	60
ctgtctgtcc	gtgtgtgagc	taagcctcat	ctgtatctcc	ttgtgatggc	gtgaaggaaa	120
ctccatggcag	atttccagacc	tggtgatgct	gtacagaaca	caggtggcct	gcttccatgc	180
gttccttagct	tcaagaaagt	agaatgaacc	gaagcattcc	tggtgaggtt	gatgaatcag	240
aaccataccc	aagtctagttg	ctgaaaccaa	tcccagaata	ttccccggaa	gaggaatcag	300
aaccacctgc	tcctaaatata	aggaacatgg	ccaccaacag	ctctctgtca	cccaaatcgc	360
ttccaaatcc	ctccggagac	ttttctcaag	ctcactcaac	cgtgaaactg	gcaaatcacc	420
agccgcctgt	atcccgagcg	gtcacctgcc	tgccagctca	actttctgag	gacagtgaag	480
acagtttctg	caggagacac	ccaggcctgg	gcaaaagctt	ccctctggg	tgctctgcag	540
tcagcgagcc	tgctctgtg	tctgtgtgtg	gagccctccc	tcagagcat	cagttttcat	600

00673395.125700

ttatgga	acgtaata	tggtggt	ctcagctt	agcggtct	cctgacact	660
gcatgact	agacaaat	gaccaaagt	tacctaagt	ctcagcag	tccttgggg	720
gtagccagg	gatggtgca	cgccccagc	ctncacagg	accgagagg	ctcggatct	780
ccaacatga	acacgggata	tgattccac	ccccaggat	tcctgggcat	caggcagct	840
gaaagggccc	tgncctccac	ctcgtgtgt	tacccccag	acotccccag	acotcagg	900
tcaggaggat	tcctctcagt	tgaacctcag	aggtatccag	catgtgcaca	gatgtgcct	960
cccaatcttt	ccccacatgc	tcctatggaac	tccattacc	attgtcctgg	aagtcccgtg	1020
caccaggtgc	ncatattggc	atgactacc	tcgagcagcc	taccagcaag	tgatccagcc	1080
ggctctgcct	gggncagccc	ctnngcctg	agccagtg	agaggcctgc	acccgtgtg	1140
gaannngtta	tcctgaatta	tcccagcccc	tgggaccaag	aagagaggcc	cgccacagaga	1200
gactgtctct	ttccggggct	tccaaggcac	caggaccagc	cacatcacca	gccacctaat	1260
agagctgggt	ctcctgggga	gtccttgga	tgccctgcag	agctgagacc	acagggtccc	1320
cagctccctg	ccccagctgc	tgtgcttaga	ccccctagca	acotccagc	cagaggaaact	1380
ctaaaaacaa	gcaatttgcc	agaagaattg	cggaagtct	ttatcactta	ttcgatggac	1440
acagctatgg	aggtgtgtga	attcgtgaac	ttttgtgtg	taaatggctt	ccaaactgca	1500
attgancant	atttgaggat	agaatccgag	gcattgatat	cattnaaatg	gatggagcgc	1560
taccttangg	gataagaccg	tgatgataat	cgtagcaatc	agccccnaaa	ntacaaaanc	1620
aggacgtng	naaggnccgt	gangtcnca	gctggacgag	gatgagcatg	gcttacatac	1680
taagtacatt	catcgatga	tgagattga	gttcataaaa	caagggaagca	tgaatttcag	1740
attcatccct	gtgctcttcc	caaatgcta	gaaggagcat	gtgcccactc	ggcttcagaa	1800
caactcatgt	ctacagctgg	cccaagaaatn	aaaaaaaaca	tcctgctgcg	gctgctnag	1860
agaggaagag	tatgtggctc	ctccacgggg	gcctctgccc	acncttcagg	gtggttccct	1920
tgtganacc	gttcatcccc	agatcactga	ggccnaggcc	atgtttgggn	gccttgttct	1980
gnacagcatt	ctggctgagg	ctnngtctgt	agcannctcc	tggtgtgttt	ttnttctgtt	2040
cnctccccga	ngaagctccc	tggnncccc	anggaaacct	gtgtgcaga	gctgtcccc	2100
ggagacctcc	nacacanc	tggncttga	agtggagtct	gtgnactgnc	tctgcattnc	2160
tctgtctttt	aaaaaaaaca	ttgcaggtgn	cagctgtccc	atatgttncc	tcctnagacag	2220
ntttgtgtgn	gtncattctt	ngggctctc	agtgcttagc	aagttagata	tgtaagggat	2280
gtnggcagca	aatggaaatg	actacaaa	ctctctatc	aatcaactta	ggctactttt	2340
atgagttagc	cagatgcttg	tgatcctca	ngacaaaact	gattcatgca	caataataa	2400
aatgtttact	cttttgtaaa	aaaaaaaa	aaaa			2434

<210> 553

<400> 553

000

<210> 554

<211> 1457

<212> DNA

<213> homo sapiens

<400> 554

actaaccag	agttgtggca	ttattaatta	tcactgggtc	tcttaactcg	aaaacggggg	60
accocagagg	caaggaaatt	tcattatccc	tatatgtggc	ttaaacttaa	aggagtatat	120
ccactactca	gagcttagta	caagggtcgg	ggtgaagtta	catataactc	ggggcgtttta	180
ccataccagg	gacccacact	caacaatgac	tgttgaagac	caaaaggagat	acctagggtc	240
agattataat	aaatcaccca	gcaccacctg	aatgtattat	ccacaaagat	atagcaataa	300
taaaaggttat	atatacatat	atttatcttg	gtaacctgag	ggctaataaac	gtggaatacg	360
ataattcttc	tcaagaggtc	catctgttag	aaagggaacc	aaaaggacag	tggttgtgtt	420
gcataaaaata	tggtttaaagt	ggagttggga	acaaaagggtg	gtttctcttag	ctctttccac	480
atctctcttt	gataaggact	gaaacctctg	tgattcatga	taaacgtttc	cttttttttt	540
ttttttggca	gcggggagag	gaaaagagga	gaaaatgggg	tttgagacc	atggcttacc	600
tttctctgct	ttgacccatc	acaccccat	tcctctctct	tcctctctcc	cgctgccaaa	660
aaaaaaaaaa	aggaaccgtt	tatcatgaat	caacagggtt	tcagtcctta	tcaaaagagag	720
atgtggaaag	agctaaagaa	accacccctt	gttcccaact	ccactttacc	catattttat	780
gcaacacaaa	cactgtccct	ttgggtccct	ttcttcacga	tggacccctt	gagaagaatt	840
ctgtatttcc	acgttttttag	ccctcaggtt	accaagataa	atatattgat	atataacctt	900
tattatttgt	atatctttgt	ggataataca	ttcaggtggt	gctgggtgat	tattataaat	960
ctgaaacctag	gatatccctt	tggtcttcca	cagtcattgt	ccctgggtatg	ctcgtgtatg	1020
gtaaaaagcc	aggtataatg	taacttccac	ccagcctttg	tactaagctc	ttgatagtg	1080
atatactctt	ttaagtttag	cccaatata	gggtaatgga	aatttctcgc	cctctgggtt	1140



ccccattttt actattaaga agaccagtga taatttaata atgccaccaaa ctctggcttal200  
 gtttaagttag agtgtgaact gtgtgggcaag agagcctcacc acctcactag gtgcagagag1260  
 cccaggcctt atgtttaaaat catgcaacttg aaaagcaaac cttaatctgc aaagacagca1320  
 gcaagcatta tacgggtcatt ttgaatgac cctttgaaag ttttttttg gttgggttgg1380  
 tttaaaatca agcctgaggc tgggtggaaa caggtagcct acacacacca aattgggggt1440  
 ggtcccgagg gaattgt 1457

<210> 555  
 <211> 741  
 <212> DNA  
 <213> homo sapiens

<400> 555

cctcctaaaa gactgggaaa gcagctttgg gctttgggtc ctccataaaa aaccaaggcg 60  
 gatgacttgg ggtttggatc cccttcggat gtoactgaa aaagccttag cagacctgat120  
 tgagaaggaa ctgtcccggt caaagaccaa ccttcctctt cgccccacat ctcttcagaal180  
 ctccctctca cacactacaa ccgccaaaag tcccaggctc tggattctgt catcctgtgt240  
 cagctacaaa tgcgaattct ctaaatagta ccttttcagt ctgtgccccag aggtttccctc300  
 aatttcagca gcaccgagcg gtttataatt cattcagttt tccaggccag gcagcccgct360  
 atccttggat ggcctttcca ncgcaatagc atcatgcnac ttgaaccaca cagcaaaccc420  
 cacctcaaat agtaatttct tggacttgaa tctcccgcca cagcacaaca caggtctggg480  
 agggatccct gtgacggggg aagaagaggt gaaggtttcg accatgccac tgtcaacctc540  
 ttccattca ttacaacaag gacagcagcc tacaagtctc cacactactg tggcctgaca600  
 acagaactga gaggagagga ttagactctg ggggtgcttg atgggcaact ggatttttgc660  
 atgattcctt tatgattttg cttttaatgt atacaccag aagagccaat ataaacgttc720  
 ctcatgctca aaaaaaaaaa a 741

<210> 556  
 <400> 556  
 000

<210> 557  
 <400> 557  
 000

<210> 558  
 <400> 558  
 000

<210> 559  
 <400> 559  
 000

<210> 560  
 <400> 560  
 000

<210> 561  
 <211> 470  
 <212> PRT  
 <213> homo sapiens

<400> 561

Thr	Asp	Gln	Pro	Asn	Ile	Gln	Ser	Val	Lys	Ile	His	Ser	Leu	Pro	Leu
1				5					10					15	
Arg	Asn	Pro	Asn	Lys	Gly	Cys	Glu	Cys	Pro	Pro	Arg	Arg	Asp	Gly	Phe
			20					25					30		
Gly	Phe	Ile	Lys	Cys	Val	Asp	Arg	Asp	Val	Arg	Met	Phe	Phe	His	Phe
		35					40					45			

00673305122700

Ser	Glu 50	Ile	Leu	Asp	Gly	Asn 55	Gln	Leu	His	Ile	Ala 60	Asp	Glu	Val	Glu	
Phe 65	Thr	Val	Val	Pro	Asp 70	Met	Leu	Ser	Ala	Gln 75	Arg	Asn	His	Ala	Ile 80	
Arg	Ile	Lys	Lys	Leu 85	Pro	Lys	Gly	Thr	Val 90	Ser	Phe	His	Ser	His 95	Ser	
Asp	His	Arg	Phe 100	Leu	Gly	Thr	Val	Glu 105	Lys	Glu	Ala	Thr	Phe 110	Ser	Asn	
Pro	Lys	Thr 115	Thr	Ser	Pro	Asn	Lys 120	Gly	Lys	Glu	Lys	Glu 125	Ala	Glu	Asp	
Gly	Ile 130	Ile	Ala	Tyr	Asp	Asp 135	Cys	Gly	Val	Lys	Leu 140	Thr	Ile	Ala	Phe	
Gln 145	Ala	Lys	Asp	Val	Glu 150	Gly	Ser	Thr	Ser	Pro 155	Gln	Ile	Gly	Asp	Lys 160	
Val	Glu	Phe	Ser	Ile 165	Ser	Asp	Lys	Gln	Arg 170	Pro	Gly	Gln	Gln	Val 175	Ala	
Thr	Cys	Val	Arg 180	Leu	Leu	Gly	Arg	Asn 185	Ser	Asn	Ser	Lys	Arg 190	Leu	Leu	
Gly	Tyr	Val 195	Ala	Thr	Leu	Lys	Asp 200	Asn	Phe	Gly	Phe	Ile 205	Glu	Thr	Ala	
Asn 210	His	Asp	Lys	Glu	Ile	Phe 215	Phe	His	Tyr	Ser	Glu 220	Phe	Ser	Gly	Asp	
Val 225	Asp	Ser	Leu	Glu	Leu 230	Gly	Asp	Met	Val	Glu 235	Tyr	Ser	Leu	Ser	Lys 240	
Gly	Lys	Gly	Asn	Lys 245	Val	Ser	Ala	Glu	Lys 250	Val	Asn	Lys	Thr	His 255	Ser	
Val	Asn	Gly	Ile 260	Thr	Glu	Glu	Ala	Asp 265	Pro	Thr	Ile	Tyr	Ser 270	Gly	Lys	
Val	Ile	Arg 275	Pro	Leu	Arg	Ser	Val 280	Asp	Pro	Thr	Gln	Thr 285	Glu	Tyr	Gln	
Gly	Met 290	Ile	Glu	Ile	Val	Glu 295	Glu	Gly	Asp	Met	Lys 300	Gly	Glu	Val	Tyr	
Pro 305	Phe	Gly	Ile	Val	Gly 310	Met	Ala	Asn	Lys	Gly 315	Asp	Cys	Leu	Gln	Lys 320	
Gly	Glu	Ser	Val	Lys 325	Phe	Gln	Leu	Cys	Val 330	Leu	Gly	Gln	Asn	Ala 335	Gln	
Thr	Met	Ala	Tyr 340	Asn	Ile	Thr	Pro	Leu 345	Arg	Arg	Ala	Thr	Val 350	Glu	Cys	
Val	Lys	Asp 355	Gln	Phe	Gly	Phe	Ile 360	Asn	Tyr	Glu	Val	Gly 365	Asp	Ser	Lys	
Lys	Leu 370	Phe	Phe	His	Val	Lys 375	Glu	Val	Gln	Asp	Gly 380	Ile	Glu	Leu	Gln	

Ala 385	Gly	Asp	Glu	Val	Glu 390	Phe	Ser	Val	Ile	Leu 395	Asn	Gln	Arg	Thr	Gly 400
Lys	Cys	Ser	Ala	Cys 405	Asn	Val	Trp	Arg	Val 410	Cys	Glu	Gly	Pro	Lys 415	Ala
Val	Ala	Ala	Pro 420	Arg	Pro	Asp	Arg	Leu 425	Val	Asn	Arg	Leu	Lys 430	Asn	Ile
Thr	Leu	Asp 435	Asp	Ala	Ser	Ala	Pro 440	Arg	Leu	Met	Val	Leu 445	Arg	Gln	Pro
Arg	Gly 450	Pro	Asp	Asn	Ser	Met 455	Gly	Phe	Gly	Ala	Glu 460	Arg	Lys	Ile	Arg
Gln 465	Ala	Gly	Val	Ile	Asp 470										

<210> 562

<211> 126

<212> PRT

<213> homo sapiens

<400> 562

Leu 1	Asn	Ala	Ile	Leu 5	Asn	Phe	Phe	His	Met 10	Glu	Lys	Glu	Leu	Leu 15	Ala
Ile	Ser	Tyr	Phe 20	Ile	Val	Asn	Glu	Ala 25	Lys	Leu	Ile	Phe	His 30	Thr	Phe
His	Cys	Gly 35	Pro	Ala	Gln	Gly	Cys 40	Asp	Val	Val	Ser	His 45	Ser	Leu	Cys
Ile	Leu 50	Ala	Gln	Asp	Thr	Gln 55	Leu	Glu	Leu	Asp	Ala 60	Leu	Pro	Phe	Leu
Gln 65	Ala	Ile	Pro	Phe	Val 70	Gly	His	Pro	Asn	Asp 75	Ala	Lys	Trp	Ile	Asp 80
Leu	Thr	Phe	His	Ile 85	Ala	Leu	Leu	His	Asn 90	Leu	Asn	His	Ser	Leu 95	Val
Leu	Ser	Leu	Cys 100	Trp	Ile	Asn	Thr	Pro 105	Gln	Gly	Ala	Asn	Tyr 110	Phe	Ala
Arg	Val	Asn 115	Gly	Gly	Ile	Ser	Phe 120	Leu	Ser	Asn	Ala	Ile 125	His		

<210> 563

<211> 85

<212> PRT

<213> homo sapiens

<400> 563

Lys 1	Ser	His	Thr	Ser 5	Cys	Asn	Leu	Leu	Ser 10	Arg	Pro	Leu	Phe	Val 15	Thr
Asn	Thr	Lys	Phe 20	Asn	Leu	Ile	Ser	Tyr 25	Leu	Arg	Arg	Ser	Arg 30	Ser	Phe

09673395.122700

His	Ile	Leu	Gly	Leu	Lys	Ser	Asn	Ser	Gln	Phe	His	Pro	Thr	Val	Ile
		35					40					45			
Ile	Ser	Asn	Asn	Ala	Ile	Leu	Ser	Leu	Leu	Leu	Phe	Ala	Phe	Ile	Trp
	50					55					60				
Ala	Ser	Gly	Phe	Arg	Ile	Gly	Lys	Ser	Gly	Phe	Phe	Phe	Tyr	Arg	Ala
65					70					75					80
Gln	Lys	Thr	Val	Ile											
				85											

<210> 564

<211> 549

<212> PRT

<213> homo sapiens

<400> 564

Leu	Tyr	Pro	Asn	Phe	Leu	Val	Asn	Glu	Leu	Ile	Leu	Lys	Gln	Lys	Gln
1				5					10					15	
Arg	Phe	Glu	Glu	Lys	Arg	Phe	Lys	Leu	Asp	His	Ser	Val	Ser	Ser	Thr
			20					25					30		
Asn	Gly	His	Arg	Trp	Gln	Ile	Phe	Gln	Asp	Trp	Leu	Gly	Thr	Asp	Gln
		35					40					45			
Asp	Asn	Leu	Asp	Leu	Ala	Asn	Val	Asn	Leu	Met	Leu	Glu	Leu	Leu	Val
	50					55					60				
Gln	Lys	Lys	Lys	Gln	Leu	Glu	Ala	Glu	Ser	His	Ala	Ala	Gln	Leu	Gln
65					70					75					80
Ile	Leu	Met	Glu	Phe	Leu	Lys	Val	Ala	Arg	Arg	Asn	Lys	Arg	Glu	Gln
				85					90					95	
Leu	Glu	Gln	Ile	Gln	Lys	Glu	Leu	Ser	Val	Leu	Glu	Glu	Asp	Ile	Lys
			100					105					110		
Arg	Val	Glu	Glu	Met	Ser	Gly	Leu	Tyr	Ser	Pro	Val	Ser	Glu	Asp	Ser
		115					120					125			
Thr	Val	Pro	Gln	Phe	Glu	Ala	Pro	Ser	Pro	Ser	His	Ser	Ser	Ile	Ile
	130					135					140				
Asp	Ser	Thr	Glu	Tyr	Ser	Gln	Pro	Pro	Gly	Phe	Ser	Gly	Ser	Ser	Gln
145					150					155					160
Thr	Lys	Lys	Gln	Pro	Trp	Tyr	Asn	Ser	Thr	Leu	Ala	Ser	Arg	Arg	Lys
				165					170					175	
Arg	Leu	Thr	Ala	His	Phe	Glu	Asp	Leu	Glu	Gln	Cys	Tyr	Phe	Ser	Thr
			180					185					190		
Arg	Met	Ser	Arg	Ile	Ser	Asp	Asp	Ser	Arg	Thr	Ala	Ser	Gln	Leu	Asp
		195					200					205			
Glu	Phe	Gln	Glu	Cys	Leu	Ser	Lys	Phe	Thr	Arg	Tyr	Asn	Ser	Val	Arg
	210					215					220				
Pro	Leu	Ala	Thr	Leu	Ser	Tyr	Ala	Ser	Asp	Leu	Tyr	Asn	Gly	Ser	Ser
225					230					235					240

00673685.122700

00673305.122700

Ile	Val	Ser	Ser	Ile	Glu	Phe	Asp	Arg	Asp	Cys	Asp	Tyr	Phe	Ala	Ile
				245					250					255	
Ala	Gly	Val	Thr	Lys	Lys	Ile	Lys	Val	Tyr	Glu	Tyr	Asp	Thr	Val	Ile
			260					265					270		
Gln	Asp	Ala	Val	Asp	Ile	His	Tyr	Pro	Glu	Asn	Glu	Met	Thr	Cys	Asn
		275					280					285			
Ser	Lys	Ile	Ser	Cys	Ile	Ser	Trp	Ser	Ser	Tyr	His	Lys	Asn	Leu	Leu
	290					295					300				
Ala	Ser	Ser	Asp	Tyr	Glu	Gly	Thr	Val	Ile	Leu	Trp	Asp	Gly	Phe	Thr
305					310					315					320
Gly	Gln	Arg	Ser	Lys	Val	Tyr	Gln	Glu	His	Glu	Lys	Arg	Cys	Trp	Ser
				325					330					335	
Val	Asp	Phe	Asn	Leu	Met	Asp	Pro	Lys	Leu	Leu	Ala	Ser	Gly	Ser	Asp
			340					345					350		
Asp	Ala	Lys	Val	Lys	Leu	Trp	Ser	Thr	Asn	Leu	Asp	Asn	Ser	Val	Ala
		355					360					365			
Ser	Ile	Glu	Ala	Lys	Ala	Asn	Val	Cys	Cys	Val	Lys	Phe	Ser	Pro	Ser
	370					375					380				
Ser	Arg	Tyr	His	Leu	Ala	Phe	Gly	Cys	Ala	Asp	His	Cys	Val	His	Tyr
385					390					395					400
Tyr	Asp	Leu	Arg	Asn	Thr	Lys	Gln	Pro	Ile	Met	Val	Phe	Lys	Gly	His
				405					410					415	
Arg	Lys	Ala	Val	Ser	Tyr	Ala	Lys	Phe	Val	Ser	Gly	Glu	Glu	Ile	Val
			420					425					430		
Ser	Ala	Ser	Thr	Asp	Ser	Gln	Leu	Lys	Leu	Trp	Asn	Val	Gly	Lys	Pro
		435					440					445			
Tyr	Cys	Leu	Arg	Ser	Phe	Lys	Gly	His	Ile	Asn	Glu	Lys	Asn	Phe	Val
	450					455					460				
Gly	Leu	Ala	Ser	Asn	Gly	Asp	Tyr	Ile	Ala	Cys	Gly	Ser	Glu	Asn	Asn
465					470					475					480
Ser	Leu	Tyr	Leu	Tyr	Tyr	Lys	Gly	Leu	Ser	Lys	Thr	Leu	Leu	Thr	Phe
				485					490					495	
Lys	Phe	Asp	Thr	Val	Lys	Ser	Val	Leu	Asp	Lys	Asp	Arg	Lys	Glu	Asp
			500					505					510		
Asp	Thr	Asn	Glu	Phe	Val	Ser	Ala	Val	Cys	Trp	Arg	Ala	Leu	Pro	Asp
		515					520					525			
Gly	Glu	Ser	Asn	Val	Leu	Ile	Ala	Ala	Asn	Ser	Gln	Gly	Thr	Ile	Lys
	530					535					540				
Val	Leu	Glu	Leu	Val											
545															

&lt;210&gt; 565

&lt;211&gt; 132

<212> PRT  
<213> homo sapiens

<400> 565

Thr	Leu	Tyr	Phe	Val	Tyr	Ile	Asp	Met	Cys	Asn	Ser	Gln	Arg	Gly	Trp
1				5					10					15	
Glu	Ile	Arg	Thr	Leu	Gln	Ile	Ile	His	Cys	Tyr	Ile	Ile	Val	His	Ile
			20					25					30		
Cys	Tyr	Phe	Val	Thr	Phe	Val	Phe	Ser	Phe	Val	Phe	Phe	Phe	Phe	Phe
		35					40					45			
Phe	Phe	Phe	Phe	Cys	Gly	Ser	Ile	Asn	Phe	Tyr	Cys	Phe	Val	Ile	Tyr
	50					55					60				
Phe	Tyr	Ser	Lys	Glu	Phe	Val	Ser	Leu	Ser	Gln	Lys	Leu	Asp	Asn	Thr
65					70					75					80
Thr	Lys	Ser	Ser	Asn	Val	His	Gly	Val	Thr	Leu	Met	Val	Glu	Ser	Trp
				85					90					95	
Leu	Gly	Ile	Pro	Asn	Val	Pro	Lys	Val	Ile	Lys	Glu	Gly	Lys	Glu	Lys
			100					105					110		
Lys	Lys	Lys	Ile	Phe	Lys	Thr	Asn	Pro	Lys	Pro	Met	Met	Thr	Leu	Gly
		115					120					125			
Arg	Asp	Ile	Thr												
	130														

<210> 566  
<211> 90  
<212> PRT  
<213> homo sapiens

<400> 566

Gly	Thr	Val	Leu	Ser	Ser	Leu	Thr	Gly	Glu	Tyr	Lys	Pro	Leu	Ile	Ser
1				5					10					15	
Ser	Thr	Leu	Leu	Ile	Ser	Ser	Ser	Lys	Thr	Leu	Ser	Ser	Phe	Trp	Ile
			20					25					30		
Cys	Ser	Ser	Cys	Ser	Leu	Leu	Phe	Leu	Leu	Ala	Thr	Leu	Arg	Asn	Ser
		35					40					45			
Ile	Arg	Ile	Cys	Ser	Trp	Ala	Ala	Cys	Asp	Ser	Ala	Ser	Ser	Cys	Phe
	50					55					60				
Phe	Phe	Cys	Thr	Ser	Asn	Ser	Asn	Ile	Arg	Leu	Thr	Leu	Ala	Lys	Ser
65					70				75						80
Arg	Leu	Ser	Trp	Ser	Val	Pro	Asn	Gln	Ser						
				85					90						

<210> 567  
<211> 331  
<212> PRT  
<213> homo sapiens

<400> 567

00673305.122700

Ser 1	Ala	Asn	His	Lys 5	Leu	Glu	Val	Asn	Gly 10	Thr	Asp	Gly	Leu	Ala 15	Pro
Val	Glu	Val	Glu 20	Glu	Leu	Leu	Arg	Gln 25	Ala	Ser	Glu	Arg	Asn 30	Ser	Lys
Ser	Pro	Thr 35	Glu	Tyr	His	Glu	Pro 40	Val	Tyr	Ala	Asn	Pro 45	Phe	Tyr	Arg
Pro	Thr 50	Thr	Pro	Gln	Arg	Glu 55	Thr	Val	Thr	Pro	Gly 60	Pro	Asn	Phe	Gln
Glu 65	Arg	Ile	Lys	Ile	Lys 70	Thr	Asn	Gly	Leu	Gly 75	Ile	Gly	Val	Asn	Glu 80
Ser	Ile	His	Asn	Met 85	Gly	Asn	Gly	Leu	Ser 90	Glu	Glu	Arg	Gly	Asn 95	Asn
Phe	Asn	His	Ile 100	Ser	Pro	Ile	Pro	Pro 105	Val	Pro	His	Pro	Arg 110	Ser	Val
Ile	Gln	Gln 115	Ala	Glu	Glu	Lys	Leu 120	His	Thr	Pro	Gln	Lys 125	Arg	Leu	Met
Thr	Pro 130	Trp	Glu	Glu	Ser	Asn 135	Val	Met	Gln	Asp	Lys 140	Asp	Ala	Pro	Ser
Pro 145	Lys	Pro	Arg	Leu	Ser 150	Pro	Arg	Glu	Thr	Ile 155	Phe	Gly	Lys	Ser	Glu 160
His	Gln	Asn	Ser	Ser 165	Pro	Thr	Cys	Gln	Glu 170	Asp	Glu	Glu	Asp	Val 175	Arg
Tyr	Asn	Ile	Val 180	His	Ser	Leu	Pro	Pro 185	Asp	Ile	Asn	Asp	Thr 190	Glu	Pro
Val	Thr	Met 195	Ile	Phe	Met	Gly	Tyr 200	Gln	Gln	Ala	Glu	Asp 205	Ser	Glu	Glu
Asp	Lys 210	Lys	Phe	Leu	Thr	Gly 215	Tyr	Asp	Gly	Ile	Ile 220	His	Ala	Glu	Leu
Val 225	Val	Ile	Asp	Asp	Glu 230	Glu	Glu	Glu	Asp	Glu 235	Gly	Glu	Ala	Glu	Lys 240
Pro	Ser	Tyr	His	Pro 245	Ile	Ala	Pro	His	Ser 250	Gln	Val	Tyr	Gln	Pro 255	Ala
Lys	Pro	Thr	Pro	Leu 260	Pro	Arg	Lys	Arg 265	Ser	Glu	Ala	Ser	Pro 270	His	Glu
Asn	Thr	Asn 275	His	Lys	Ser	Pro	His 280	Lys	Asn	Ser	Ile	Ser 285	Leu	Lys	Glu
Gln	Glu 290	Glu	Ser	Leu	Gly	Ser 295	Pro	Val	His	His	Ser 300	Pro	Phe	Asp	Ala
Gln 305	Thr	Thr	Gly	Asp	Gly 310	Thr	Glu	Asp	Pro	Ser 315	Leu	Thr	Ala	Leu	Arg 320
Met	Arg	Met	Ala	Lys 325	Leu	Gly	Lys	Lys	Val 330	Ile					

00673305-122700

<210> 568  
 <211> 216  
 <212> PRT  
 <213> homo sapiens

<400> 568

Leu	Ser	Leu	Thr	Ser	Arg	Met	Glu	Glu	Ala	Glu	Leu	Val	Lys	Gly	Arg
1				5					10					15	
Leu	Gln	Ala	Ile	Thr	Asp	Lys	Arg	Lys	Ile	Gln	Glu	Glu	Ile	Ser	Gln
			20					25					30		
Lys	Arg	Leu	Lys	Ile	Glu	Glu	Asp	Lys	Leu	Lys	His	Gln	His	Leu	Lys
		35					40					45			
Lys	Lys	Ala	Leu	Arg	Glu	Lys	Trp	Leu	Leu	Asp	Gly	Ile	Ser	Ser	Gly
	50					55					60				
Lys	Glu	Gln	Glu	Glu	Met	Lys	Lys	Gln	Asn	Gln	Gln	Asp	Gln	His	Gln
	65				70				75						80
Ile	Gln	Val	Leu	Glu	Gln	Ser	Ile	Leu	Arg	Leu	Glu	Lys	Glu	Ile	Gln
				85					90					95	
Asp	Leu	Glu	Lys	Ala	Glu	Leu	Gln	Ile	Ser	Thr	Lys	Glu	Glu	Ala	Ile
			100					105					110		
Leu	Lys	Lys	Leu	Lys	Ser	Ile	Glu	Arg	Thr	Thr	Glu	Asp	Ile	Ile	Arg
		115					120					125			
Ser	Val	Lys	Val	Glu	Arg	Glu	Glu	Arg	Ala	Glu	Glu	Ser	Ile	Glu	Asp
	130					135					140				
Ile	Tyr	Ala	Asn	Ile	Pro	Asp	Leu	Pro	Lys	Ser	Tyr	Ile	Pro	Ser	Arg
	145				150					155					160
Leu	Arg	Lys	Glu	Ile	Asn	Glu	Glu	Lys	Glu	Asp	Asp	Glu	Gln	Asn	Arg
				165					170					175	
Lys	Ala	Leu	Tyr	Ala	Met	Glu	Ile	Lys	Val	Glu	Lys	Asp	Leu	Lys	Thr
			180					185					190		
Gly	Glu	Ser	Thr	Val	Leu	Ser	Ser	Asn	Thr	Ser	Gly	His	Gln	Met	Thr
		195					200					205			
Leu	Lys	Gly	Thr	Gly	Val	Lys	Val								
	210					215									

<210> 569  
 <211> 132  
 <212> PRT  
 <213> homo sapiens

<400> 569

Leu	Glu	Lys	Leu	His	Ile	Cys	Phe	Pro	Gln	Leu	Phe	Gly	Asn	Phe	Ser
1				5					10					15	
Gln	Ile	Met	Thr	Thr	Thr	Tyr	Ser	His	Gly	Leu	Ile	Trp	Tyr	Thr	Val
			20					25					30		

00673305.122700



Met	Ile	Ile	Phe	Trp	Thr	Ser	Glu	Lys	Ile	Asn	Lys	Ile	Ser	Arg	Arg
		35					40					45			
Glu	Ile	Cys	Lys	Cys	Phe	Leu	Val	Ser	Ser	Ser	Lys	Asp	Val	Tyr	Ile
	50					55					60				
Gly	Gly	Thr	Thr	Leu	Arg	Ser	Pro	Phe	Phe	Pro	Ala	Leu	Pro	Phe	Ser
	65				70					75					80
Ser	Leu	Lys	Leu	Leu	Arg	Met	Asp	Pro	Gln	Ser	His	Leu	Gln	Leu	Ser
				85					90					95	
Glu	His	Gln	Met	Gly	Asn	Gly	Gly	Gln	Gly	Cys	Leu	Ser	Phe	Leu	Leu
			100					105					110		
Ala	Leu	Ser	Glu	Ile	Trp	Asn	Phe	Cys	Gly	Gly	Ile	Tyr	Asp	Leu	Cys
		115					120					125			
Phe	His	Glu	Asp												
		130													

<210> 570

<211> 199

<212> PRT

<213> homo sapiens

<400> 570

Asn	Phe	Val	Thr	Pro	Trp	Ser	Phe	Trp	Trp	Trp	Thr	Lys	Leu	Thr	Phe
1				5					10					15	
Phe	Phe	Pro	Leu	Ala	Leu	Lys	Lys	Ser	Ser	Arg	Val	Ser	Ser	Ser	His
			20					25					30		
Leu	Pro	Arg	Ile	Tyr	Gln	Ala	Phe	Leu	Met	Ser	Ala	Thr	Phe	Asn	Glu
		35					40					45			
Asp	Val	Gln	Ala	Leu	Lys	Glu	Leu	Ile	Leu	His	Asn	Pro	Val	Thr	Leu
	50					55					60				
Lys	Leu	Gln	Glu	Ser	Gln	Leu	Pro	Gly	Pro	Asp	Gln	Leu	Gln	Gln	Phe
	65				70					75					80
Gln	Val	Val	Cys	Glu	Thr	Glu	Glu	Asp	Lys	Phe	Leu	Leu	Leu	Tyr	Ala
				85					90					95	
Leu	Leu	Lys	Leu	Ser	Leu	Ile	Arg	Gly	Lys	Ser	Leu	Leu	Phe	Val	Asn
			100					105					110		
Thr	Leu	Glu	Arg	Ser	Tyr	Arg	Leu	Arg	Leu	Phe	Leu	Glu	Gln	Phe	Ser
		115					120					125			
Ile	Pro	Thr	Cys	Val	Leu	Asn	Gly	Glu	Leu	Pro	Leu	Arg	Ser	Arg	Cys
	130					135					140				
His	Ile	Ile	Ser	Gln	Phe	Asn	Gln	Gly	Phe	Tyr	Asp	Cys	Val	Ile	Ala
	145				150					155					160
Thr	Asp	Ala	Glu	Val	Leu	Gly	Ala	Pro	Arg	Gln	Arg	Ala	Met	Arg	Pro
				165					170					175	
Arg	Arg	Arg	Ala	Lys	Thr	Gly	Thr	Met	Ala	Ser	Arg	Phe	Leu	Glu	Arg
			180					185					190		

00673305-122700

Thr Val Val Ala Leu Gly His  
195

<210> 571  
<211> 195  
<212> PRT  
<213> homo sapiens

<400> 571

Gln	Arg	Val	Arg	Ala	Ala	Leu	Leu	Ser	Ser	Ala	Met	Glu	Asp	Ser	Glu
1				5					10					15	
Ala	Leu	Gly	Phe	Glu	His	Met	Gly	Leu	Asp	Pro	Arg	Leu	Leu	Gln	Ala
			20					25					30		
Val	Thr	Asp	Leu	Gly	Trp	Ser	Arg	Pro	Thr	Leu	Ile	Gln	Glu	Lys	Ala
		35					40					45			
Ile	Pro	Leu	Ala	Leu	Glu	Gly	Lys	Asp	Leu	Leu	Ala	Arg	Ala	Arg	Thr
	50					55					60				
Gly	Ser	Gly	Lys	Thr	Ala	Ala	Tyr	Ala	Ile	Pro	Met	Leu	Gln	Leu	Leu
65					70					75					80
Leu	His	Arg	Lys	Ala	Thr	Gly	Pro	Val	Val	Glu	Gln	Ala	Val	Arg	Gly
				85					90					95	
Leu	Val	Leu	Val	Pro	Thr	Lys	Glu	Leu	Ala	Arg	Gln	Ala	Gln	Ser	Met
			100					105					110		
Ile	Gln	Gln	Leu	Ala	Thr	Tyr	Cys	Ala	Arg	Asp	Val	Arg	Val	Ala	Asn
		115					120					125			
Val	Ser	Ala	Ala	Glu	Asp	Ser	Val	Ser	Gln	Arg	Ala	Val	Leu	Met	Glu
	130					135					140				
Lys	Pro	Asp	Val	Val	Val	Gly	Thr	Pro	Ser	Arg	Ile	Leu	Ser	His	Leu
145					150					155					160
Gln	Gln	Asp	Ser	Leu	Lys	Leu	Arg	Asp	Ser	Leu	Glu	Leu	Leu	Val	Val
				165					170					175	
Asp	Glu	Ala	Asp	Leu	Leu	Phe	Ser	Phe	Gly	Phe	Glu	Glu	Glu	Leu	Lys
			180					185						190	
Ser	Leu	Leu													
		195													

<210> 572  
<211> 76  
<212> PRT  
<213> homo sapiens

<400> 572

Asp	Ile	Gly	His	Ser	Asp	Ile	Pro	Ser	Thr	Val	Gly	Ser	Gln	Leu	Leu
1				5					10					15	
Asn	His	Gly	Leu	Cys	Leu	Pro	Cys	Gln	Leu	Leu	Gly	Arg	Asn	Lys	Asn
			20					25					30		

00673095.122700

Lys	Ala	Ser	His	Cys	Leu	Phe	Tyr	His	Arg	Thr	Cys	Arg	Leu	Pro	Met
		35					40					45			
Glu	Gln	Gln	Leu	Gln	His	Arg	Asn	Ser	Ile	Ser	Gly	Arg	Leu	Pro	Gly
	50					55					60				
Ala	Arg	Ala	Gly	Pro	Ser	Gln	Glu	Val	Leu	Pro	Phe				
65					70					75					

<210> 573  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 573

Asp	Ser	Gln	Val	Gly	Arg	Gly	Pro	Gln	Arg	Asn	Ser	Ser	Leu	His	Thr
1				5					10					15	
Gly	Arg	Ser	Val	His	Trp	Gly	Glu	Ala	Thr	Gly	Ser	Leu	Arg	His	Leu
			20					25					30		
Gln	Trp	Gly	Arg	Ala	Gln	Pro	Leu	Leu	Phe	Leu	Gly	Gly	Lys	Leu	Arg
		35					40					45			
Phe	Lys	Leu	Pro	Gly	Gly	Lys	Ser	Met	Gly	Arg	Lys	Gln	Ala	Leu	Xxx
	50					55					60				
Leu	Leu	Arg	Val	Ser	Val	Ser	Pro	Phe	Phe	Pro	Leu	Cys	Leu	Ile	Asn
65					70					75					80
Lys	Phe	His	Phe	Ser	His	Pro	Ser	Asn	Ser	Leu					
				85					90						

<210> 574  
 <211> 89  
 <212> PRT  
 <213> homo sapiens

<400> 574

Glu	Lys	Trp	Asn	Leu	Leu	Ile	Arg	His	Lys	Gly	Lys	Lys	Gly	Glu	Thr
1				5					10					15	
Glu	Thr	Leu	Ser	Lys	Xxx	Arg	Ala	Cys	Phe	Leu	Pro	Met	Asp	Phe	Pro
			20					25					30		
Pro	Gly	Ser	Leu	Asn	Arg	Ser	Phe	Pro	Pro	Arg	Lys	Arg	Arg	Gly	Trp
		35					40					45			
Ala	Leu	Pro	His	Trp	Arg	Trp	Arg	Lys	Leu	Pro	Val	Ala	Ser	Pro	Gln
	50					55					60				
Cys	Thr	Leu	Leu	Pro	Val	Cys	Arg	Leu	Glu	Phe	Leu	Trp	Gly	Pro	Leu
65					70					75					80
Pro	Thr	Trp	Leu	Ser	His	Cys	Pro	Leu							
				85											

<210> 575  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

00575355752700



<212> PRT  
<213> homo sapiens

<400> 578

Gln 1	Thr	Asp	Asn	Leu 5	Ser	Glu	Arg	Gln	Pro 10	Xxx	Gly	Lys	Xxx	Val 15	Cys
Arg	Gly	Cys	Pro 20	Gln	Gly	Glu	Cys	Ser 25	Trp	Glu	Arg	Ala	Val 30	Leu	Leu
Xxx	Pro	Gly 35	Arg	Pro	Ala	Leu	Ser 40	Xxx	Thr	Leu	Leu	Xxx 45	Lys	Xxx	Ala
Pro	Cys 50	Glu	Val	Asn	Trp	Val 55	Xxx	Val	Arg	Gly	Ser 60	Xxx	Xxx	Cys	Xxx
Gly 65	Ala	Pro	Ala	Xxx	Thr 70	Pro	Xxx	Pro	Xxx	Gln 75	Arg	Xxx	Ala	Ala	Ser 80
Ala	Xxx	Ala	Gly	Leu 85	Glu	Xxx	Ser	Xxx	Ala 90	Xxx	Ala	Gly	Xxx	Ala 95	Gly
Cys	Cys	Cys	Xxx 100	Gly	Leu	Pro	Xxx	Val 105	Trp	Ser	Xxx	Leu	Ala 110	Leu	Pro
Thr	Ala	Ser 115	Leu	Glu	Ala	Ser	Xxx 120	Xxx	Pro	Arg	Pro	Ala 125	Ala	Ser	Pro
Arg	Thr 130	Ser	Cys	Pro	Ser	Thr 135	Leu	Pro	Gln	Ala	Thr 140	Lys	Thr	Pro	Arg
Val 145	Leu	Pro	Asn	Lys	Xxx 150	Xxx	Leu	Gly	Thr	Xxx 155	Ser	Lys	Leu	Ile	Phe 160

<210> 579  
<211> 437  
<212> PRT  
<213> homo sapiens

<400> 579

Ser 1	Gln	Gly	Val	Leu 5	Ser	Ser	Asp	Gly	Val 10	Trp	Arg	Val	Lys	Ser 15	Ile
Pro	Asn	Gly	Lys 20	Gly	Ser	Ser	Pro	Leu 25	Pro	Thr	Ala	Thr	Thr 30	Pro	Lys
Pro	Leu	Ile 35	Pro	Thr	Glu	Ala	Ser 40	Ile	Arg	Val	Trp	Gly 45	Thr	Ser	Gly
Thr	Ser 50	His	Leu	His	Pro	Arg 55	Ser	Ile	Cys	Met	Ile 60	Gln	Lys	Tyr	Asn
His 65	Asp	Gly	Glu	Ala	Gly 70	Arg	Leu	Glu	Ala	Phe 75	Ser	Gln	Gly	Glu	Ser 80
Val	Leu	Lys	Glu	Pro 85	Lys	Tyr	Gln	Glu 90	Glu	Leu	Glu	Asp	Arg	Leu 95	His
Phe	Tyr	Val	Glu 100	Glu	Cys	Asp	Tyr	Leu 105	Gln	Gly	Phe	Gln	Ile 110	Leu	Cys

00673005.122700

Asp	Leu	His 115	Asp	Gly	Phe	Ser	Gly 120	Val	Gly	Ala	Lys	Ala 125	Ala	Glu	Leu
Leu	Gln 130	Asp	Glu	Tyr	Ser	Gly 135	Arg	Gly	Ile	Ile	Thr 140	Trp	Gly	Leu	Leu
Pro 145	Gly	Pro	Tyr	His	Arg 150	Gly	Glu	Ala	Gln	Arg 155	Asn	Ile	Tyr	Arg	Leu 160
Leu	Asn	Thr	Ala	Phe 165	Gly	Leu	Val	His	Leu 170	Thr	Ala	His	Ser	Ser	Leu 175
Val	Cys	Pro	Leu 180	Ser	Leu	Gly	Gly	Ser 185	Leu	Gly	Leu	Arg	Pro 190	Glu	Pro
Pro	Val	Ser 195	Phe	Pro	Tyr	Leu	His 200	Tyr	Asp	Ala	Thr	Leu 205	Pro	Phe	His
Cys	Ser 210	Ala	Ile	Leu	Ala	Thr 215	Ala	Leu	Asp	Thr	Val 220	Thr	Val	Pro	Tyr
Arg 225	Leu	Cys	Ser	Ser	Pro 230	Val	Ser	Met	Val	His 235	Leu	Ala	Asp	Met	Leu 240
Ser	Phe	Cys	Gly	Lys 245	Lys	Val	Val	Thr	Ala 250	Gly	Ala	Ile	Ile	Pro 255	Phe
Pro	Leu	Ala	Pro 260	Gly	Gln	Ser	Leu	Pro 265	Asp	Ser	Leu	Met	Gln 270	Phe	Gly
Gly	Ala	Thr 275	Pro	Trp	Thr	Pro	Leu 280	Ser	Ala	Cys	Gly	Glu 285	Pro	Ser	Gly
Thr	Arg 290	Cys	Phe	Ala	Gln	Ser 295	Val	Val	Leu	Arg	Gly 300	Tyr	Arg	Gln	Ser
Met 305	Pro	His	Lys	Pro	Gln 310	Asn	Gln	Arg	Asp	Thr 315	Ser	Thr	Leu	Cys	Pro 320
Ser	Cys	Met	Tyr	His 325	Trp	Gly	Arg	Asn	Leu 330	Gly	Ser	Val	Phe	Thr 335	Thr
Ala	Ala	Ala	Trp 340	Ser	His	Glu	Phe	Phe 345	Pro	Ser	Ala	Ala	Asp 350	Ser	Leu
Gln	Gly	Gly 355	Ser	Ser	Leu	Pro	Pro 360	Pro	Leu	Leu	Lys	Leu 365	Gln	Ser	Thr
Gly	Tyr 370	Gly	Ser	Gly	Trp	Phe 375	Pro	Gln	Gly	Ser	Arg 380	Ser	Ser	Val	Ser
Leu 385	Ser	Leu	Pro	Gln	Gln 390	Trp	Arg	Ala	Ser	Gln 395	Cys	Leu	Gly	His	Cys 400
Val	Pro	Leu	Arg	Pro 405	Cys	Thr	Arg	Pro	Trp 410	Lys	Pro	Trp	Pro	Glu 415	Thr
Ser	Pro	Asn	Ser 420	Thr	Cys	Gly	Ala	Gly 425	Pro	Ala	Ser	Trp	Met 430	Leu	Glu
Trp	Ser	Thr 435	Met	Thr											

09673395.122700

<210> 580  
 <211> 277  
 <212> PRT  
 <213> homo sapiens

<400> 580

Thr	Glu	Arg	Leu	Leu	Leu	Asp	Gly	Pro	Pro	Pro	His	Ser	Pro	Glu	Thr
1				5					10					15	
Pro	Gln	Phe	Pro	Pro	Thr	Thr	Gly	Ala	Val	Leu	Tyr	Thr	Val	Lys	Arg
			20					25					30		
Asn	Gln	Val	Gly	Pro	Glu	Val	Arg	Ser	Cys	Pro	Lys	Ala	Ser	Pro	Arg
		35					40					45			
Leu	Gln	Lys	Glu	Arg	Glu	Gly	Gln	Lys	Ala	Val	Ser	Glu	Ser	Glu	Ala
	50					55					60				
Leu	Met	Leu	Val	Trp	Asp	Ala	Ser	Glu	Thr	Glu	Lys	Leu	Pro	Gly	Thr
65					70					75					80
Val	Glu	Pro	Pro	Ala	Ser	Phe	Leu	Ser	Pro	Val	Ser	Ser	Lys	Thr	Arg
				85					90					95	
Asp	Ala	Gly	Arg	Arg	His	Val	Ser	Gly	Lys	Pro	Asp	Thr	Gln	Glu	Arg
			100					105					110		
Trp	Leu	Pro	Ser	Ser	Arg	Ala	Arg	Val	Lys	Thr	Arg	Asp	Arg	Thr	Cys
		115					120					125			
Pro	Val	His	Glu	Ser	Pro	Ser	Gly	Ile	Asp	Thr	Ser	Glu	Thr	Ser	Pro
	130					135					140				
Lys	Ala	Pro	Arg	Gly	Gly	Leu	Ala	Lys	Asp	Ser	Gly	Thr	Gln	Ala	Lys
145				150					155						160
Gly	Pro	Glu	Gly	Glu	Gln	Gln	Pro	Lys	Ala	Ala	Glu	Ala	Thr	Val	Cys
				165					170					175	
Ala	Asn	Asn	Ser	Lys	Val	Ser	Ser	Thr	Gly	Glu	Lys	Val	Val	Leu	Trp
			180					185					190		
Thr	Arg	Glu	Ala	Asp	Arg	Val	Ile	Leu	Thr	Met	Cys	Gln	Glu	Gln	Gly
	195						200					205			
Ala	Gln	Pro	Gln	Thr	Phe	Asn	Ile	Ile	Ser	Gln	Gln	Leu	Gly	Asn	Lys
	210					215					220				
Thr	Pro	Ala	Glu	Val	Ser	His	Arg	Phe	Arg	Glu	Leu	Met	Gln	Leu	Phe
225					230					235					240
His	Thr	Ala	Cys	Glu	Ala	Ser	Ser	Glu	Asp	Glu	Asp	Asp	Ala	Thr	Ser
				245					250					255	
Thr	Ser	Asn	Ala	Asp	Gln	Leu	Ser	Asp	His	Gly	Asp	Leu	Leu	Ser	Glu
			260					265					270		
Glu	Glu	Leu	Asp	Glu											
		275													

<210> 581  
 <211> 172

00673295.122700

<212> PRT  
<213> homo sapiens

<400> 581

Phe	Pro	Glu	Ser	His	Ser	Ser	Ser	Ser	Ser	10	Ser	Asp	Arg	Arg	Ser	Pro
1				5											15	
Trp	Ser	Asp	Ser	Trp	Ser	Ala	Leu	Leu	Val	Leu	Val	Ala	Ser	Ser	Ser	
			20					25					30			
Ser	Ser	Glu	Leu	Ala	Ser	Gln	Ala	Val	Trp	Lys	Ser	Cys	Met	Ser	Ser	
		35					40					45				
Arg	Lys	Arg	Trp	Glu	Thr	Ser	Ala	Gly	Val	Leu	Phe	Pro	Ser	Cys	Trp	
	50					55					60					
Glu	Met	Met	Leu	Lys	Val	Cys	Gly	Cys	Ala	Pro	Cys	Ser	Trp	His	Met	
65					70					75					80	
Val	Arg	Ile	Thr	Arg	Ser	Ala	Ser	Leu	Val	His	Arg	Thr	Thr	Phe	Ser	
				85					90					95		
Pro	Val	Glu	Leu	Thr	Leu	Leu	Leu	Leu	Ala	His	Thr	Val	Ala	Ser	Ala	
			100					105					110			
Ala	Phe	Gly	Cys	Cys	Ser	Pro	Ser	Gly	Pro	Leu	Ala	Cys	Val	Pro	Leu	
		115					120					125				
Ser	Leu	Ala	Lys	Pro	Pro	Leu	Gly	Ala	Leu	Gly	Glu	Val	Ser	Glu	Val	
		130				135					140					
Ser	Ile	Pro	Asp	Gly	Asp	Ser	Trp	Thr	Gly	His	Val	Leu	Ser	Leu	Val	
145					150					155					160	
Phe	Thr	Leu	Ala	Leu	Leu	Glu	Gly	Ser	His	Leu	Ser					
				165					170							

<210> 582  
<211> 549  
<212> PRT  
<213> homo sapiens

<400> 582

Glu	Phe	Pro	Pro	Gly	Leu	Thr	Glu	Pro	Thr	Ala	Val	Arg	Ala	Leu	Ala	
1				5					10					15		
Arg	Ala	Arg	Arg	Thr	Arg	Ala	Gly	Ser	Ala	Ser	Asp	Pro	Glu	Arg	Ser	
			20					25					30			
Pro	Gly	Ala	Met	Ala	Leu	Ser	Glu	Leu	Ala	Leu	Val	Arg	Trp	Leu	Gln	
		35					40					45				
Glu	Ser	Arg	Arg	Ser	Arg	Lys	Leu	Ile	Leu	Phe	Ile	Val	Phe	Leu	Ala	
	50					55					60					
Leu	Leu	Leu	Asp	Asn	Met	Leu	Leu	Thr	Val	Val	Val	Pro	Ile	Ile	Pro	
65					70					75					80	
Ser	Tyr	Leu	Tyr	Ser	Ile	Lys	His	Glu	Lys	Asn	Ala	Thr	Glu	Ile	Gln	
				85					90					95		

0067306-722700



Thr	Ala	Arg	Pro 100	Val	His	Thr	Ala	Ser 105	Ile	Ser	Asp	Ser	Phe 110	Gln	Ser		
Ile	Phe	Ser 115	Tyr	Tyr	Asp	Asn	Ser 120	Thr	Met	Val	Thr	Gly 125	Asn	Ala	Thr		
Arg	Asp 130	Leu	Thr	Leu	His	Gln 135	Thr	Ala	Thr	Gln	His 140	Met	Val	Thr	Asn		
Ala	Ser	Ala	Val	Pro	Ser	Asp 150	Cys	Pro	Ser	Glu 155	Asp	Lys	Asp	Leu	Leu 160		
Asn	Glu	Asn	Val	Gln 165	Val	Gly	Leu	Leu	Phe 170	Ala	Ser	Lys	Ala	Thr 175	Val		
Gln	Leu	Ile	Thr 180	Asn	Pro	Phe	Ile	Gly 185	Leu	Leu	Thr	Asn	Arg 190	Ile	Gly		
Tyr	Pro	Ile 195	Pro	Ile	Phe	Ala	Gly 200	Phe	Cys	Ile	Met	Phe 205	Val	Ser	Thr		
Ile	Met 210	Phe	Ala	Phe	Ser	Ser 215	Ser	Tyr	Ala	Phe	Leu 220	Leu	Ile	Ala	Arg		
Ser	Leu	Gln	Gly	Ile	Gly 230	Ser	Ser	Cys	Ser	Ser 235	Val	Ala	Gly	Met	Gly 240		
Met	Leu	Ala	Ser	Val 245	Tyr	Thr	Asp	Asp	Glu 250	Glu	Arg	Gly	Asn	Val 255	Met		
Gly	Ile	Ala	Leu 260	Gly	Gly	Leu	Ala	Met 265	Gly	Val	Leu	Val	Gly 270	Pro	Pro		
Phe	Gly	Ser 275	Val	Leu	Tyr	Glu	Phe 280	Val	Gly	Lys	Thr	Ala 285	Pro	Phe	Leu		
Val	Leu 290	Ala	Ala	Leu	Val	Leu 295	Leu	Asp	Gly	Ala	Ile 300	Gln	Leu	Phe	Val		
Leu	Gln	Pro	Ser	Arg 310	Val	Gln	Pro	Glu	Ser	Gln 315	Lys	Gly	Thr	Pro	Leu 320		
Thr	Thr	Leu	Leu	Lys 325	Asp	Pro	Tyr	Ile	Leu 330	Ile	Ala	Ala	Gly	Ser 335	Ile		
Ser	Phe	Ala	Asn 340	Met	Gly	Ile	Ala	Met 345	Leu	Glu	Pro	Ala	Leu 350	Pro	Ile		
Trp	Met	Met 355	Glu	Thr	Met	Cys	Ser 360	Arg	Lys	Trp	Gln	Leu 365	Gly	Val	Ala		
Phe	Leu 370	Pro	Ala	Ser	Ile	Ser 375	Tyr	Leu	Ile	Gly	Thr 380	Asn	Ile	Phe	Gly		
Ile	Leu	Ala	His	Lys	Met 390	Gly	Arg	Trp	Leu	Cys 395	Ala	Leu	Leu	Gly	Met 400		
Ile	Ile	Val	Gly	Val 405	Ser	Ile	Leu	Cys	Ile 410	Pro	Phe	Pro	Lys	Asn 415	Ile		
Tyr	Gly	Leu	Ile 420	Ala	Pro	Asn	Phe	Gly 425	Val	Gly	Phe	Ala	Asn 430	Gly	Met		

Val	Asp	Ser	Ser	Met	Met	Pro	Ile	Met	Gly	Tyr	Leu	Val	Asp	Leu	Arg	
		435					440					445				
His	Val	Ser	Val	Tyr	Gly	Ser	Val	Tyr	Ala	Ile	Ala	Asp	Val	Ala	Phe	
	450					455					460					
Cys	Met	Gly	Tyr	Ala	Ile	Gly	Pro	Ser	Ala	Gly	Gly	Ala	Ile	Ala	Lys	
	465				470					475					480	
Ala	Ile	Gly	Phe	Pro	Trp	Leu	Met	Thr	Ile	Ile	Gly	Ile	Ile	Asp	Ile	
				485					490					495		
Leu	Phe	Ala	Pro	Leu	Cys	Phe	Phe	Leu	Arg	Ser	Pro	Pro	Ala	Lys	Glu	
			500					505					510			
Glu	Lys	Met	Ala	Ile	Leu	Met	Asp	His	Asn	Cys	Pro	Ile	Lys	Thr	Lys	
		515					520					525				
Met	Tyr	Thr	Gln	Asn	Asn	Ile	Gln	Ser	Tyr	Pro	Ile	Gly	Glu	Asp	Glu	
	530					535					540					
Glu	Ser	Glu	Ser	Asp												
	545															

<210> 583  
 <211> 121  
 <212> PRT  
 <213> homo sapiens

<400> 583

Tyr	Leu	Leu	Ser	His	Trp	Asn	Gln	Tyr	Phe	Trp	Asp	Thr	Cys	Thr	Gln	
1				5					10					15		
Asn	Gly	Glu	Val	Ala	Leu	Cys	Ser	Ser	Gly	Asn	Asp	Asn	Cys	Trp	Ser	
			20					25					30			
Gln	His	Phe	Met	Tyr	Ser	Ile	Ser	Lys	Lys	His	Leu	Trp	Thr	His	Ser	
		35					40					45				
Ser	Glu	Leu	Trp	Ser	Trp	Phe	Cys	Lys	Trp	Asn	Gly	Gly	Phe	Val	Asn	
	50					55					60					
Asp	Ala	Tyr	His	Gly	Leu	Pro	Arg	Arg	Pro	Ala	Ala	Arg	Val	Arg	Leu	
	65				70					75					80	
Trp	Glu	Cys	Val	Arg	His	Cys	Gly	Cys	Gly	Ile	Leu	Tyr	Gly	Val	Cys	
				85					90					95		
Tyr	Arg	Ser	Phe	Cys	Trp	Trp	Cys	Tyr	Cys	Lys	Gly	Asn	Trp	Ile	Ser	
			100					105					110			
Met	Ala	His	Asp	Asn	Tyr	Trp	Asp	Asn								
		115					120									

<210> 584  
 <211> 106  
 <212> PRT  
 <213> homo sapiens

<400> 584

Asp	Gly	Gly	Ser	Val	His	Trp	Pro	Gly	Arg	Leu	Asp	Phe	Cys	Ser	Ile	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

00673395-122700

1			5			10			15						
Leu	Leu	Met	Leu 20	Asn	Ala	Val	Gln	Ile 25	Thr	Trp	Asp	Asp	Gly 30	Asp	His
Asp	Ser	Glu 35	Gln	His	Val	Val	Gln 40	Gln	Arg	Gln	Glu 45	His	Asp	Glu	
Gln	Asp 50	Glu	Leu	Pro	Arg	Ala 55	Ala	Ala	Leu	Leu	Gln 60	Pro	Ala	Asp	Gln
Arg 65	Gln	Leu	Ala	Gln	Gly 70	His	Gly	Ser	Gly	Ala 75	Pro	Leu	Gly	Val	Ala 80
Cys	Ala	Ala	Cys	Pro 85	Gly	Pro	Pro	Cys	Pro 90	Arg	Gln	Arg	Pro	His 95	Arg
Ser	Gly	Leu	Arg 100	Gln	Ser	Gly	Arg	Glu 105	Phe						

<210> 585  
 <211> 409  
 <212> PRT  
 <213> homo sapiens

<400> 585

Lys 1	Ser	Arg	Leu	Ser 5	Val	Thr	Leu	Met	Pro 10	Val	Gln	Leu	Ser	Glu 15	His
Pro	Glu	Trp	Asn 20	Glu	Ser	Met	His	Ser 25	Leu	Arg	Ile	Ser	Val 30	Gly	Gly
Leu	Pro	Val 35	Leu	Ala	Ser	Met	Thr 40	Lys	Ala	Ala	Asp	Pro 45	Arg	Phe	Arg
Pro	Arg 50	Trp	Lys	Val	Ile	Leu 55	Thr	Phe	Phe	Val	Gly 60	Ala	Ala	Ile	Leu
Trp 65	Leu	Leu	Cys	Ser	His 70	Arg	Pro	Ala	Pro	Gly 75	Arg	Pro	Pro	Thr	His 80
Asn	Ala	His	Asn	Trp 85	Arg	Leu	Gly	Gln	Ala 90	Pro	Ala	Asn	Trp	Tyr 95	Asn
Asp	Thr	Tyr	Pro 100	Leu	Ser	Pro	Pro	Gln 105	Arg	Thr	Pro	Ala	Gly 110	Ile	Arg
Tyr	Arg	Ile 115	Ala	Val	Ile	Ala	Asp 120	Leu	Asp	Thr	Glu	Pro 125	Thr	Ala	Gln
Asp	Glu 130	Asn	Thr	Trp	Arg	Ser 135	Asp	Leu	Lys	Lys	Gly 140	Tyr	Leu	Thr	Leu
Ser 145	Asp	Ser	Gly	Asp	Lys 150	Val	Ala	Val	Glu	Trp 155	Asp	Lys	Asp	His	Gly 160
Val	Leu	Glu	Ser	His 165	Leu	Ala	Glu	Lys	Gly 170	Arg	Gly	Met	Glu	Leu 175	Ser
Asp	Leu	Ile	Val 180	Phe	Asn	Gly	Lys	Leu 185	Tyr	Ser	Val	Asp	Asp 190	Arg	Thr

00673305.102700

Gly	Val	Val	Tyr	Gln	Ile	Glu	Gly	Ser	Lys	Ala	Val	Pro	Trp	Val	Ile
		195					200					205			
Leu	Ser	Asp	Gly	Asp	Gly	Thr	Val	Glu	Lys	Gly	Phe	Lys	Ala	Glu	Trp
	210					215					220				
Leu	Ala	Val	Lys	Asp	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Leu	Gly	Lys	Glu
	225				230					235					240
Trp	Thr	Thr	Thr	Thr	Gly	Asp	Val	Val	Asn	Glu	Asn	Pro	Glu	Trp	Val
				245					250					255	
Lys	Val	Val	Gly	Tyr	Lys	Gly	Ser	Val	Asp	His	Glu	Asn	Trp	Val	Ser
			260					265					270		
Asn	Tyr	Asn	Ala	Leu	Arg	Ala	Ala	Ala	Gly	Ile	Gln	Pro	Pro	Ala	Asn
		275					280					285			
Leu	Ile	His	Glu	Ser	Ala	Cys	Trp	Ser	Asp	Thr	Leu	Gln	Arg	Trp	Phe
	290					295					300				
Phe	Leu	Pro	Arg	Arg	Ala	Ser	Gln	Glu	Arg	Tyr	Ser	Glu	Lys	Asp	Asp
	305				310					315					320
Glu	Arg	Lys	Gly	Ala	Asn	Leu	Leu	Leu	Ser	Ala	Ser	Pro	Asp	Phe	Gly
				325					330					335	
Asp	Ile	Ala	Val	Ser	His	Val	Gly	Ala	Val	Val	Pro	Thr	His	Gly	Phe
		340						345					350		
Ser	Ser	Phe	Lys	Phe	Ile	Pro	Asn	Thr	Asp	Asp	Gln	Ile	Ile	Val	Ala
		355					360					365			
Leu	Lys	Ser	Glu	Glu	Asp	Ser	Gly	Arg	Val	Ala	Ser	Tyr	Ile	Met	Ala
	370					375					380				
Phe	Thr	Leu	Asp	Gly	Arg	Phe	Leu	Leu	Pro	Glu	Thr	Lys	Ile	Gly	Ser
	385				390					395					400
Val	Lys	Tyr	Glu	Gly	Ile	Glu	Phe	Ile							
				405											

<210> 586

<211> 249

<212> PRT

<213> homo sapiens

<400> 586

Lys	Leu	Ser	Pro	Asp	Gly	Leu	Ala	Gln	Cys	Phe	Arg	Phe	Glu	Leu	Asn
1				5					10					15	
Glu	Leu	Asp	Ala	Phe	Val	Phe	His	Ala	Ser	Asp	Leu	Gly	Leu	Arg	Gln
			20					25					30		
Gln	Glu	Ala	Pro	Val	Gln	Arg	Glu	Gly	His	Asp	Val	Gly	Gly	Asp	Ser
		35					40					45			
Ala	Ala	Val	Leu	Leu	Gly	Phe	Glu	Gly	His	Asn	Asp	Leu	Val	Val	Gly
	50					55					60				
Val	Gly	Asp	Glu	Leu	Glu	Gly	Arg	Glu	Ala	Val	Ser	Gly	Asp	His	Arg
65					70					75					80

00673305.122700

Pro	Asp	Val	Ala	His 85	Ser	Asp	Val	Ala	Glu 90	Val	Arg	Gly	Gly	Ala 95	Gln
Gln	Gln	Val	Gly 100	Ala	Leu	Ala	Leu	Val 105	Val	Leu	Leu	Ala	Val 110	Ala	Leu
Leu	Ala	Gly 115	Ala	Ala	Arg	Gln	Glu 120	Glu	Pro	Ala	Leu	Gln 125	Arg	Val	Thr
Pro	Ala 130	Gly	Arg	Leu	Met	Asp 135	Glu	Val	Ser	Trp	Arg 140	Leu	Asp	Ala	Gly
Ser 145	Ser	Pro	Gln	Gly	Val 150	Val	Val	Gly	His	Pro 155	Val	Leu	Val	Val	His 160
Ala	Ala	Leu	Val	Ala 165	His	His	Leu	His	Pro 170	Leu	Arg	Val	Leu	Val	His 175
His	Ile	Thr	Arg 180	Ser	Gly	Arg	Pro	Leu 185	Leu	Ala	Gln	Ala	Ala 190	His	Val
Gln	Thr	Leu 195	Val	Leu	His	Cys	Gln 200	Pro	Phe	Gly	Leu	Glu 205	Ala	Phe	Leu
His	Gly 210	Ala	Val	Ala	Val	Gly 215	Gln	Asn	His	Pro	Gly 220	His	Gly	Phe	Ala
Ala 225	Phe	Asp	Leu	Val	Asp 230	Asp	Pro	Arg	Pro	Val 235	Ile	His	Gly	Val	Glu 240
Phe	Pro	Ile	Glu	Asn 245	Asn	Gln	Val	Gly							

<210> 587

<211> 157

<212> PRT

<213> homo sapiens

<400> 587

Leu 1	Glu	Phe	Phe	Ile 5	Pro	Cys	Leu	Gly	Ser 10	Val	Asn	Glu	Ala	Cys 15	Leu
Phe	Pro	Gly	Val 20	Ser	Phe	His	Gly	Leu 25	Tyr	Phe	Ser	Ser	Ser 30	Ser	Gly
Ser	Phe	Ala 35	Gly	Ser	Ser	Leu	Trp 40	Lys	Leu	His	Glu	Arg 45	Trp	Leu	Gly
Leu	Gly 50	Phe	Ala	Gly	Val	Tyr 55	Ser	Arg	Val	Lys 60	Glu	Trp	Asp	Leu	
Arg 65	Pro	Arg	Leu	Gly	Thr 70	Thr	Gln	Ala	Glu	Lys 75	Gly	Arg	Phe	His	His 80
Ser	Gln	Cys	Pro	Pro 85	His	Ser	Asn	Tyr	Leu 90	Thr	Pro	Thr	Pro	Thr 95	Leu
Thr	Pro	Thr	Pro 100	Pro	Arg	Asp	Arg	Gln 105	Gly	Cys	His	Gly	Gly 110	Pro	Glu
Gly	Ala	Gly	Ser	Gly	Cys	Pro	Cys	Ala	Gly	Pro	Ser	Gln	Thr	Ser	Pro

00673667122700

115

120

125

Pro	Leu	Lys	Leu	Lys	His	Ser	Cys	Glu	Glu	Gly	Ser	Glu	Glu	Gly	Pro
	130					135					140				
Leu	Ser	His	Gly	Cys	Leu	Phe	Pro	Pro	Leu	Cys	His	Arg			
145					150					155					

&lt;210&gt; 588

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 588

Asn	Thr	Met	Ala	Val	Ala	Ala	Val	Lys	Trp	Val	Met	Ser	Lys	Arg	Thr
1				5					10					15	
Ile	Leu	Lys	His	Leu	Phe	Pro	Val	Gln	Asn	Gly	Ala	Leu	Tyr	Cys	Val
			20					25					30		
Cys	His	Lys	Ser	Thr	Tyr	Ser	Pro	Leu	Pro	Asp	Asp	Tyr	Asn	Cys	Asn
		35					40					45			
Val	Glu	Leu	Ala	Leu	Thr	Ser	Asp	Gly	Arg	Thr	Ile	Val	Cys	Tyr	His
	50					55					60				
Pro	Ser	Val	Asp	Ile	Pro	Tyr	Glu	His	Thr	Lys	Pro	Ile	Pro	Arg	Pro
65					70					75					80
Asp	Pro	Val	His	Asn	Asn	Glu	Glu	Thr	His	Asp	Gln	Val	Leu	Lys	Thr
				85					90					95	
Arg	Leu	Glu	Glu	Lys	Val	Glu	His	Leu	Glu	Glu	Gly	Pro	Met	Ile	Glu
			100					105					110		
Gln	Leu	Ser	Lys	Met	Phe	Phe	Thr	Thr	Lys	His	Arg	Trp	Tyr	Pro	His
		115					120					125			
Gly	Arg	Tyr	His	Arg	Cys	Arg	Lys	Asn	Leu	Asn	Pro	Pro	Lys	Asp	Arg
	130					135					140				

&lt;210&gt; 589

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 589

Ile	His	Gln	Thr	Ala	Phe	Ser	Gln	Met	Ala	Asn	Glu	Ala	His	Phe	Ser
1				5					10					15	
Leu	Ile	Pro	Pro	Gly	Thr	Ser	Ala	Ser	Ser	Val	Phe	Trp	Arg	Ile	Gln
			20					25					30		
Ile	Leu	Thr	Thr	Ser	Val	Ile	Pro	Ser	Met	Arg	Ile	Pro	Thr	Val	Leu
		35					40					45			
Ser	Ser	Lys	Glu	His	Phe	Ala	Lys	Leu	Phe	Tyr	His	Arg	Ser	Phe	Leu
	50					55					60				
Lys	Val	Phe	Asn	Phe	Phe	Phe	Gln	Ser	Gly	Phe	Gln	His	Leu	Ile	Met
65						70				75					80

Cys	Phe	Phe	Ile	Ile 85	Met	His	Arg	Ile	Trp 90	Pro	Arg	Asp	Arg	Phe 95	Cys
Val	Phe	Ile	Trp 100	Asn	Val	His	Arg	Arg 105	Val	Val	Ala	Tyr	Tyr 110	Cys	Pro
Ala	Ile	Arg 115	Ser	Gln	Ser	Lys	Leu 120	Tyr	Val	Ala	Ile	Ile 125	Val	Ile	Trp

<210> 590  
 <211> 61  
 <212> PRT  
 <213> homo sapiens

<400> 590

Lys 1	Leu	Val	Cys	Leu 5	Glu	Ala	Asp	Ser	Lys 10	Ser	Ser	Phe	Ser	Ser 15	Glu
His	Leu	Phe	Ser 20	Tyr	His	Leu	Ile	Ser 25	Ile	Leu	Lys	His	His 30	Gly	Cys
Ser	Cys	Ser 35	Lys	Met	Gly	Asp	Val 40	Lys	Glu	Asn	Tyr	Leu 45	Glu	Thr	Phe
Ile	Ser 50	Ser	Pro	Lys	Trp	Ser 55	Phe	Ile	Leu	Cys	Leu 60	Ser			

<210> 591  
 <211> 173  
 <212> PRT  
 <213> homo sapiens

<400> 591

Ala 1	Gln	Glu	Ser	Pro 5	Trp	Gln	Leu	Cys	Arg 10	Gly	Ala	Arg	Thr	Ser 15	Lys
Arg	Lys	Leu	Pro 20	Lys	Leu	Gly	Met	Glu 25	Gln	His	Cys	Asn	Glu 30	Met	Cys
Pro	Pro	Ser 35	Ser	Leu	Phe	Leu	Pro 40	Gly	Ala	Tyr	Lys	Ala 45	Gln	Met	Tyr
Ser	Asp 50	Val	Trp	Thr	Asn	Thr 55	Lys	Lys	Lys	Lys	Lys 60	Lys	Lys	Lys	Lys
Lys 65	Ala	Phe	Leu	Ser	His 70	Arg	His	Lys	Thr	Gln 75	Ile	Ile	Tyr	Cys	Tyr 80
Glu	Ala	Leu	Phe	Thr 85	Asn	Gly	Gln	Phe	Leu 90	His	Phe	Ile	Ala	Ala 95	Cys
Glu	Arg	Leu	Pro 100	Asp	Gly	Arg	Pro	Ile 105	Ser	Leu	Val	Leu	Gln 110	Thr	Ser
Ser	Gln	Ala 115	Ala	Phe	Tyr	Gln	Lys 120	Gly	Glu	Asn	Ser	Cys 125	Leu	Ser	Phe
Leu	Lys 130	Asn	Ala	Phe	Leu	Tyr 135	Leu	Ser	Ile	Arg	His 140	Tyr	Thr	Ser	Glu

00673305-122700

Leu 145	Tyr	Lys	Arg	Pro	Gly 150	Gly	Thr	Met	Ser	Leu 155	Val	Asp	Thr	Phe	His 160
Cys	Ser	Val	Ala	Pro 165	Phe	Leu	Ala	Trp	Glu 170	Ala	Ser	Ala			

<210> 592  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 592

Thr 1	Cys	Glu	Pro	Phe 5	Arg	Asn	Pro	Gln	Val 10	Gly	Lys	Asp	Pro	Thr 15	Pro
Ser	Leu	Arg	Ile 20	Ile	Cys	Leu	Ala	Ile 25	Thr	Gly	Ser	Trp	Lys 30	Cys	Phe
Leu	Gly	Cys 35	Val	Lys	Ile	Asn	Gln 40	Gly	Gly	Met	Lys	His 45	Ile	Phe	Leu
Ala	Thr 50	Lys	Leu	Glu	Phe	Leu 55	Arg	Glu	Gln	Met	Gln 60	Arg	Asp	Leu	Leu
Leu 65	Leu	Ala	Arg	Leu	Gln 70	Gly	Pro	Leu	Trp	Ser 75	His	Thr	Glu	Ala	Val 80
Thr	Gly	His	Lys	Pro 85	Arg	Arg	Ala	Arg	Gly 90	Ser	Cys	Ala	Glu	Ala 95	Pro
Gly	Pro	Leu	Ser 100	Gly	Ser	Phe	Pro	Ser 105							

<210> 593  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 593

Thr 1	Cys	Glu	Pro	Phe 5	Arg	Asn	Pro	Gln	Val 10	Gly	Lys	Asp	Pro	Thr 15	Pro
Ser	Leu	Arg	Ile 20	Ile	Cys	Leu	Ala	Ile 25	Thr	Gly	Ser	Trp	Lys 30	Cys	Phe
Leu	Gly	Cys 35	Val	Lys	Ile	Asn	Gln 40	Gly	Gly	Met	Lys	His 45	Ile	Phe	Leu
Ala	Thr 50	Lys	Leu	Glu	Phe	Leu 55	Arg	Glu	Gln	Met	Gln 60	Arg	Asp	Leu	Leu
Leu 65	Leu	Ala	Arg	Leu	Gln 70	Gly	Pro	Leu	Trp	Ser 75	His	Thr	Glu	Ala	Val 80
Thr	Gly	His	Lys	Pro 85	Arg	Arg	Ala	Arg	Gly 90	Ser	Cys	Ala	Glu	Ala 95	Pro
Gly	Pro	Leu	Ser 100	Gly	Ser	Phe	Pro	Ser 105							

<210> 594

00673305.122700



<211> 172  
 <212> PRT  
 <213> homo sapiens

<400> 594

Thr 1	Pro	Ala	Leu	Arg 5	Ala	Arg	Ser	Leu	Arg 10	Asp	Arg	Cys	Ala	Arg 15	Ala
Pro	Cys	Pro	His 20	Gly	Gly	Gln	Gln	Arg 25	Arg	Arg	Arg	Arg	Leu 30	Asn	Ala
Glu	Gly	Ala 35	Glu	Gly	Ala	Arg	Gly 40	Gly	Gly	Ser	Ser	Tyr 45	Ser	Glu	Met
Ala	Glu 50	Thr	Val	Ala	Asp	Thr 55	Arg	Arg	Leu	Ile	Thr 60	Lys	Pro	Gln	Asn
Leu 65	Asn	Asp	Ala	Tyr	Gly 70	Pro	Pro	Ser	Asn	Phe 75	Leu	Glu	Ile	Asp	Val 80
Ser	Asn	Pro	Gln	Thr 85	Val	Gly	Val	Gly	Arg 90	Gly	Arg	Phe	Thr	Thr 95	Tyr
Glu	Ile	Arg	Val 100	Lys	Thr	Asn	Leu	Pro 105	Ile	Phe	Lys	Leu	Lys 110	Glu	Ser
Thr	Val	Arg 115	Arg	Arg	Tyr	Ser	Asp 120	Phe	Glu	Trp	Leu	Arg 125	Ser	Glu	Leu
Glu	Arg 130	Glu	Ser	Lys	Val	Val 135	Val	Pro	Pro	Leu	Pro 140	Gly	Lys	Ala	Phe
Leu 145	Arg	Gln	Phe	Leu	Leu 150	Glu	Glu	Met	Met	Glu 155	Tyr	Leu	Met	Thr	Ile 160
Leu	Leu	Arg	Lys	Glu 165	Asn	Lys	Gly	Trp	Ser 170	Ser	Leu				

<210> 595  
 <211> 127  
 <212> PRT  
 <213> homo sapiens

<400> 595

Ser 1	Ala	Ala	Gly	Cys 5	Gln	Pro	Arg	Ser	Pro 10	Pro	Phe	Arg	Cys	Ser 15	Cys
Cys	Arg	Arg	Arg 20	Gly	Leu	Pro	Pro	Pro 25	Pro	Pro	Arg	Ser	Ala 30	Ala	Ala
Ala	Gly	Ala 35	Ala	Ala	Arg	Arg	Gly 40	Asp	Thr	Gly	Leu	Ala 45	Arg	Ser	Gly
Arg	Glu 50	Glu	Asn	Glu	His 55	Val	Glu	Arg	Ala	Phe	Thr 60	Pro	His	Ala	Lys
Leu 65	Leu	Pro	Ala	Pro	Leu 70	Lys	Leu	Pro	Pro	Pro 75	Ser	Pro	Gly	Glu	Lys 80
Arg	Leu	Thr	Ser	Trp 85	Asn	Ala	Thr	Pro	Gly 90	Ser	Arg	Glu	Ala	Arg 95	Pro

006733667122700

Arg	Leu	Gly	Arg	Gly	Thr	Ala	Asp	Trp	Gly	Val	Arg	Arg	Ser	Gly	Val
			100					105					110		
Met	Gly	Leu	Gly	Val	Ala	Asn	Arg	Phe	Arg	Pro	Asp	Tyr	Ser	Ala	
		115					120					125			

<210> 596  
 <211> 123  
 <212> PRT  
 <213> homo sapiens

<400> 596

Phe	Thr	Ser	Gln	Pro	Phe	Lys	Val	Thr	Val	Ser	Ser	Ser	Asn	Ser	Arg
1				5					10					15	
Phe	Phe	Gln	Leu	Glu	Asn	Arg	Lys	Ile	Cys	Leu	Asp	Pro	Asp	Phe	Val
			20					25					30		
Ser	Gly	Glu	Ala	Ala	Pro	Ala	Asp	Pro	His	Arg	Leu	Arg	Val	Ala	His
		35					40					45			
Ile	Asp	Leu	Glu	Glu	Val	Ala	Gly	Gly	Ser	Val	Gly	Val	Ile	Gln	Val
	50					55					60				
Leu	Arg	Leu	Gly	Asp	Gln	Pro	Pro	Gly	Val	Ser	His	Gly	Leu	Arg	His
	65				70					75				80	
Phe	Ala	Val	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Ser	Leu	Arg	Pro	Leu	Arg
				85					90					95	
Val	Gln	Pro	Pro	Pro	Pro	Ala	Leu	Leu	Pro	Ala	Val	Gly	Thr	Arg	Gly
			100					105					110		
Ser	Arg	Ala	Ala	Val	Ala	Lys	Arg	Thr	Ser	Thr					
		115					120								

<210> 597  
 <211> 262  
 <212> PRT  
 <213> homo sapiens

<400> 597

Ser	Cys	Gly	Asp	Val	Glu	Gln	Lys	Ile	Gln	Phe	Lys	Arg	Glu	Thr	Ala
1				5					10					15	
Ser	Leu	Lys	Leu	Leu	Pro	His	Gln	Pro	Arg	Ile	Val	Glu	Met	Lys	Lys
			20					25					30		
Gly	Ser	Asn	Gly	Tyr	Gly	Phe	Tyr	Leu	Arg	Ala	Gly	Ser	Glu	Gln	Lys
		35					40					45			
Gly	Gln	Ile	Ile	Lys	Asp	Ile	Asp	Ser	Gly	Ser	Pro	Ala	Glu	Glu	Ala
	50					55					60				
Gly	Leu	Lys	Asn	Asn	Asp	Leu	Val	Val	Ala	Val	Asn	Gly	Glu	Ser	Val
	65				70					75					80
Glu	Thr	Leu	Asp	His	Asp	Ser	Val	Val	Glu	Met	Ile	Arg	Lys	Gly	Gly
				85					90					95	

00673305-12700



1			5			10			15						
Pro	Pro	Ala	Pro 20	Asn	Cys	Gly	Asp	Glu 25	Glu	Arg	Lys	Gln	Trp 30	Leu	Trp
Phe	Leu	Ser 35	Glu	Gly	Arg	Leu	Arg 40	Thr	Glu	Arg	Ser	Asn 45	His	Gln	Gly
His	Arg 50	Phe	Trp	Lys	Ser	Ser 55	Arg	Gly	Gly	Trp	Leu 60	Glu	Glu	Gln	

<210> 600  
 <211> 336  
 <212> PRT  
 <213> homo sapiens

<400> 600

Lys 1	Leu	Asn	Phe	Asn 5	Thr	Met	Arg	Cys	Cys 10	His	Ile	Cys	Lys	Leu 15	Pro
Gly	Arg	Val	Met 20	Gly	Ile	Arg	Val	Leu 25	Arg	Leu	Ser	Leu	Val 30	Val	Ile
Leu	Val	Leu 35	Leu	Leu	Val	Ala	Gly 40	Ala	Leu	Thr	Ala	Leu 45	Leu	Pro	Ser
Val	Lys 50	Glu	Asp	Lys	Met	Leu 55	Met	Leu	Arg	Arg	Glu 60	Ile	Lys	Ser	Gln
Gly 65	Lys	Ser	Thr	Met	Asp 70	Ser	Phe	Thr	Leu	Ile 75	Met	Gln	Thr	Tyr	Asn 80
Arg	Thr	Asp	Leu	Leu 85	Leu	Lys	Leu	Leu	Asn 90	His	Tyr	Gln	Ala	Val 95	Pro
Asn	Leu	His	Lys 100	Val	Ile	Val	Val	Trp 105	Asn	Asn	Ile	Gly	Glu 110	Lys	Ala
Pro	Asp	Glu 115	Leu	Trp	Asn	Ser	Leu 120	Gly	Pro	His	Pro	Ile 125	Pro	Val	Ile
Phe	Lys 130	Gln	Gln	Thr	Ala	Asn 135	Arg	Met	Arg	Asn	Arg 140	Leu	Gln	Val	Phe
Pro 145	Glu	Leu	Glu	Thr	Asn 150	Ala	Val	Leu	Met	Val 155	Asp	Asp	Asp	Thr	Leu 160
Ile	Ser	Thr	Pro	Asp 165	Leu	Val	Phe	Ala	Phe 170	Ser	Val	Trp	Gln	Gln 175	Phe
Pro	Asp	Gln	Ile 180	Val	Gly	Phe	Val	Pro 185	Arg	Lys	His	Val	Ser 190	Thr	Ser
Ser	Gly	Ile 195	Tyr	Ser	Tyr	Gly	Ser 200	Phe	Glu	Met	Gln	Ala 205	Pro	Gly	Ser
Gly	Asn 210	Gly	Asp	Gln	Tyr	Ser 215	Met	Val	Leu	Ile	Gly 220	Ala	Ser	Phe	Phe
Asn 225	Ser	Lys	Tyr	Leu	Glu 230	Leu	Phe	Gln	Arg	Gln 235	Pro	Ala	Ala	Val	His 240

00673705-122700

Ala	Leu	Ile	Asp	Asp 245	Thr	Gln	Asn	Cys	Asp 250	Asp	Ile	Ala	Met	Asn 255	Phe	
Ile	Ile	Ala	Lys 260	His	Ile	Gly	Lys	Thr 265	Ser	Gly	Ile	Phe	Val 270	Lys	Pro	
Val	Asn	Met 275	Asp	Asn	Leu	Glu	Lys 280	Glu	Thr	Asn	Ser	Gly 285	Tyr	Ser	Gly	
Met	Trp 290	His	Arg	Ala	Glu	His 295	Ala	Leu	Gln	Arg	Ser 300	Tyr	Cys	Ile	Asn	
Lys 305	Leu	Val	Asn	Ile	Tyr 310	Asp	Ser	Met	Pro	Leu 315	Arg	Tyr	Ser	Asn	Ile 320	
Met	Ile	Ser	Gln	Phe 325	Gly	Phe	Pro	Tyr	Ala 330	Asn	Tyr	Lys	Arg	Lys 335	Ile	

<210> 601  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 601

His 1	Ala	Leu	Lys	Ile 5	Leu	Gln	His	Tyr	Asp 10	Phe	Pro	Val	Trp	Phe 15	Ser	
Ile	Cys	Gln	Leu 20	Gln	Lys	Lys	Asn	Ile 25	Lys	Val	Lys	Gln	Thr 30	Lys	Thr	
Asn	Leu	Lys 35	Thr	Ala	Trp	His	Leu 40	Ser	Ser	Phe	Ser	Met 45	Leu	Cys	Ile	
Phe 50	Leu	Ser	Asn	Ile	Met	Asn 55	Phe	Ile	Tyr	Ser	Arg 60	Ser	Leu	Tyr	Asn	
Arg 65	Lys	Lys	Ser	Ala	Val 70	Leu	Leu	Gly	Tyr	Lys 75	Ile	His	Ile	Thr	Phe 80	
Glu	Ser	Gln	Glu	Val 85	Gly	Leu	Ile	Gln	Leu 90	Gly	Leu	Leu	Met	Lys 95	Ser	
Phe	His	Pro	Gly 100	Ile												

<210> 602  
 <211> 90  
 <212> PRT  
 <213> homo sapiens

<400> 602

Phe 1	Lys	Ser	Phe	Asn 5	Lys	Arg	Ser	Val	Leu 10	Leu	Tyr	Val	Cys	Ile 15	Met	
Arg	Val	Lys	Glu 20	Ser	Met	Val	Asp	Leu 25	Pro	Trp	Asp	Phe	Ile 30	Ser	Leu	
Arg	Asn	Met 35	Ser	Ile	Leu	Ser	Ser 40	Leu	Thr	Leu	Gly	Ser 45	Lys	Ala	Val	
Lys	Ala	Pro	Ala	Thr	Ser	Asn	Asn	Thr	Arg	Met	Thr	Thr	Lys	Asp	Asn	

00673335.122700

50					55					60					
Arg 65	Ser	Thr	Arg	Ile	Pro 70	Ile	Thr	Leu	Pro	Gly 75	Ser	Leu	Gln	Met	Trp 80
Gln	His	Leu	Ile	Val 85	Leu	Lys	Phe	Asn	Phe 90						

<210> 603  
 <211> 163  
 <212> PRT  
 <213> homo sapiens

<400> 603

Ile 1	Tyr	Gly	Val	Ser 5	Phe	Leu	Ile	Phe	Asn 10	Ile	Lys	Asn	Ile	Tyr 15	Val
Ser	Val	Ile	Pro 20	Cys	Gln	Gly	Cys	Leu 25	Leu	Val	Cys	Leu	Arg 30	Phe	Cys
Phe	Ile	Phe 35	Ile	His	Val	Val	Val 40	Ile	Phe	Ser	Ser	Gln 45	Phe	Leu	Leu
Val	Ser 50	Pro	Phe	Pro	Gly	Ser 55	Phe	Leu	Leu	Leu	Leu 60	Leu	Ser	Val	Gly
Asp 65	Asp	Lys	Leu	Val	Ser 70	Leu	Arg	Ala	Leu	His 75	Leu	Trp	Ile	Phe	Leu 80
Xxx	Ser	Leu	Thr 85	Gln	Pro	Ala	Pro	Val 90	Gly	Ser	Gly	Pro	Val 95	Leu	
Arg	Leu	Pro	Arg 100	Ser	Leu	Phe	His 105	Leu	Gln	Val	Cys	Leu	Pro 110	Xxx	Pro
Ala	Pro	Gly 115	Leu	Ala	Pro	Ala 120	Ala	Ala	Cys	Pro	Ser	Glu 125	Ala	Leu	Leu
Ser	Pro 130	Pro	Gly	Ser	His	Gly 135	Trp	Phe	Pro	Leu	Ser 140	Gln	Leu	Val	Ser
Leu 145	Asn	Pro	Lys	Pro	Leu 150	Arg	Asn	Trp	Gly	Leu 155	Val	Ser	Gly	Thr	Cys 160
Cys	Tyr	Gln													

<210> 604  
 <211> 150  
 <212> PRT  
 <213> homo sapiens

<400> 604

Pro 1	Leu	Ser	Phe	Leu 5	Met	Tyr	Lys	Thr	Leu 10	Leu	Ser	Gly	Leu	Glu 15	Phe
Glu	His	Leu	Trp 20	Xxx	Phe	Ile	Tyr	Phe 25	Ala	Xxx	Val	Cys	Gly 30	Gln	Ser
Asn	Ile	Phe 35	Pro	Lys	Tyr	Ile	Leu 40	Pro	Arg	Lys	Xxx	Lys 45	Lys	Gln	Ile

00673305-122700

Arg	Xxx 50	Phe	Asp	Xxx	Lys	Xxx 55	Asn	Arg	Pro	Xxx	Lys 60	Gly	Ala	Xxx	Thr
Trp	65	Ser	Arg	Ala	Trp	Xxx 70	Arg	Gly	Lys	Ala	Xxx 75	Arg	Gly	Gln	Cys 80
Cys	Gly	Gln	Ile	Cys 85	Ala	Tyr	Phe	Ile	Thr 90	Gly	Val	Lys	Xxx	Lys 95	Gln
Ser	Xxx	Ile	Asp 100	Val	Xxx	Arg	Ile	Tyr 105	Thr	Val	Xxx	Arg	Asn 110	Xxx	Arg
Xxx	Xxx	Phe 115	Xxx	Lys	Asn	Arg	Asn 120	Thr	Xxx	Trp	Xxx	Xxx 125	Phe	Tyr	His
Xxx	Xxx 130	Tyr	Thr	Phe	Ser	Leu 135	Trp	Xxx	Asn	Xxx	Leu 140	Thr	Lys	Leu	Xxx
Phe	Lys	Ile	Lys	Leu	Met 145										

<210> 605  
 <211> 108  
 <212> PRT  
 <213> homo sapiens  
 <400> 605

Leu	Asp	Phe	Lys	Xxx 5	Gln	Phe	Cys	Glu	Ser 10	Ile	Xxx	Pro	Gln	Ala 15	Lys
Cys	Val	Xxx	Xxx 20	Met	Ile	Lys	Xxx	Xxx 25	Pro	Xxx	Xxx	Ile	Pro 30	Val	Phe
Leu	Lys	Xxx 35	Val	Pro	Xxx	Ile	Ser 40	Xxx	His	Cys	Ile	Tyr 45	Pro	Xxx	Asp
Ile	Asn 50	Xxx	Thr	Leu	Phe	Ser 55	Phe	Tyr	Ser	Ser	Asn 60	Lys	Val	Gly	Thr
Asp	Leu	Ser	Thr	Thr	Asn 70	Leu	Pro	Ser	Xxx	Cys 75	Leu	Ala	Ser	Xxx	Pro 80
Cys	Ser	Ala	Pro	Gly 85	Xxx	Xxx	Pro	Leu	Xxx 90	Xxx	Pro	Val	Xxx	Phe 95	Xxx
Val	Lys	Xxx	Pro 100	Asn	Leu	Leu	Leu	Ala 105	Phe	Ser	Trp				

<210> 606  
 <211> 203  
 <212> PRT  
 <213> homo sapiens  
 <400> 606

Gly	Pro	Ser	Ala	Leu 5	Val	His	Ser	Val	Arg 10	Pro	Asp	Leu	Cys	Ser 15	Asn
Pro	Leu	Ser	Cys 20	Gly	Ser	Leu	Ala	Cys 25	Met	Ala	Tyr	Thr	Gly 30	Glu	Leu
Gly	Leu	Trp	Ala	Val	Gln	Thr	Gln	Gly	Ser	His	Phe	Ala	Phe	Pro	Leu

0067305-122700

00673305-122700

35					40					45					
Leu	Ser	Pro	Phe	Ser	Ile	Leu	Ala	Leu	Arg	Gln	Asn	Phe	Ser	Gln	Arg
	50					55					60				
Arg	Thr	Leu	Cys	Cys	Pro	Arg	Ser	Ala	Val	Ile	Leu	Pro	Phe	Leu	Pro
65					70					75					80
Ser	Phe	His	Pro	Ser	Ser	Ala	Gln	Met	Lys	Ser	Ser	Arg	Asn	Ser	Ser
				85					90					95	
Phe	Leu	Pro	Leu	Trp	Asp	Ser	Glu	Thr	Gly	Asn	Leu	Gln	Gly	Gly	Val
			100					105					110		
Phe	Pro	Ser	Pro	Leu	Phe	Leu	Phe	Ser	Thr	Pro	Arg	Gly	Thr	Lys	Ala
		115					120					125			
Ala	Val	Pro	Thr	Ser	Gly	Thr	Glu	Leu	His	Thr	Ile	Val	Gly	Lys	Leu
	130					135					140				
Gln	Gly	Pro	Leu	Leu	Leu	Val	Leu	Arg	Ala	His	Leu	Cys	Tyr	Trp	Ser
145					150					155					160
Phe	Trp	Gln	Lys	Arg	Lys	Met	Ile	Glu	Pro	Arg	Val	Ala	Pro	Glu	Cys
				165					170					175	
Ser	Ser	Leu	Thr	Val	Glu	Gly	Pro	Lys	Leu	Val	Phe	Arg	Ala	His	Pro
			180					185					190		
Arg	Arg	Glu	Val	Ile	Arg	Cys	His	Ala	Phe	Cys					
		195					200								

<210> 607

<211> 154

<212> PRT

<213> homo sapiens

<400> 607

Glu	Val	Arg	Gln	Lys	Glu	Trp	Cys	Leu	Leu	Trp	Ser	Phe	Pro	Phe	Pro
1				5						10				15	
Gly	Ala	Gly	Leu	Cys	Ala	Lys	Leu	Gly	Pro	Gln	His	Ile	Trp	Ser	Thr
			20					25					30		
Leu	Leu	Val	Gly	Ala	Arg	Pro	Glu	His	Leu	Thr	Gln	Pro	Val	His	Thr
		35					40					45			
Ala	Pro	Arg	Val	Pro	Pro	Leu	Ser	Gln	Ala	Gly	Pro	Thr	Ala	Pro	Gly
	50					55					60				
Ser	Ala	Asp	Lys	Gly	Met	Ala	Cys	Pro	Leu	Arg	Cys	Gln	Asn	Ser	Ile
65					70					75					80
Gln	Lys	Ala	Pro	Pro	Gln	Val	Asp	Val	Val	Pro	Gly	Ala	Gly	Glu	Glu
			85						90					95	
Ser	Gly	Thr	Thr	Thr	Leu	Ala	Val	Asn	Leu	Ser	Asn	Arg	Gly	Leu	Gly
			100					105					110		
Phe	Leu	Val	Ala	Ala	Ser	Cys	Pro	Gly	Leu	Glu	Val	His	Arg	Ser	Arg
		115					120					125			



Gly	Val	Pro	Leu	Gly	Thr	Lys	Asp	Met	Pro	His	Trp	Gly	Cys	Asn	Gly
	130					135					140				
Glu	Lys	Ser	Gly	Lys	Leu	Gly	Ala	Gln	Leu						
145					150										

<210> 608  
 <211> 123  
 <212> PRT  
 <213> homo sapiens

<400> 608

Cys	Gly	Val	Leu	Ser	Leu	Arg	Trp	Val	Gln	Gln	Pro	Trp	Phe	Leu	Trp
1				5					10					15	
Gly	Leu	Arg	Ile	Arg	Ile	Val	Gly	Arg	Glu	Lys	Leu	Leu	Leu	Glu	Asp
			20					25					30		
Phe	Leu	Ser	Gln	Ser	Pro	Arg	Glu	Val	Glu	Arg	Arg	Asn	Phe	Cys	Trp
		35					40					45			
Thr	Ser	Ser	Gly	Gln	Arg	Lys	Asp	Gly	Met	Lys	Val	Glu	Lys	Ala	Glu
	50					55					60				
Leu	Gln	Leu	Ser	Gly	Asp	Asn	Lys	Glu	Phe	Phe	Ser	Gly	Lys	Ser	Phe
65					70					75					80
Val	Leu	Glu	Gln	Gly	Trp	Lys	Met	Gly	Thr	Thr	Lys	Glu	Lys	Gln	Ser
				85					90					95	
Val	Thr	Leu	Gly	Phe	Gly	Gln	Pro	Arg	Gly	Pro	Ala	Pro	Gln	Tyr	Lys
			100					105					110		
Pro	Tyr	Arg	Pro	Gly	Thr	His	Arg	Arg	Val	Asp					
		115					120								

<210> 609  
 <211> 88  
 <212> PRT  
 <213> homo sapiens

<400> 609

Leu	Val	Glu	Pro	Asn	Gly	Leu	Phe	Trp	Phe	His	Phe	Ser	Ala	Ser	Arg
1				5					10					15	
Arg	Gln	Asn	Lys	Glu	Ser	His	Ser	Lys	Met	Phe	Ile	Val	Asp	Asn	Met
			20					25					30		
Ser	Leu	Lys	Val	Val	Pro	Leu	Cys	Ser	Tyr	Ser	Thr	Glu	Glu	Met	Ile
		35					40					45			
His	Ile	Pro	Ile	Ile	Asp	Met	Val	Ser	Gln	Ser	Glu	Glu	Ser	Phe	Arg
	50					55					60				
Arg	Leu	His	Lys	Tyr	Val	Leu	Cys	Thr	Cys	Pro	Met	Leu	Gly	Asn	Arg
65					70				75						80
Lys	Ile	Ile	Val	Ile	Asp	Lys	Thr								
				85											

<210> 610

00673305-132700

<211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 610

Ser	Cys	Phe	His	Lys	Leu	Ser	Thr	Gln	Glu	Pro	Asp	Gly	Lys	Lys	Asn
1				5					10					15	
Lys	Asn	Tyr	Ala	Asp	Asn	Tyr	Arg	Lys	Ile	Asn	Pro	Asn	Leu	Val	Lys
			20					25					30		
Leu	Val	Lys	Ala	Cys	Thr	Phe	Gln	Arg	Phe	Ile	Arg	Thr	Gly	Leu	Asn
		35					40					45			
Arg	Glu	Phe	Leu	Leu	Asn	Lys	Met	Ala	Leu	Thr	Leu	Val	Pro	Arg	Asn
	50					55					60				
Trp	Asn	Pro	Gln	Arg	Ser	Tyr	Thr	Gly	Asp	Asn	Ser	Ala	Leu	Ile	Leu
65					70					75					80

<210> 611  
 <211> 71  
 <212> PRT  
 <213> homo sapiens

<400> 611

Met	Gly	Ile	Thr	His	Glu	Cys	Val	Ile	Leu	Leu	Gly	Ala	Ser	Ala	Asn
1				5					10					15	
Ser	Leu	Thr	Val	Val	Pro	Ser	Leu	Thr	Leu	Pro	Val	His	His	Leu	Arg
			20					25					30		
Arg	Leu	Asp	Pro	Ser	Leu	Thr	Ser	Pro	Phe	Leu	Lys	Pro	Val	Ser	Phe
		35					40					45			
Ser	Leu	Leu	Pro	Asn	Trp	Leu	Trp	Leu	Phe	Leu	Gln	Pro	Phe	His	Ser
	50					55					60				
Arg	Ala	Ile	Phe	Ala	Lys	Glu									
65					70										

<210> 612  
 <211> 395  
 <212> PRT  
 <213> homo sapiens

<400> 612

Ala	Pro	Met	Arg	Pro	Glu	Arg	Pro	Arg	Pro	Arg	Gly	Ser	Ala	Pro	Gly
1				5					10					15	
Pro	Met	Glu	Thr	Pro	Pro	Trp	Asp	Pro	Ala	Arg	Asn	Asp	Ser	Leu	Pro
			20					25					30		
Pro	Thr	Leu	Thr	Pro	Ala	Val	Pro	Pro	Tyr	Val	Lys	Leu	Gly	Leu	Thr
		35					40					45			
Val	Val	Tyr	Thr	Val	Phe	Tyr	Ala	Leu	Leu	Phe	Val	Phe	Ile	Tyr	Val
	50					55					60				
Gln	Leu	Trp	Leu	Val	Leu	Arg	Tyr	Arg	His	Lys	Arg	Leu	Ser	Tyr	Gln

002227 985 122700

65				70				75				80			
Ser	Val	Phe	Leu	Phe 85	Leu	Cys	Leu	Phe	Trp 90	Ala	Ser	Leu	Arg	Thr 95	Val
Leu	Phe	Ser	Phe 100	Tyr	Phe	Lys	Asp	Phe 105	Val	Ala	Ala	Asn	Ser 110	Leu	Ser
Pro	Phe	Val 115	Phe	Trp	Leu	Leu	Tyr 120	Cys	Phe	Pro	Val	Cys 125	Leu	Gln	Phe
Phe	Thr 130	Leu	Thr	Leu	Met	Asn 135	Leu	Tyr	Phe	Thr	Gln 140	Val	Ile	Phe	Lys
Ala 145	Lys	Ser	Lys	Tyr	Ser 150	Pro	Glu	Leu	Leu	Lys 155	Tyr	Arg	Leu	Pro	Leu 160
Tyr	Leu	Ala	Ser	Leu 165	Phe	Ile	Ser	Leu	Val 170	Phe	Leu	Leu	Val	Asn 175	Leu
Thr	Cys	Ala	Val 180	Leu	Val	Lys	Thr	Gly 185	Asn	Trp	Glu	Arg	Lys 190	Val	Ile
Val	Ser	Val 195	Arg	Val	Ala	Ile	Asn 200	Asp	Thr	Leu	Phe	Val 205	Leu	Cys	Ala
Val	Ser 210	Leu	Ser	Ile	Cys	Leu 215	Tyr	Lys	Ile	Ser	Lys 220	Met	Ser	Leu	Ala
Asn 225	Ile	Tyr	Leu	Glu	Ser 230	Lys	Gly	Ser	Ser	Val 235	Cys	Gln	Val	Thr	Ala 240
Ile	Gly	Val	Thr	Val 245	Ile	Leu	Leu	Tyr	Thr 250	Ser	Arg	Ala	Cys	Tyr 255	Asn
Leu	Phe	Ile	Leu 260	Ser	Phe	Ser	Gln	Asn 265	Lys	Ser	Val	His	Ser 270	Phe	Asp
Tyr	Asp	Trp 275	Tyr	Asn	Val	Ser	Asp 280	Gln	Ala	Asp	Leu	Lys 285	Asn	Gln	Leu
Gly	Asp 290	Ala	Gly	Tyr	Val	Leu 295	Phe	Gly	Val	Val	Leu 300	Phe	Val	Trp	Glu
Leu 305	Leu	Pro	Thr	Thr	Leu 310	Val	Val	Tyr	Phe	Phe 315	Arg	Val	Arg	Asn	Pro 320
Thr	Lys	Asp	Leu	Thr 325	Asn	Pro	Gly	Met	Val 330	Pro	Ser	His	Gly	Phe 335	Ser
Pro	Arg	Ser	Tyr 340	Phe	Phe	Asp	Asn	Pro 345	Arg	Arg	Tyr	Asp	Ser 350	Asp	Asp
Asp	Leu	Ala 355	Trp	Asn	Ile	Ala	Pro 360	Gln	Gly	Leu	Gln	Gly 365	Gly	Phe	Ala
Pro	Asp 370	Tyr	Tyr	Asp	Trp	Gly 375	Gln	Gln	Thr	Asn	Ser 380	Phe	Leu	Ala	Gln
Ala 385	Gly	Thr	Leu	Gln	Arg 390	Leu	Asn	Phe	Gly	Ser 395					

<211> 213  
 <212> PRT  
 <213> homo sapiens

<400> 613

Ala 1	Arg	Cys	Ala	Glu 5	Thr	Pro	Ala	Gly	Ala 10	Ala	Ala	Ala	Val	Ser 15	Pro
Asp	Glu	Ala	Arg 20	Ala	Ser	Pro	Ala	Ala 25	Arg	Gln	Arg	Pro	Arg 30	Pro	Asp
Gly	Asp	Pro 35	Ala	Val	Gly	Pro	Ser 40	Pro	Gln	Arg	Leu	Ala 45	Ala	Ala	His
Ala	Asp 50	Pro	Gly	Arg	Ala	Pro 55	Leu	Arg	Glu	Ala	Trp 60	Pro	His	Arg	Arg
Leu 65	His	Arg	Val	Leu	Arg 70	Ala	Ala	Leu	Arg	Val 75	His	Leu	Arg	Ala	Ala 80
Leu	Ala	Gly	Ala	Ala 85	Leu	Pro	Pro	Gln	Ala 90	Ala	Gln	Leu	Pro	Glu 95	Arg
Leu	Pro	Leu	Ser 100	Leu	Pro	Leu	Leu	Gly 105	Leu	Pro	Ala	Asp	Arg 110	Pro	Leu
Leu	Leu	Leu 115	Leu	Gln	Arg	Leu	Arg 120	Gly	Gly	Gln	Phe	Ala 125	Gln	Pro	Leu
Arg	Leu 130	Leu	Ala	Ala	Leu	Leu 135	Leu	Pro	Cys	Val	Pro 140	Ala	Val	Phe	His
Pro 145	His	Ala	Asp	Glu	Leu 150	Val	Leu	His	Ala	Gly 155	Asp	Phe	Gln	Ser	Gln 160
Val	Lys	Ile	Phe	Ser 165	Arg	Ile	Thr	Gln	Ile 170	Pro	Val	Ala	Pro	Leu 175	Pro
Gly	Leu	Pro	Leu 180	His	Gln	Pro	Cys	Phe 185	Pro	Val	Gly	Glu	Phe 190	Asn	Leu
Cys	Cys	Ala 195	Gly	Lys	Asp	Gly	Lys 200	Leu	Gly	Glu	Glu	Gly 205	Tyr	Arg	Leu
Cys	Ala 210	Ser	Gly	His											

<210> 614  
 <211> 161  
 <212> PRT  
 <213> homo sapiens

<400> 614

Leu 1	Gly	Phe	Glu	Asn 5	His	Leu	Arg	Glu	Val 10	Gln	Val	His	Gln	Arg 15	Glu
Gly	Glu	Lys	Leu 20	Gln	Ala	His	Arg	Glu 25	Ala	Val	Glu	Gln	Pro 30	Glu	Asp
Glu	Gly	Ala 35	Glu	Arg	Ile	Gly	Arg 40	His	Glu	Val	Phe	Glu 45	Val	Glu	Gly

00573395.122700

Glu	Glu	Asp	Gly	Pro	Gln	Gly	Gly	Pro	Glu	Glu	Ala	Glu	Lys	Glu	Glu
	50					55					60				
Asp	Ala	Leu	Val	Ala	Glu	Pro	Leu	Val	Ala	Val	Thr	Gln	His	Gln	Pro
65					70				75						80
Glu	Leu	His	Val	Asp	Glu	His	Glu	Glu	Gln	Arg	Val	Glu	His	Gly	Val
				85					90					95	
Asp	Asp	Gly	Glu	Ala	Lys	Leu	His	Val	Gly	Gly	His	Gly	Arg	Gly	Gln
			100					105					110		
Arg	Gly	Arg	Gln	Arg	Val	Val	Ala	Gly	Trp	Val	Pro	Arg	Arg	Gly	Leu
		115					120					125			
His	Arg	Ala	Gly	Gly	Ala	Ala	Ala	Arg	Pro	Gly	Thr	Leu	Gly	Pro	His
	130					135					140				
Arg	Gly	Ser	Arg	Pro	Pro	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Arg	Ile	Ala
145					150					155					160

Pro

<210> 615  
 <211> 102  
 <212> PRT  
 <213> homo sapiens

<400> 615

His	Lys	Lys	Thr	Ser	Ser	Tyr	Ser	Gly	Val	Thr	Val	Cys	Ser	Tyr	Asp
1				5					10					15	
Ser	Ile	Ile	Arg	Leu	Lys	Ala	Gly	Glu	Ile	Cys	Val	Gln	Phe	Asn	Arg
			20					25					30		
Thr	Gln	Leu	Lys	Gly	Arg	Gln	Val	Gly	Trp	Glu	Arg	Lys	Leu	Leu	Ser
		35					40					45			
Gly	Gly	Ile	Arg	Gly	Asn	Gln	Ser	Lys	Thr	Lys	Phe	Tyr	Cys	Leu	Gln
	50					55					60				
Phe	Asn	Ser	Ile	Ile	Ala	Ile	Met	Cys	Ser	Gly	Lys	His	Ile	Pro	Val
65					70					75					80
Leu	Leu	Asp	Arg	Val	Ser	Phe	Pro	Phe	Ser	Gly	Thr	Lys	Met	Val	Glu
				85					90					95	
Gly	Ile	Ile	Asn	Pro	Thr										
			100												

<210> 616  
 <211> 86  
 <212> PRT  
 <213> homo sapiens

<400> 616

Val	Thr	Cys	Leu	Ser	Leu	Tyr	Val	Glu	Thr	Asn	Phe	Thr	Met	Ile	Thr
1				5					10					15	
Asp	Leu	Cys	Asn	Ile	Ser	Ser	Leu	Asn	Phe	His	Thr	Ile	Leu	Lys	Cys

00673333-122760





20							25							30						
Asp	Ala	Leu	Pro	Gly	His	Ser	Lys	Pro	Ser	Arg	Ser	Met	Glu	Ser	Ser					
		35					40					45								
Pro	Arg	Lys	Gly	Ser	Lys	Lys	Lys	Pro	Val	Lys	Val	Glu	Ala	Pro	Glu					
		50				55					60									
Tyr	Ile	Pro	Ile	Ser	Asp	Asp	Pro	Lys	Ser	Ser	Ala	Lys	Lys	Lys	Met					
					70					75					80					
Lys	Ser	Lys	Lys	Lys	Val	Glu	Gln	Pro	Val	Ile	Glu	Glu	Pro	Ala	Leu					
					85				90					95						
Lys	Arg	Lys	Thr	Arg	Lys	Lys	Arg	Lys	Glu	Ser	Gly	Val	Ala	Gly	Asp					
			100						105				110							
Pro	Trp	Arg	Glu	Glu	Thr	Asp	Thr	Asp	Leu	Glu	Val	Val	Leu	Glu	Lys					
		115					120					125								
Lys	Gly	Asn	Met	Asp	Glu	Ala	His	Ile	Asp	Gln	Val	Arg	Arg	Lys	Ala					
		130				135					140									
Leu	Gln	Glu	Glu	Ile	Asp	Arg	Glu	Ser	Gly	Lys	Thr	Glu	Ala	Ser	Glu					
					150					155					160					
Thr	Arg	Lys	Trp	Thr	Gly	Thr	Gln	Phe	Gly	Gln	Trp	Asp	Thr	Ala	Gly					
				165					170					175						
Phe	Glu	Asn	Glu	Asp	Gln	Lys	Leu	Lys	Phe	Leu	Arg	Leu	Met	Gly	Gly					
			180					185					190							
Phe	Lys	Asn	Leu	Ser	Pro	Ser	Phe	Ser	Arg	Pro	Ala	Ser	Thr	Ile	Ala					
		195					200					205								
Arg	Pro	Asn	Met	Ala	Leu	Gly	Lys	Lys	Ala	Ala	Asp	Ser	Leu	Gln	Gln					
		210				215					220									
Asn	Leu	Gln	Arg	Asp	Tyr	Asp	Arg	Ala	Met	Ser	Leu	Glu	Val	Gln	Pro					
					230					235					240					
Gly	Ser	Arg	Leu	Ala	Val	Phe	Ser	Thr	Ala	Pro	Asn	Lys	Ile	Phe	Tyr					
				245					250					255						
Ile	Asp	Arg	Asn	Ala	Ser	Lys	Ser	Val	Lys	Leu	Glu	Asp								
			260					265												

```
<210> 620
<211> 218
<212> PRT
<213> homo sapiens
```

<400> 620

Val 1	Arg	Val	Cys	Phe 5	Leu	Pro	Pro	Arg	Val 10	Ser	Cys	Tyr	Pro	Thr 15	Leu
Phe	Pro	Leu	Leu 20	Pro	Arg	Leu	Pro	Phe 25	Gln	Ser	Trp	Leu	Leu 30	Asp	Asp
Trp	Leu	Leu 35	Tyr	Leu	Leu	Phe	Gly 40	Leu	His	Leu	Phe	Leu 45	Cys	Gly	Gly



Leu	Arg	Val	Ile	Thr	Tyr	Gly	Asp	Val	Phe	Arg	Ser	Leu	Asn	Phe	Asp
	50					55					60				
Trp	Leu	Leu	Phe	Thr	Ser	Phe	Pro	Arg	Ala	Ala	Leu	His	Gly	Pro	Gly
65					70				75						80
Gly	Leu	Gly	Val	Ala	Trp	Glu	Gly	Ile	Ser	Leu	Leu	Val	Asp	Phe	Phe
				85					90					95	
Phe	Leu	Leu	His	Leu	Pro	Ile	Val	Phe	Ser	Gly	Ala	Leu	Pro	Xxx	Ser
			100					105					110		
Val	Ser	Xxx	Pro	Lys	Ala	Ala	Cys	Ser	Ser	Ser	Phe	Phe	Pro	Thr	Xxx
		115					120					125			
Ala	Ser	Val	Pro	Asn	Ile	Pro	Gly	Leu	Pro	Gly	Leu	Thr	Glu	Pro	Arg
	130					135					140				
Val	Leu	Asp	Arg	Glu	Gly	Xxx	Trp	Gly	Pro	Gly	Xxx	Pro	Phe	Phe	Ser
	145				150					155					160
Phe	Leu	Xxx	Phe	Phe	Glu	Leu	Leu	Ala	Asn	Ser	Gly	Phe	Leu	Leu	Thr
				165					170					175	
Leu	Ser	Xxx	Gly	Xxx	Gly	Glu	Val	Phe	Thr	Pro	Glu	Ala	Trp	Asp	Met
			180					185					190		
Ala	Arg	Gly	Asp	Phe	Leu	Xxx	Phe	Leu	Phe	Pro	Thr	Glu	Glu	Leu	Gln
		195					200					205			
Val	Ala	Lys	His	Leu	Leu	Pro	Glu	Ala	Gly						
	210					215									

<210> 621  
 <211> 389  
 <212> PRT  
 <213> homo sapiens

<400> 621

Ala	Ala	Gly	Ala	Cys	Gly	Ala	Arg	Gly	Ser	Gly	Arg	Arg	Gly	Ser	Tyr
1				5					10					15	
Val	Pro	Glu	Val	Arg	Cys	Gly	Ala	Pro	Gly	Gly	Ala	Ala	Gly	Thr	Gly
			20					25					30		
Ala	Pro	Arg	Ser	Cys	Cys	Cys	Gln	Thr	Asn	Pro	Gly	Pro	Pro	Ser	Ser
		35					40					45			
Leu	Arg	Arg	Ala	Phe	Arg	Arg	Arg	Glu	Leu	Pro	Phe	Pro	Ala	Cys	His
	50					55					60				
Glu	Ile	Gly	Leu	Gly	Ala	Glu	Ala	Gly	Ser	Gly	Pro	Pro	Pro	Ala	Pro
65					70					75					80
Ala	Ala	Arg	Glu	Ser	Arg	Ser	Arg	Ala	Met	Glu	Glu	Glu	Ala	Ser	Ser
				85					90					95	
Pro	Gly	Leu	Gly	Cys	Ser	Lys	Pro	His	Leu	Glu	Lys	Leu	Thr	Leu	Gly
			100					105					110		
Ile	Thr	Arg	Ile	Leu	Glu	Ser	Ser	Pro	Gly	Val	Thr	Glu	Val	Thr	Ile
		115					120					125			

09673305.122700

Ile	Glu	Lys	Pro	Pro	Ala	Glu	Arg	His	Met	Ile	Ser	Ser	Trp	Glu	Gln
	130					135					140				
Lys	Asn	Asn	Cys	Val	Met	Pro	Glu	Asp	Val	Lys	Asn	Phe	Tyr	Leu	Met
	145				150					155					160
Thr	Asn	Gly	Phe	His	Met	Thr	Trp	Ser	Val	Lys	Leu	Asp	Glu	His	Ile
				165					170					175	
Ile	Pro	Leu	Gly	Ser	Met	Ala	Ile	Asn	Ser	Ile	Ser	Lys	Leu	Thr	Gln
			180					185					190		
Leu	Thr	Gln	Ser	Ser	Met	Tyr	Ser	Leu	Pro	Asn	Ala	Pro	Thr	Leu	Ala
		195					200					205			
Asp	Leu	Glu	Asp	Asp	Thr	His	Glu	Ala	Ser	Asp	Asp	Gln	Pro	Glu	Lys
	210					215					220				
Pro	His	Phe	Asp	Ser	Arg	Ser	Val	Ile	Phe	Glu	Leu	Asp	Ser	Cys	Asn
	225				230					235					240
Gly	Ser	Gly	Lys	Val	Cys	Leu	Val	Tyr	Lys	Ser	Gly	Lys	Pro	Ala	Leu
				245					250					255	
Ala	Glu	Asp	Thr	Glu	Ile	Trp	Phe	Leu	Asp	Arg	Ala	Leu	Tyr	Trp	His
			260					265					270		
Phe	Leu	Thr	Asp	Thr	Phe	Thr	Ala	Tyr	Tyr	Arg	Leu	Leu	Ile	Thr	His
		275					280					285			
Leu	Gly	Leu	Pro	Gln	Trp	Gln	Tyr	Ala	Phe	Thr	Ser	Tyr	Gly	Ile	Ser
	290					295					300				
Pro	Gln	Ala	Lys	Gln	Trp	Phe	Ser	Met	Tyr	Lys	Pro	Ile	Thr	Tyr	Asn
	305				310					315					320
Thr	Asn	Leu	Leu	Thr	Glu	Glu	Thr	Asp	Ser	Phe	Val	Asn	Lys	Leu	Asp
				325					330					335	
Pro	Ser	Lys	Val	Phe	Lys	Ser	Lys	Asn	Lys	Ile	Val	Ile	Pro	Lys	Lys
			340					345					350		
Lys	Gly	Pro	Val	Gln	Pro	Ala	Gly	Gly	Gln	Lys	Gly	Pro	Ser	Gly	Pro
		355					360					365			
Ser	Gly	Pro	Ser	Thr	Ser	Ser	Thr	Ser	Lys	Ser	Ser	Ser	Gly	Ser	Gly
	370					375					380				
Asn	Pro	Thr	Arg	Lys											
	385														

<210> 622

<211> 109

<212> PRT

<213> homo sapiens

<400> 622

Ala	Arg	Pro	Ala	Pro	Ala	Gly	Arg	Glu	Gly	Arg	Gly	Glu	Gly	Glu	Ala
1				5					10					15	
Thr	Ser	Arg	Arg	Cys	Gly	Val	Gly	His	Arg	Ala	Gly	Pro	Arg	Glu	Pro

09672305-122700

20					25					30					
Ala	Pro	His	Gly	Ala	Ala	Ala	Val	Arg	Pro	Thr	Pro	Gly	Pro	His	His
		35					40					45			
His	Cys	Ala	Ala	Leu	Ser	Gly	Ala	Glu	Asn	Tyr	Arg	Ser	Arg	His	Ala
	50					55					60				
Met	Lys	Leu	Ala	Ser	Ala	Leu	Arg	Arg	Gly	Pro	Ala	Leu	His	Pro	Leu
	65					70				75					80
Pro	Pro	Arg	Ala	Asn	Arg	Gly	Arg	Glu	Pro	Trp	Arg	Arg	Arg	His	Arg
				85						90					95
Pro	Arg	Gly	Trp	Ala	Ala	Ala	Ser	Arg	Thr	Trp	Arg	Ser			
			100					105							

<210> 623  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 623

Arg	Ser	Ala	Gly	Gly	Phe	Ser	Met	Met	Val	Thr	Ser	Val	Thr	Pro	Gly
1				5					10					15	
Glu	Asp	Ser	Arg	Met	Arg	Val	Met	Pro	Arg	Val	Ser	Phe	Ser	Arg	Cys
			20					25					30		
Gly	Leu	Leu	Gln	Pro	Ser	Pro	Gly	Asp	Asp	Ala	Ser	Ser	Ser	Met	Ala
		35					40					45			
Arg	Asp	Arg	Asp	Ser	Arg	Ala	Ala	Gly	Ala	Gly	Gly	Gly	Pro	Asp	Pro
	50					55					60				
Ala	Ser	Ala	Pro	Arg	Pro	Ile	Ser	Trp	His	Ala	Gly	Asn	Gly	Ser	Ser
	65				70					75					80
Arg	Arg	Leu	Lys	Ala	Arg	Arg	Ser	Asp	Asp	Gly	Gly	Pro	Gly	Leu	Val
				85					90					95	

<210> 624  
 <211> 218  
 <212> PRT  
 <213> homo sapiens

<400> 624

Cys	Cys	Thr	Glu	His	Arg	Trp	Pro	Ala	Ser	Met	Pro	Pro	Gln	Leu	Gln
1				5					10					15	
Glu	Thr	Arg	Met	Asn	Arg	Ser	Ile	Pro	Val	Glu	Val	Asp	Glu	Ser	Glu
			20					25					30		
Pro	Tyr	Pro	Ser	Gln	Leu	Leu	Lys	Pro	Ile	Pro	Glu	Tyr	Ser	Pro	Glu
		35					40					45			
Glu	Glu	Ser	Glu	Pro	Pro	Ala	Pro	Asn	Ile	Arg	Asn	Met	Ala	Pro	Asn
	50					55					60				
Ser	Leu	Ser	Ala	Pro	Thr	Met	Leu	His	Asn	Ser	Ser	Gly	Asp	Phe	Ser
	65				70					75					80

Gln	Ala	His	Ser	Thr 85	Leu	Lys	Leu	Ala	Asn 90	His	Gln	Arg	Pro	Val 95	Ser	
Arg	Gln	Val	Thr 100	Cys	Leu	Arg	Thr	Gln 105	Val	Leu	Glu	Asp	Ser 110	Glu	Asp	
Ser	Phe	Cys 115	Arg	Arg	His	Pro	Gly 120	Leu	Gly	Lys	Ala	Phe 125	Pro	Ser	Gly	
Cys	Ser 130	Ala	Val	Ser	Glu	Pro 135	Ala	Ser	Glu	Ser	Val 140	Val	Gly	Ala	Leu	
Pro 145	Ala	Glu	His	Gln	Phe 150	Ser	Phe	Met	Glu	Lys 155	Arg	Asn	Gln	Trp	Leu 160	
Val	Ser	Gln	Leu	Ser 165	Ala	Ala	Ser	Pro	Asp 170	Thr	Gly	His	Asp	Ser 175	Asp	
Lys	Ser	Asp	Gln 180	Ser	Leu	Pro	Asn	Ala 185	Ser	Ala	Asp	Ser	Leu 190	Gly	Gly	
Ser	Gln	Glu 195	Met	Val	Gln	Arg	Pro 200	Gln	Pro	Xxx	Gln	Glu 205	Pro	Ser	Arg	
Pro	Gly 210	Ser	Ala	Asn	His	Arg 215	His	Gly	Ile							

<210> 625

<211> 212

<212> PRT

<213> homo sapiens

<400> 625

Asn 1	Leu	Gln	Ile	Thr 5	Ser	Gly	Leu	Tyr	Pro 10	Gly	Arg	Ser	Pro	Ala 15	Cys	
Ala	Leu	Lys	Phe 20	Trp	Arg	Thr	Val	Lys 25	Thr	Val	Ser	Ala	Gly 30	Asp	Thr	
Gln	Ala	Trp 35	Ala	Lys	Leu	Ser	Leu 40	Leu	Gly	Ala	Leu	Gln 45	Ser	Ala	Ser	
Leu	Arg 50	Leu	Ser	Leu	Trp	Leu 55	Glu	Pro	Ser	Leu	Gln 60	Ser	Ile	Ser	Phe	
His 65	Leu	Trp	Lys	Asn 70	Val	Ile	Asn	Gly	Trp	Tyr 75	Leu	Ser	Phe	Gln 80	Arg	
Leu	Leu	Leu	Thr 85	Leu	Ala	Met	Thr	Gln	Thr 90	Asn	Gln	Thr	Lys 95	Val	Tyr	
Leu	Met	Pro	Gln 100	Gln	Thr	Pro	Trp	Ala 105	Val	Ala	Arg	Arg	Trp 110	Cys	Asn	
Gly	Pro	Ser 115	Leu	His	Arg	Asn	Arg 120	Ala	Gly	Leu	Asp	Leu 125	Pro	Thr	Ile	
Asp	Thr 130	Gly	Tyr	Asp	Ser	Gln 135	Pro	Gln	Asp	Val	Leu 140	Gly	Ile	Arg	Gln	
Leu	Glu	Arg	Pro	Leu	Xxx	Leu	Thr	Ser	Val	Cys	Tyr	Pro	Gln	Asp	Leu	

00673305-122700

145					150					155				160
Pro	Arg	Pro	Leu	Arg	Ser	Arg	Glu	Phe	Pro	Gln	Phe	Glu	Pro	Gln
				165					170					175
Tyr	Pro	Ala	Cys	Ala	Gln	Met	Leu	Pro	Pro	Asn	Leu	Ser	Pro	His
			180					185					190	Ala
Pro	Trp	Asn	Tyr	His	Tyr	His	Cys	Pro	Gly	Ser	Pro	Asp	His	Gln
		195					200					205		Val
Xxx	Ile	Trp	Pro											
	210													

<210> 626  
 <400> 626  
 000

<210> 627  
 <400> 627  
 000

<210> 628  
 <400> 628  
 000

<210> 629  
 <400> 629  
 000

<210> 630  
 <211> 184  
 <212> PRT  
 <213> homo sapiens

<400> 630

Phe	Met	Ile	Asn	Val	Ser	Phe	Phe	Phe	Phe	Leu	Ala	Ala	Gly	Arg	Gly
1				5					10					15	
Lys	Glu	Glu	Glu	Met	Gly	Cys	Asp	Gly	Ser	Lys	Ala	Gly	Lys	Val	Ser
			20					25					30		
His	Gly	Pro	Gln	Thr	Pro	Phe	Pro	Pro	Leu	Ser	Leu	Ser	Pro	Leu	Pro
		35					40					45			
Lys	Lys	Lys	Lys	Lys	Glu	Thr	Phe	Ile	Met	Asn	Gln	Gln	Gly	Phe	Ser
	50					55					60				
Pro	Tyr	Gln	Arg	Glu	Met	Trp	Lys	Glu	Leu	Lys	Lys	Pro	Pro	Phe	Val
	65				70					75					80
Pro	Asn	Ser	Thr	Leu	Pro	Ile	Phe	Tyr	Ala	Thr	Gln	Thr	Leu	Ser	Phe
				85					90					95	
Trp	Val	Pro	Phe	Leu	Gln	Met	Asp	Leu	Leu	Arg	Arg	Ile	Ile	Val	Phe
			100					105					110		
His	Val	Phe	Ser	Pro	Gln	Val	Thr	Lys	Ile	Asn	Ile	Cys	Ile	Tyr	Asn
		115					120				125				
Leu	Tyr	Tyr	Cys	Tyr	Ile	Phe	Val	Asp	Asn	Thr	Phe	Arg	Trp	Cys	Trp
	130					135					140				

00673365-12200

Val	Ile	Tyr	Tyr	Asn	Leu	Asn	Leu	Gly	Ile	Ser	Phe	Gly	Leu	Pro	Gln
145					150					155					160
Ser	Leu	Leu	Arg	Trp	Gly	Pro	Trp	Tyr	Gly	Lys	Thr	Pro	Arg	Tyr	Asn
				165					170					175	
Val	Thr	Ser	Pro	Gln	Pro	Leu	Tyr								
			180												

<210> 631  
 <211> 138  
 <212> PRT  
 <213> homo sapiens

<400> 631

Gly	Pro	Trp	Leu	Thr	Phe	Pro	Ala	Phe	Asp	Pro	Ser	His	Pro	Ile	Ser
1				5					10					15	
Ser	Ser	Phe	Pro	Leu	Pro	Ala	Ala	Lys	Lys	Lys	Lys	Lys	Glu	Thr	Phe
			20					25					30		
Ile	Met	Asn	Gln	Gln	Gly	Phe	Ser	Pro	Tyr	Gln	Arg	Glu	Met	Trp	Lys
		35					40					45			
Glu	Leu	Lys	Lys	Pro	Pro	Phe	Val	Pro	Asn	Ser	Thr	Leu	Pro	Ile	Phe
	50					55					60				
Tyr	Ala	Thr	Gln	Thr	Leu	Ser	Phe	Trp	Val	Pro	Phe	Leu	Gln	Met	Asp
	65				70					75				80	
Leu	Leu	Arg	Arg	Ile	Ile	Val	Phe	His	Val	Phe	Ser	Pro	Gln	Val	Thr
				85					90					95	
Lys	Ile	Asn	Ile	Cys	Ile	Tyr	Asn	Leu	Tyr	Tyr	Cys	Tyr	Ile	Phe	Val
			100					105					110		
Asp	Asn	Thr	Phe	Arg	Trp	Cys	Trp	Val	Ile	Tyr	Tyr	Asn	Leu	Asn	Leu
		115					120					125			
Gly	Ile	Ser	Phe	Gly	Leu	Pro	Gln	Ser	Cys						
	130					135									

<210> 632  
 <211> 91  
 <212> PRT  
 <213> homo sapiens

<400> 632

Trp	Val	Lys	Gly	Arg	Lys	Gly	Lys	Pro	Trp	Ser	Ser	Asn	Pro	Ile	Ser
1				5					10					15	
Ser	Ser	Phe	Pro	Leu	Pro	Ala	Ala	Lys	Lys	Lys	Lys	Lys	Gly	Asn	Val
			20					25					30		
Tyr	His	Glu	Ser	Thr	Gly	Phe	Gln	Ser	Leu	Ser	Lys	Arg	Asp	Val	Glu
		35					40					45			
Arg	Ala	Lys	Glu	Thr	Thr	Leu	Cys	Ser	Gln	Leu	His	Phe	Thr	His	Ile
	50					55					60				

00673305-152700

Leu Cys Asn Thr Asn Thr Val Leu Leu Gly Pro Phe Leu Thr Asp Gly  
 65 70 80  
 Pro Leu Glu Lys Asn Tyr Arg Ile Pro Arg Phe  
 85 90

<210> 633  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 633

Arg Asn His Ala Lys Ile Gln Leu Pro Met Gln Ala Pro Gln Ser Leu  
 1 5 10 15  
 Ile Leu Ser Ser Gln Phe Cys Cys Gln Ala Thr Val Val Trp Arg Leu  
 20 25 30  
 Val Gly Cys Cys Pro Cys Cys Asn Glu Trp Glu Glu Val Asp Ser Gly  
 35 40 45  
 Met Val Glu Thr Phe Thr Ser Ser Ser Pro Ala Thr Gly Ile Pro Pro  
 50 55 60  
 Arg Pro Val Leu Cys Cys Gly Gly Arg Phe Lys Ser Lys Lys Leu Leu  
 65 70 75 80  
 Phe Glu Val Gly Phe Ala Val Trp Phe Lys Xxx His Asp Ala Ile Ala  
 85 90 95  
 Xxx Glu Arg Pro Ser Lys Asp Ser Gly Leu Pro Gly Leu Glu Asn  
 100 105 110

<210> 634  
 <211> 89  
 <212> PRT  
 <213> homo sapiens

<400> 634

Leu Arg Arg Asn Cys Pro Val Gln Arg Pro Thr Phe Pro Phe Ala Pro  
 1 5 10 15  
 His Leu Phe Arg Thr Pro Leu His Thr Leu Gln Pro Pro Lys Val Pro  
 20 25 30  
 Gly Ser Gly Phe Leu His Pro Ala Ala Ala Thr Asn Ala Asn Ser Leu  
 35 40 45  
 Asn Ser Thr Phe Ser Val Leu Pro Gln Arg Phe Pro Gln Phe Gln Gln  
 50 55 60  
 His Arg Ala Val Tyr Asn Ser Phe Ser Phe Pro Gly Gln Ala Ala Arg  
 65 70 75 80  
 Tyr Pro Trp Met Ala Phe Pro Xxx Gln  
 85

<210> 635  
 <211> 89  
 <212> PRT  
 <213> homo sapiens

0067305-122700

<400> 635

Phe	Ile	Gln	Phe	Ser	Arg	Pro	Gly	Ser	Pro	Leu	Ser	Leu	Asp	Gly	Leu
1				5					10					15	
Ser	Xxx	Ala	Ile	Ala	Ser	Cys	Xxx	Leu	Asn	His	Thr	Ala	Asn	Pro	Thr
			20					25					30		
Ser	Asn	Ser	Asn	Phe	Leu	Asp	Leu	Asn	Leu	Pro	Pro	Gln	His	Asn	Thr
		35					40					45			
Gly	Leu	Gly	Gly	Ile	Pro	Val	Ala	Gly	Glu	Glu	Glu	Val	Lys	Val	Ser
	50					55					60				
Thr	Met	Pro	Leu	Ser	Thr	Ser	Ser	His	Ser	Leu	Gln	Gln	Gly	Gln	Gln
65					70					75					80
Pro	Thr	Ser	Leu	His	Thr	Thr	Val	Ala							
				85											

276

265

295

312

00673335-122700



**IN THE UNITED STATES DESIGNATED/ELECTED OFFICE**

International Application No. : PCT/DE99/01174  
 International Filing Date : 15 April 1999  
 Priority Date(s) Claimed : 17 April 1998  
 Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.  
 Title: HUMAN NUCLEIC ACID SEQUENCES FROM ENDOMETRIAL TUMOR TISSUE

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
 Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend this application as follows:

**IN THE CLAIMS:**

Claims 5 and 6, line 1: Change "claims 1 to 4" to -- claim 3 --.

Claim 7: Please rewrite as follows:

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim[s 1 to 6]3, in such a sufficient amount that they hybridize with the sequences [according to claims 1 to 6] of claim 3 or a sequence having 90% homology thereto.

Claims 8 and 9, line 1: Change "claims 1 to 7" to -- claim 3 --.

Claim 10, lines 1 and 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 11, line 2: Change "claims 1 to 9" to -- claim 3 --.

Claim 13, lines 1 and 2: Change "claims 11 and 12" to -- claim 11 --.

Claim 14, lines 1 and 2: Change "claims 1 to 10" to -- claim 3 --.

Claim 16, line 3: Change "claims 1 to 10" to -- claim 3 --.

Claim 18, line 1: Change "claims 16 or 17" to -- claim 16 --.

Claim 19, line 2: Change "claims 16 to 18" to -- claim 16 --.

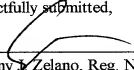
Claim 27, line 3: After "630-635" insert -- of claim 23 --.

Claim 28, line 3: After "555" insert -- of claim 3 --.  
Claim 29, line 2: After "555" insert -- of claim 3 --.  
Claims 30 and 31, line 2: After "630-635" insert -- of claim 23 --.  
Claim 32, line 3: After "630-635" insert -- of claim 23 --.  
Claims 33 and 34, line 1: Change "claims 1 to 10" to -- claim 3 --.  
Claim 35 line 4: After "555" insert -- of claim 3 --.  
Claim 38, line 1: Change "claims 1 to 7" to -- claim 3 --.

### Remarks

The purpose of this Preliminary Amendment is to eliminate multiple and improper multiple dependent claims to avoid additional fees. Applicants reserve the right to reintroduce claims directed to canceled combined subject matter.

Respectfully submitted,

  
\_\_\_\_\_  
Anthony J. Zelano, Reg. No. 27,969  
Attorney for Applicants  
MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
Arlington Courthouse Plaza 1  
2200 Clarendon Boulevard, Suite 1400  
Arlington, VA 22201  
Direct Dial: 703-812-5311  
Facsimile: 703-243-6410  
Email: zelano@mwzb.com

AJZ:ack

Filed: OCTOBER 17, 2000

K:\pat\sch\1780\prelim amdt

09/678385

WO 99/54461

PCT/DE99/01174

**Human Nucleic Acid Sequences from Endometrial Tumor Tissue**

The invention relates to human nucleic acid sequences from endometrial tumors, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer in women is the endometrial tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

0957385-12200

0067355.122700

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which play a role as candidate genes in endometrial tumors, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-126 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

09573505-122700

The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which are expressed elevated in the endometrial tumor.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic,

00673305.122700

such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>λ</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

00673355-102700

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of ORF ID Nos. 142-528 and Seq. ID Nos. ORF 561-575, 577-625, and 630-635 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

09573305.1.22700



The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 according to the invention can also be used as tools for finding active ingredients against endometrial tumors, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 for expression of polypeptides, which can be used as tools for finding active ingredients against endometrial tumors.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 142-528 and Seq. ID Nos. 561-575, 577-625, and 630-635 as pharmaceutical agents in the gene therapy for treatment of uterus tumors or for the production of a pharmaceutical agent for treatment of uterus tumors.

00673555-132700

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-141 and Seq. ID Nos. 531-552, 554, and 555, genomic BAC, PAC and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq.

00673335.122700

ID Nos. 531-552, 554, and 555, for use as vehicles for gene transfer.

002227.56227960

## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

09673395.122700

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

09673395-122700

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

#### **Example 1**

##### **Search for Tumor-related Candidate Genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

00673305-122700

Figures 2b1-2b4 illustrate the lengthening of the uterus tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

00673305-122700

**Example 2****Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1. Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 136 was found, which occurs 15.6 x more strongly in the endometrial tumor than in normal tissue.

00673305-122700



09/673395

529 Rec'd PCT/PTC 17 OCT 2000

The result is as follows:

Electronic Northern for SEQ. ID NO.: 136

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0102	0.0038	2.7221	0.3674
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0090	0.0078	1.1513	0.8686
Endocrine tissue	0.0000	0.0150	0.0000	undef
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0059	0.0031	1.9199	0.5209
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0114	0.0041	2.7942	0.3579
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0103	0.0120	0.8567	1.1673
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0104			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0142	Skin-muscle	0.0000
Suprarenal gland	0.0108	Testicles	0.0000
Kidney	0.0254	Lung	0.0164
Placenta	0.0000	Nerves	0.0060
Prostate	0.0061	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0125

00673395.122700

In an analogous procedure, the following Northern were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0038	0.0056	0.6905	1.4634
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0031	0.9599	1.0417
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0068	0.1055	0.0640	15.6211
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

00673365.152760

Electronic Northern for SEQ. ID NO.: 2

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.3166	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673305-12200

Electronic Northern for SEQ. ID NO.: 3

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0078	0.0231	0.2774	3.6055
Ovary	0.0090	0.0198	0.4764	2.0992
Endocrine tissue	0.0031	0.0000	undef	0.0000
Gastrointestinal	0.0030	0.0052	0.5756	1.7372
Brain	0.0085	0.0176	0.4852	2.0611
Hematopoietic	0.0019	0.0093	0.2071	4.8289
Skin	0.0118	0.0123	0.9599	1.0417
Hepatic	0.0027	0.0000	undef	0.0000
Heart	0.0073	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0058	0.0117	0.4920	2.0326
Muscle-skeleton	0.0073	0.0020	3.5562	0.2812
Kidney	0.0097	0.0153	0.6303	1.5866
Pancreas	0.0034	0.0240	0.1428	7.0040
Penis	0.0136	0.0274	0.4956	2.0176
Prostate	0.0050	0.0000	undef	0.0000
Uterus-endometrium	0.0090	0.0000	undef	0.0000
Uterus-myometrium	0.0109	0.0149	0.7312	1.3677
Uterus-general	0.0068	0.1583	0.0427	23.4317
Breast hyperplasia	0.0076	0.0272	0.2806	3.5642
Prostate hyperplasia	0.0102	0.0000	undef	0.0000
Seminal vesicle	0.0160			
Sensory organs	0.0119			
White blood cells	0.0178			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0278	Breast	0.0272
Gastrointestinal	0.0194	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0114
Lung	0.0145	Skin-muscle	0.0194
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0124	Lung	0.0164
Placenta	0.0121	Nerves	0.0120
Prostate	0.0249	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

00673395.122700

Electronic Northern for SEQ. ID NO.: 4

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast				
Small intestine	0.0039	0.0000	undef	0.0000
Ovary	0.0026	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0165	0.0000	undef
Gastrointestinal	0.0030	0.0000	undef	0.0000
Brain	0.0017	0.0000	undef	0.0000
Hematopoietic	0.0077	0.0000	undef	0.0000
Skin	0.0015	0.0021	0.7200	1.3890
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0048	0.0000	undef	0.0000
Lung	0.0011	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0021	0.0020	1.0161	0.9842
Kidney	0.0193	0.0077	2.5211	0.3967
Pancreas	0.0000	0.0060	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0017	0.0000	undef	0.0000
Uterus-endometrium	0.0030	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.1053	0.0000	undef
Breast hyperplasia	0.0076	0.0068	1.1223	0.8911
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0000			
Sensory organs	0.0030			
White blood cells	0.0000			
Cervix	0.0017			
	0.0213			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Fetal	0.0041
Heart-blood vessels	0.0000	Gastrointestinal	0.0000
Lung	0.0036	Hematopoietic	0.0000
Suprarenal gland	0.0036	Skin-muscle	0.0032
Kidney	0.0000	Testicles	0.0000
Placenta	0.0000	Lung	0.0082
Prostate	0.0000	Nerves	0.0020
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0000
		Uterus_n	0.0167

09573395-122700

## Electronic Northern for SEQ. ID NO.: 5

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0038	0.0038	1.0208	0.9796
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0093	0.0000	undef
Hematopoietic	0.0015	0.0021	0.7200	1.3890
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0053	0.0137	0.3855	2.5941
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0193	0.0000	undef	0.0000
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0017	0.0055	0.2991	3.3428
Prostate	0.0060	0.0267	0.2246	4.4517
Uterus-endometrium	0.0065	0.0021	3.0709	0.3256
Uterus-myometrium	0.0135	0.1055	0.1280	7.8106
Uterus-general	0.0051	0.0068	0.0000	undef
Breast hyperplasia	0.0096	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0078			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0759
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0035	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

00673395-122700

Electronic Northern for SEQ. ID NO.: 6

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0156	0.0077	2.0339	0.4917
Small intestine	0.0051	0.0075	0.6805	1.4694
Ovary	0.0123	0.0331	0.3707	2.6973
Endocrine tissue	0.0120	0.0104	1.1513	0.8686
Gastrointestinal	0.0085	0.0075	1.1321	0.8833
Brain	0.0096	0.0278	0.3451	2.8974
Hematopoietic	0.0133	0.0164	0.8100	1.2346
Skin	0.0120	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0170	0.0000	undef	0.0000
Lung	0.0058	0.0117	0.4920	2.0326
Stomach-esophagus	0.0197	0.0164	1.2066	0.8288
Muscle-skeleton	0.0193	0.0000	undef	0.0000
Kidney	0.0034	0.0180	0.1904	5.2530
Pancreas	0.0054	0.0274	0.1983	5.0439
Penis	0.0066	0.0053	1.1966	0.8357
Prostate	0.0240	0.0267	0.8985	1.1129
Uterus-endometrium	0.0044	0.0192	0.2275	4.3961
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0229	0.0272	0.8417	1.1881
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0192			
Seminal vesicle	0.0059			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0104			
	0.0106			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0250	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0354
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0245
Hepatic	0.0260	Gastrointestinal	0.0244
Heart-blood vessels	0.0178	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0551
Suprarenal gland	0.0000	Testicles	0.0386
Kidney	0.0000	Lung	0.0082
Placenta	0.0121	Nerves	0.0069
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0167
		Uterus_n	

00673395-122700

Electronic Northern for SEQ. ID NO.: 7

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0026	0.0019	1.3611	0.7347
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0026	2.3025	0.4343
Gastrointestinal	0.0051	0.0000	undef	0.0000
Brain	0.0096	0.0139	0.6903	1.4437
Hematopoietic	0.0037	0.0092	0.4000	2.5001
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0097	0.0153	0.6303	1.5866
Kidney	0.0000	0.0120	0.0000	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0150	0.0000	undef	0.0000
Uterus-endometrium	0.0087	0.0043	2.0473	0.4885
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

Breast	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0000
Hematopoietic	0.0097
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0155
Sensory Organs	0.0000
Uterus_n	

00673395-122700



## Electronic Northern for SEQ. ID NO.: 8

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0000	0.0019	0.0000	undef
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0000	0.0021	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0009			
Cervix	0.0000			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	% frequency	LIBRARIES
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0068
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0203
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0047
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0057
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0050
Sensory organs	0.0000	Sensory Organs	0.0137
		Uterus_n	0.0000

00573305-122700

Electronic Northern for SEQ. ID NO.: 9

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0005
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395.122700

Electronic Northern for SEQ. ID NO.: 10

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory Organs	0.0000
Uterus_n	

09673095 122700

Electronic Northern for SEQ. ID NO.: 11

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0090	0.0188	0.4764	2.0992
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0000	0.0000	undef	undef
Prostate	0.0131	0.0213	0.6142	1.6282
Uterus-endometrium	0.0000	0.1593	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0178			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0154
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0342
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

0067305-122700

Electronic Northern for SEQ. ID NO.: 12

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395.122700

Electronic Northern for SEQ. ID NO.: 13

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef undef	
Small intestine	0.0038	0.0019	2.0416 0.4898	
Ovary	0.0061	0.0000	undef 0.0000	
Endocrine tissue	0.0000	0.0208	0.0000 undef	
Gastrointestinal	0.0034	0.0201	0.1698 5.8889	
Brain	0.0057	0.0000	undef 0.0000	
Hematopoietic	0.0000	0.0072	1.1314 0.8839	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0037	0.0000	undef 0.0000	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0021	0.0000	undef 0.0000	
Lung	0.0058	0.0000	undef 0.0000	
Stomach-esophagus	0.0010	0.0020	0.5080 1.9684	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0051	0.0000	undef 0.0000	
Pancreas	0.0054	0.0000	undef 0.0000	
Penis	0.0017	0.0000	undef 0.0000	
Prostate	0.0030	0.0000	undef 0.0000	
Uterus-endometrium	0.0065	0.0043	1.5354 0.6513	
Uterus-myometrium	0.0068	0.1583	0.0427 23.4317	
Uterus-general	0.0152	0.0000	undef 0.0000	
Breast hyperplasia	0.0051	0.0000	undef 0.0000	
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0143			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0250

00673395.122700

Electronic Northern for SEQ. ID NO.: 14

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

00673365-122700

## Electronic Northern for SEQ. ID NO.: 15

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00573355-122700



Electronic Northern for SEQ. ID NO.: 16

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6399
Breast	0.0153	0.0188	0.8166	1.2245
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0182	0.4934	2.0268
Endocrine tissue	0.0187	0.0100	1.8679	0.5354
Gastrointestinal	0.0192	0.0324	0.5917	1.6901
Brain	0.0067	0.0205	0.3240	3.0866
Hematopoietic	0.0147	0.0379	0.3882	2.5762
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0143	0.0323	0.4412	2.2666
Heart	0.0148	0.0275	0.5397	1.8529
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0156	0.0102	1.5241	0.6561
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0154	0.0120	1.2850	0.7782
Kidney	0.0407	0.0068	5.9478	0.1681
Pancreas	0.0132	0.0110	1.1966	0.8357
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0153	0.0085	1.7913	0.5582
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0178			
Sensory organs	0.0353			
White blood cells	0.0165			
Cervix	0.0319			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast 0.0476
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.1114
Hematopoietic	Endocrine tissue 0.0245
Skin	Fetal 0.0175
Hepatic	Gastrointestinal 0.0244
Heart-blood vessels	Hematopoietic 0.0114
Lung	Skin-muscle 0.0292
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0082
Placenta	Nerves 0.0020
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0310
	Uterus_n 0.0167

00673395.122700

Electronic Northern for SEQ. ID NO.: 17

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0111	0.0031	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0016	Hematopoietic	0.0000
Lung	0.0016	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0100
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0208
		Uterus_n	

00573305.122700

Electronic Northern for SEQ. ID NO.: 18

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0078	0.0256	0.3051	3.2777
Small intestine	0.0090	0.0113	0.7939	1.2595
Ovary	0.0092	0.0000	undef	0.0000
Endocrine tissue	0.0090	0.0286	0.3140	3.1849
Gastrointestinal	0.0255	0.0050	5.0944	0.1963
Brain	0.0096	0.0185	0.5177	1.9316
Hematopoietic	0.0044	0.0082	0.5400	1.8520
Skin	0.0134	0.0379	0.3529	2.8338
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0285	0.0194	1.4706	0.6800
Testicles	0.0042	0.0275	0.1542	6.4853
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0083	0.0184	0.4516	2.2144
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0060	0.0000	undef
Pancreas	0.0109	0.0274	0.3965	2.5219
Penis	0.0017	0.0110	0.1496	6.6857
Prostate	0.0060	0.0533	0.1123	8.9035
Uterus-endometrium	0.0262	0.0192	1.3648	0.7327
Uterus-myometrium	0.0068	0.1583	0.0427	23.4317
Uterus-general	0.0000	0.0068	0.0000	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0297			
Sensory organs	0.0356			
White blood cells	0.0000			
Cervix	0.0113			
	0.0000			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0152
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0064
Hepatic	Gastrointestinal	0.0244
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0389
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0000
Placenta	Nerves	0.0080
Prostate	Prostate	0.0274
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0458

00673395.122700

Electronic Northern for SEQ. ID NO.: 19

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0102	1.9068	0.5244
Breast	0.0115	0.0132	0.8750	1.1429
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0119	0.0125	0.9509	1.0516
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0096	0.0041	2.3399	0.4274
Hematopoietic	0.0080	0.0379	0.2117	4.7230
Skin	0.0330	0.2542	0.1300	7.6946
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0127	0.0000	undef	0.0000
Testicles	0.0115	0.0468	0.2460	4.0652
Lung	0.0052	0.0082	0.6350	1.5747
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0087	0.0106	0.8189	1.2211
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0458	0.0000	undef	0.0000
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0353			
White blood cells	0.0113			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

04673395-122700

Electronic Northern for SEQ. ID NO.: 20

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.2111	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

0067355-162700

Electronic Northern for SEQ. ID NO.: 21

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

00673305.122700

## Electronic Northern for SEQ. ID NO.: 22

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0128	0.0000	undef
Breast	0.0051	0.0075	0.6805	1.4694
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0104	0.5756	1.7372
Endocrine tissue	0.0102	0.0125	0.8151	1.2268
Gastrointestinal	0.0172	0.0093	1.8638	0.5365
Brain	0.0052	0.0010	5.0397	0.1994
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0201	0.0412	0.4883	2.0480
Testicles	0.0288	0.0234	1.2299	0.8130
Lung	0.0114	0.0184	0.6209	1.6105
Stomach-esophagus	0.0097	0.0077	1.2605	0.7933
Muscle-skeleton	0.0086	0.0180	0.4759	2.1012
Kidney	0.0217	0.0000	undef	0.0000
Pancreas	0.0149	0.0221	0.6731	1.4857
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0065	0.0170	0.3839	2.6051
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0192	0.0000	undef	undef
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0130			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0227
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0030
Prostate	0.0249	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

00673395-12700

Electronic Northern for SEQ. ID NO.: 23

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	0.0000
Brain	0.0007	0.0041	0.1800	5.5559
Hematopoietic	0.0000	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	0.0000
Heart	0.0032	0.0137	0.2313	4.3235
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0205	0.0000	undef
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0154
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

00673345-122700



Electronic Northern for SEQ. ID NO.: 24

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0077	0.0000	undef
Small intestine	0.0064	0.0019	3.4026	0.2939
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0025	2.7170	0.3681
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0118	0.0031	3.8398	0.2604
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9584
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0109	0.0000	undef	0.0000
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0085	0.5118	1.9538
Uterus-myometrium	0.0000	0.1583	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0194
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0080
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus_n	0.0000

00573355.12700

Electronic Northern for SEQ. ID NO.: 25

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0064	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0026	1.1513	0.8586
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0046	0.0000	undef	0.0000
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0041	0.0000	undef
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0051	0.0000	undef	0.0000
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064	0.0000	undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

Electronic Northern for SEQ. ID NO.: 26

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0038	0.0185	0.2071	4.8289
Brain	0.0037	0.0031	1.1999	0.8334
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0062	0.0041	1.5241	0.6561
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0136	0.0068	1.9926	0.5044
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0954	0.1067	9.3678
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0140
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0680
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0070
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00573305.122700

Electronic Northern for SEQ. ID NO.: 27

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0059	0.0041	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0232
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

00673365.426700

Electronic Northern for SEQ. ID NO.: 28  
 NORMAL TUMOR Ratios  
 % frequency % frequency N/T T/N

Bladder				
Breast	0.0000	0.0051	0.0000	undef
Small intestine	0.0153	0.0094	1.6333	0.6123
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0130	0.2303	4.3431
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0030	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0184	0.0000	undef	0.0000
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0020	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0060	1.4278	0.7004
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0068	0.1035	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0256		undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS  
 % frequency

STANDARDIZED/SUBTRACTED  
 LIBRARIES  
 % frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0105
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0520	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0060
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

00573465-122700

Electronic Northern for SEQ. ID NO.: 29

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0128	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0038	0.0046	0.8283	1.2072
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0061	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0085	0.2559	3.9077
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0012
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0000
Prostate	Prostate	0.0137
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

00673396142200

Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0104	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0064	0.6824	1.4654
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

00673395-122700

Electronic Northern for SEQ. ID NO.: 31

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0013	0.0056	0.2269	4.4083
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0078	0.0000	undef
Gastrointestinal	0.0017	0.0050	0.3396	2.9444
Brain	0.0038	0.0046	0.8283	1.2072
Hematopoietic	0.0037	0.0041	0.8999	1.1112
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0063	0.0000	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0034	0.0060	0.5711	1.7510
Pancreas	0.0027	0.0137	0.1993	5.0439
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0000	0.0267	0.0000	undef
Uterus-endometrium	0.0022	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.1053	0.0000	undef
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0224			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0010
Placenta	0.0182	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

09573395.122700



Electronic Northern for SEQ. ID NO.: 32  
 NORMAL TUMOR Ratios  
 % frequency % frequency N/T T/N

Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0038	0.0000	undef
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0068	0.0030	1.3585	0.7361
Brain	0.0038	0.0000	undef	0.0000
Hematopoietic	0.0022	0.0041	0.5400	1.8520
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0129	0.3676	2.7200
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0020	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0054	0.0000	undef	0.0000
Penis	0.0000	0.0110	0.0000	undef
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0006
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0020
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

09673305.122700

## Electronic Northern for SEQ. ID NO.: 33

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.2639	0.0256	39.0528
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0154
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673335-12700

## Electronic Northern for SEQ. ID NO.: 34

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0010	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673335-12700

Electronic Northern for SEQ. ID NO.: 35

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0026	0.0038	0.6805	1.4694
Ovary	0.0000	0.0163	0.0000	undef
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0034	0.0000	undef	0.0000
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0021	0.3600	2.7779
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0082	0.1270	7.8735
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0034	0.0000	undef	0.0000
Pancreas	0.0081	0.0479	0.1699	5.8843
Penis	0.0000	0.0000	undef	undef
Prostate	0.0060	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0021	2.0473	0.4885
Uterus-myometrium	0.0068	0.2639	0.0256	39.0528
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0052			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0340
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

00673305.122700

Electronic Northern for SEQ. ID NO.: 36

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0038	0.0019	2.0416	0.4898
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0034	0.0000	undef	0.0000
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0015	0.0010	1.4399	0.6945
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0032
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673005.725700

Electronic Northern for SEQ. ID NO.: 37

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0010	0.0000	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395.122700

Electronic Northern for SEQ. ID NO.: 38

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0023
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0000

006733061-102700

Electronic Northern for SEQ. ID NO.: 39

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0052	0.5756	1.7372
Endocrine tissue	0.0000	0.0075	0.0000	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0404	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0020	3.5562	0.2812
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0269	0.1066	0.2527	3.9571
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

00672356-162700



Electronic Northern for SEQ. ID NO.: 40

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0030	0.0156	0.1919	5.2117
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0096	0.0231	0.4142	2.4145
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00573305-122700

Electronic Northern for SEQ. ID NO.: 41

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0057
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673005-122700

## Electronic Northern for SEQ. ID NO.: 42

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0051	0.0113	0.4537	2.2042
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0136	0.0251	0.5434	1.8403
Gastrointestinal	0.0153	0.0185	0.8283	1.2072
Brain	0.0118	0.0041	2.8798	0.3472
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0064	0.0275	0.2313	4.3235
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0187	0.0164	1.1431	0.8748
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0081	0.0205	0.3965	2.5219
Pancreas	0.0182	0.0055	3.2906	0.3039
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0131	0.0213	0.6142	1.6282
Uterus-endometrium	0.0135	0.1583	0.0854	11.7158
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0199			
Cervix	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0399
Lung	0.0072	Skin-muscle	0.0454
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0000	Lung	0.0082
Placenta	0.0182	Nerves	0.0301
Prostate	0.0499	Prostate	0.0068
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0167

00673305.122700

## Electronic Northern for SEQ. ID NO.: 43

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0102	1.1441	0.8741
Small intestine	0.0102	0.0226	0.4537	2.2042
Ovary	0.0123	0.0165	0.7415	1.3487
Endocrine tissue	0.0030	0.0078	0.3838	2.6058
Gastrointestinal	0.0136	0.0150	0.9057	1.1042
Brain	0.0153	0.0046	3.3134	0.3018
Hematopoietic	0.0074	0.0103	0.7200	1.3890
Skin	0.0053	0.0379	0.1412	7.0845
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0143	0.0129	1.1029	0.9067
Testicles	0.0074	0.0137	0.5397	1.8529
Lung	0.0173	0.0000	undef	0.0000
Stomach-esophagus	0.0125	0.0164	0.7621	1.3122
Muscle-skeleton	0.0097	0.0153	0.6303	1.5866
Kidney	0.0154	0.0060	2.5700	0.3891
Pancreas	0.0109	0.0137	0.7930	1.2610
Penis	0.0083	0.0276	0.2991	3.3428
Prostate	0.0150	0.0533	0.2808	3.5614
Uterus-endometrium	0.0196	0.0149	1.3161	0.7598
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0136	0.0000	undef
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0208			
Sensory organs	0.0178			
White blood cells	0.0706			
Cervix	0.0251			
	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0272
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0557
Hematopoietic	0.0118	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0402
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0000	Hematopoietic	0.0342
Lung	0.0217	Skin-muscle	0.0486
Suprarenal gland	0.0254	Testicles	0.0309
Kidney	0.0185	Lung	0.0328
Placenta	0.0303	Nerves	0.0100
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0310
		Uterus_n	0.0291

05673305-122700

Electronic Northern for SEQ. ID NO.: 44

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

0567355.122700

Electronic Northern for SEQ. ID NO.: 45

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0094	0.1361	7.3472
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0017	0.0100	0.1698	5.8889
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0052	0.0062	0.8400	1.1905
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0053	0.0412	0.1285	7.7824
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0052	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0221	0.0748	13.3713
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0087	0.0085	1.0236	0.9769
Uterus-endometrium	0.0000	0.1593	0.0000	undef
Uterus-myometrium	0.0152	0.0204	0.7482	1.3366
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0072	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0182	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00673005.122700

Electronic Northern for SEQ. ID NO.: 46

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00573305.122700

Electronic Northern for SEQ. ID NO.: 47

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0010	1.4399	0.6945
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0060	0.2856	3.5020
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0152	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
0.0000	Breast	0.0000
0.0000	Ovary_n	0.0000
0.0000	Ovary_t	0.0000
0.0000	Endocrine tissue	0.0000
0.0000	Fetal	0.0006
0.0000	Gastrointestinal	0.0000
0.0000	Hematopoietic	0.0000
0.0000	Skin-muscle	0.0000
0.0000	Testicles	0.0000
0.0000	Lung	0.0000
0.0000	Nerves	0.0000
0.0000	Prostate	0.0000
0.0000	Sensory Organs	0.0000
	Uterus_n	0.0000

00673305.122700



Electronic Northern for SEQ. ID NO.: 48

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.2111	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673235.122700

Electronic Northern for SEQ. ID NO.: 49

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0163	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0030	0.3396	2.9444
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0065
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 50

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

00675355.122700

Electronic Northern for SEQ. ID NO.: 51

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

09573395.122700

Electronic Northern for SEQ. ID NO.: 52

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0044	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0040
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

09673355 122700

## Electronic Northern for SEQ. ID NO.: 53

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0051	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0015	0.0031	0.4900	2.0835
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0441	0.0000	undef	0.0000
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0064	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0060	0.2856	3.5020
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0267	0.0000	undef
Uterus-endometrium	0.0044	0.0000	undef	0.0000
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032	0.0954	0.0000	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0017
Hepatic	Gastrointestinal	0.0244
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0082
Placenta	Nerves	0.0010
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

09673305.122700

Electronic Northern for SEQ. ID NO.: 54

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0106	0.2047	4.8846
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0012	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0000

00673305.122700

Electronic Northern for SEQ. ID NO.: 55

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef undef	
Small intestine	0.0013	0.0019	0.6805	1.4694
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0026	2.3025	0.4343
Gastrointestinal	0.0017	0.0050	0.3396	2.9444
Brain	0.0057	0.0093	0.6213	1.6096
Hematopoietic	0.0022	0.0041	0.5400	1.8520
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9594
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0054	0.0068	0.7930	1.2610
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0087	0.0000	undef	0.0000
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0030
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00673306172200



## Electronic Northern for SEQ. ID NO.: 56

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0117	0.0128	0.9153	1.0926
Small intestine	0.0051	0.0132	0.3899	2.5715
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0102	0.0125	0.8151	1.2268
Brain	0.0134	0.0046	2.8992	0.3449
Hematopoietic	0.0103	0.0113	0.9163	1.0913
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0134	0.0000	undef
Testicles	0.0085	0.0000	undef	0.0000
Lung	0.0173	0.0234	0.7380	1.3551
Stomach-esophagus	0.0145	0.0123	1.1854	0.8436
Muscle-skeleton	0.0097	0.0077	1.2605	0.7933
Kidney	0.0063	0.0000	undef	0.0000
Pancreas	0.0190	0.0000	undef	0.0000
Penis	0.0050	0.0055	0.8974	1.1143
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0085	0.2559	3.9077
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0068	1.1223	0.8911
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0030			
Sensory organs	0.0178			
White blood cells	0.0000			
Cervix	0.0052			
	0.0000			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0260	Gastrointestinal	0.0365
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

00573305.122700

Electronic Northern for SEQ. ID NO.: 57

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0038	0.0075	0.5104	1.9593
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0185	0.4142	2.4145
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.1908	0.0000	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0050
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

09673355.122700

## Electronic Northern for SEQ. ID NO.: 58

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1655	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673305-122700

## Electronic Northern for SEQ. ID NO.: 59

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0281	0.0226	1.2476	0.8015
Ovary	0.0307	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0065	0.0000	undef	0.0000
Brain	0.0153	0.0324	0.4733	2.1127
Hematopoietic	0.0044	0.0072	0.6171	1.6205
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0257	0.0000	undef	0.0000
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0061	0.0000	undef
Muscle-skeleton	0.0000	0.0153	0.0000	undef
Kidney	0.0154	0.0180	0.8567	1.1673
Pancreas	0.0217	0.0068	3.1722	0.3152
Penis	0.0000	0.0166	0.0000	undef
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0135	0.1055	0.1280	7.8106
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			
Cervix	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0476
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0181	Testicles	0.0000
Kidney	0.0254	Lung	0.0082
Placenta	0.0000	Nerves	0.0050
Prostate	0.0303	Nerves	0.0137
Sensory organs	0.0000	Prostate	0.0000
	0.0000	Sensory Organs	0.0208
		Uterus_n	

09673395-122700

## Electronic Northern for SEQ. ID NO.: 60

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0102	1.5254	0.6555
Breast	0.0115	0.0207	0.5568	1.7960
Small intestine	0.0215	0.0165	1.2976	0.7707
Ovary	0.0240	0.0260	0.9210	1.0858
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0172	0.0139	1.2425	0.8048
Brain	0.0170	0.0246	0.6900	1.4494
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0238	0.0194	1.2255	0.8160
Heart	0.0180	0.0275	0.6553	1.5260
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0156	0.0164	0.9526	1.0498
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0081	0.0411	0.1983	5.0439
Pancreas	0.0116	0.0055	2.0940	0.4775
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0131	0.0043	3.0709	0.3256
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0426			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
% frequency	% frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

0.0000	0.0000
0.0139	0.0000
0.0125	0.0000
0.0157	0.0245
0.0000	0.0151
0.0260	0.0122
0.0213	0.0000
0.0036	0.0194
0.0000	0.0000
0.0062	0.0246
0.0061	0.0211
0.0000	0.0274
0.0126	0.0000
	0.0125

00073305-12200

Electronic Northern for SEQ. ID NO.: 61

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0128	0.0000	undef
Small intestine	0.0000	0.0056	0.0000	undef
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0119	0.0075	1.5849	0.6309
Brain	0.0057	0.0000	undef	0.0000
Hematopoietic	0.0059	0.0072	0.8228	1.2153
Skin	0.0067	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0048	0.0129	0.3676	2.7200
Testicles	0.0053	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0031	0.0020	1.5241	0.6561
Muscle-skeleton	0.0193	0.0000	undef	0.0000
Kidney	0.0017	0.0120	0.1428	7.0040
Pancreas	0.0136	0.0000	undef	0.0000
Penis	0.0033	0.0276	0.1197	8.3571
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0153	0.0170	0.8957	1.1165
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032	0.0000	undef	undef
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0136
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0000
Hepatic	0.0000	Fetal	0.0058
Heart-blood vessels	0.0000	Gastrointestinal	0.0122
Lung	0.0036	Hematopoietic	0.0057
Suprarenal gland	0.0000	Skin-muscle	0.0000
Kidney	0.0000	Testicles	0.0154
Placenta	0.0000	Lung	0.0000
Prostate	0.0124	Nerves	0.0030
Sensory organs	0.0061	Prostate	0.0000
	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

00677305.122700

Electronic Northern for SEQ. ID NO.: 62

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673305-122700

Electronic Northern for SEQ. ID NO.: 63

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0051	1.5254	0.6555
Breast	0.0038	0.0094	0.4083	2.4491
Small intestine	0.0031	0.0331	0.0927	10.7893
Ovary	0.0150	0.0208	0.7195	1.3898
Endocrine tissue	0.0136	0.0100	1.3585	0.7361
Gastrointestinal	0.0230	0.0046	4.9700	0.2012
Brain	0.0096	0.0082	1.1699	0.8547
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0052	0.0041	1.2701	0.7873
Stomach-esophagus	0.0387	0.0077	5.0421	0.1983
Muscle-skeleton	0.0051	0.0120	0.4283	2.3347
Kidney	0.0081	0.0274	0.2974	3.3626
Pancreas	0.0083	0.0110	0.7479	1.3371
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0044	0.0043	1.0236	0.9769
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
% frequency	% frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

00673305.122700



Electronic Northern for SEQ. ID NO.: 64

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

09673395-122700

Electronic Northern for SEQ. ID NO.: 65

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0244	0.0137	1.7843	0.5604
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 66

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00873705.122700

Electronic Northern for SEQ. ID NO.: 67

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0038	0.0000	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0097
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 68

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0038	0.0188	0.2042	4.8982
Small intestine	0.0153	0.0331	0.4634	2.1579
Ovary	0.0120	0.0208	0.5756	1.7372
Endocrine tissue	0.0136	0.0125	1.0868	0.9201
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0052	0.0041	1.2599	0.7937
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0847	0.0000	undef
Hepatic	0.0095	0.0194	0.4902	2.0400
Heart	0.0307	0.0275	1.1179	0.8945
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0042	0.0286	0.1452	6.8893
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0120	0.4283	2.3347
Kidney	0.0054	0.0137	0.3965	2.5219
Pancreas	0.0116	0.0110	1.0470	0.9551
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0106	0.4095	2.4423
Uterus-endometrium	0.0135	0.1583	0.0854	11.7158
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0102	0.1908	0.0534	18.7357
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0130			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0105
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0421
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0082
Placenta	Nerves	0.0030
Prostate	Prostate	0.0137
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0083

0067395-122700

Electronic Northern for SEQ. ID NO.: 69

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1053	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0010
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

00673305-122700

Electronic Northern for SEQ. ID NO.: 70

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

00673305-122700

## Electronic Northern for SEQ. ID NO.: 71

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0230	0.0000	undef
Breast	0.0051	0.0056	0.9074	1.1021
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0060	0.0182	0.3289	3.0402
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0728	0.0185	3.9346	0.2542
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8528	0.5368
Stomach-esophagus	0.0387	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0035	0.5983	1.6714
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0608
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395.122700



Electronic Northern for SEQ. ID NO.: 72

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0309	Lung	0.0000
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

09673305.162700

## Electronic Northern for SEQ. ID NO.: 73

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0078	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0021	0.0061	0.3387	2.9526
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0043	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0072
Suprarenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast	0.0136
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lung	0.0000
Nerves	0.0010
Prostate	0.0137
Sensory Organs	0.0000
Uterus_n	0.0000

00673395-122700

Electronic Northern for SEQ. ID NO.: 74

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder	0.0078	0.0051	1.5254	0.6555
Breast	0.0051	0.0075	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0119	0.0125	0.9509	1.0516
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0059	0.0051	1.1519	0.8681
Hematopoietic	0.0187	0.0379	0.4940	2.0241
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0073	0.0041	1.7781	0.5624
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0120	0.0000	undef
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0043	1.5354	0.6513
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0035			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0065
Lung	0.0072	Skin-muscle	0.0154
Suprarenal gland	0.0000	Testicles	0.0246
Kidney	0.0124	Lung	0.0010
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0077
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 75

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0078	1.1513	0.8686
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0019	0.0231	0.0828	12.0723
Brain	0.0089	0.0031	2.8798	0.3472
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0061	0.5080	1.9684
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
% frequency	% frequency	
0.0000	Breast	0.0000
0.0000	Ovary_n	0.0000
0.0000	Ovary_t	0.0000
0.0000	Endocrine tissue	0.0000
0.0000	Fetal	0.0151
0.0000	Gastrointestinal	0.0000
0.0036	Hematopoietic	0.0114
0.0000	Skin-muscle	0.0130
0.0254	Testicles	0.0000
0.0000	Lung	0.0082
0.0000	Nerves	0.0060
0.0000	Prostate	0.0137
0.0000	Sensory Organs	0.0000
	Uterus_n	0.0208

00673395.122700

Electronic Northern for SEQ. ID NO.: 76

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.2111	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

00673395-122700

## Electronic Northern for SEQ. ID NO.: 77

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

Electronic Northern for SEQ. ID NO.: 78

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0213			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673335.122700

Electronic Northern for SEQ. ID NO.: 79

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0050	0.3396	2.9444
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0032	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast 0.0068
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0164
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0042
	Uterus_n

00673365.122100



Electronic Northern for SEQ. ID NO.: 80

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0055	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.1583	0.0000	undef
Uterus-general	0.0000	0.0068	0.0000	undef
Breast hyperplasia	0.0032	0.0000	undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0278	Breast	0.0068
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00573305-122700

Electronic Northern for SEQ. ID NO.: 81

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00573395.122700

## Electronic Northern for SEQ. ID NO.: 82

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0077	0.0150	0.5104	1.9593
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0208	0.4317	2.3163
Endocrine tissue	0.0068	0.0150	0.4528	2.2083
Gastrointestinal	0.0268	0.0231	1.1597	0.8623
Brain	0.0081	0.0123	0.6600	1.5152
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0011	0.0412	0.0257	38.9118
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0031	0.0123	0.2540	3.9367
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0060	1.7133	0.5837
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0166	0.2991	3.3428
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0305	0.0554	0.5512	1.8143
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0253
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0507	Lung	0.0082
Placenta	0.0000	Nerves	0.0131
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

00673305-122700

Electronic Northern for SEQ. ID NO.: 83

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0050
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

00673305.122700

Electronic Northern for SEQ. ID NO.: 84

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
0.0000	Breast	0.0000
0.0000	Ovary_n	0.0000
0.0000	Ovary_t	0.0000
0.0000	Endocrine tissue	0.0000
0.0000	Fetal	0.0006
0.0000	Gastrointestinal	0.0000
0.0000	Hematopoietic	0.0000
0.0000	Skin-muscle	0.0000
0.0254	Testicles	0.0000
0.0000	Lung	0.0000
0.0000	Nerves	0.0000
0.0000	Prostate	0.0000
0.0000	Sensory Organs	0.0000
	Uterus_n	

007227.9652960

Electronic Northern for SEQ. ID NO.: 85

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

09673395.122700

Electronic Northern for SEQ. ID NO.: 86

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395.122700

Electronic Northern for SEQ. ID NO.: 87

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0128	0.0075	1.7013	0.5878
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0030	0.0078	0.3838	2.6058
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0033	0.0139	0.2761	3.6217
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0031	0.0000	undef	0.0000
Lung	0.0097	0.0077	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0050	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0044	0.0149	0.2925	3.4192
Prostate	0.0068	0.1055	0.0640	15.6211
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0192			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0106			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0068
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0122
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0082
Placenta	Nerves	0.0000
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

00673395 122700



Electronic Northern for SEQ. ID NO.: 88

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0050	0.0000	undef
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0007	0.0010	0.7200	1.3890
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0020	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0017			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673336-762700

Electronic Northern for SEQ. ID NO.: 89

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0013	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

00573395-122700

Electronic Northern for SEQ. ID NO.: 90

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1053	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

00573395.122700

## Electronic Northern for SEQ. ID NO.: 91

	NORMAL	TUMOR	Ratios	T/N
	% frequency	% frequency	N/T	
Bladder	0.0000	0.0000	undef undef	
Breast	0.0030	0.0038	2.3818 0.4198	
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0030	0.0052	0.5756 1.7372	
Endocrine tissue	0.0034	0.0025	1.3585 0.7361	
Gastrointestinal	0.0096	0.0000	undef 0.0000	
Brain	0.0037	0.0021	1.7999 0.5556	
Hematopoietic	0.0027	0.0000	undef 0.0000	
Skin	0.0110	0.0847	0.1300 7.6946	
Hepatic	0.0095	0.0065	1.4706 0.6800	
Heart	0.0042	0.0000	undef 0.0000	
Testicles	0.0000	0.0117	0.0000 undef	
Lung	0.0010	0.0020	0.5080 1.9684	
Stomach-esophagus	0.0000	0.0077	0.0000 undef	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0027	0.0000	undef 0.0000	
Pancreas	0.0017	0.0166	0.0997 10.0285	
Penis	0.0030	0.0000	undef 0.0000	
Prostate	0.0000	0.0021	0.0000 undef	
Uterus-endometrium	0.0000	0.1055	0.0000 undef	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0026			
White blood cells	0.0106			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0041
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0057
Lung	Skin-muscle	0.0065
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0050
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0125

00673395-122700

Electronic Northern for SEQ. ID NO.: 92

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395.122700

## Electronic Northern for SEQ. ID NO.: 93

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0040	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673305.122700

## Electronic Northern for SEQ. ID NO.: 94

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0035	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0208

00673395-122700

## Electronic Northern for SEQ. ID NO.: 95

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00672305.122700



Electronic Northern for SEQ. ID NO.: 96

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0023
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0068
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

09673395.122700

Electronic Northern for SEQ. ID NO.: 97

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4634
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0010
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 98

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0026	1.1513	0.8686
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0330	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0533	0.0000	undef
Prostate	0.0022	0.0021	1.0236	0.3769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0053	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

0067395-122700

Electronic Northern for SEQ. ID NO.: 99

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673305.122700

Electronic Northern for SEQ. ID NO.: 100

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0022	0.0010	2.1599	0.4630
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0020	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

00673305-122700

Electronic Northern for SEQ. ID NO.: 101

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

00672306-12200

## Electronic Northern for SEQ. ID NO.: 102

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

00673395.122700

Electronic Northern for SEQ. ID NO.: 103

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0064	0.0000	undef	0.0000
Ovary	0.0000	0.0165	0.0000	undef
Endocrine tissue	0.0000	0.0078	0.0000	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0015	0.0021	0.7200	1.3890
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0032	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0010	0.0041	0.2540	3.9367
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	% frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0032
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0040
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

00673395-122700



## Electronic Northern for SEQ. ID NO.: 104

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

006775001122700

## Electronic Northern for SEQ. ID NO.: 105

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0090	0.0038	2.3818	0.4196
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0052	0.5756	1.7372
Gastrointestinal	0.0034	0.0025	1.3585	0.7361
Brain	0.0096	0.0000	undef	0.0000
Hematopoietic	0.0037	0.0021	1.7999	0.5556
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0110	0.0847	0.1300	7.6946
Heart	0.0095	0.0065	1.4706	0.6800
Testicles	0.0042	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0010	0.0020	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0027	0.0000	undef	undef
Pancreas	0.0017	0.0166	0.0997	10.0285
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0106			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0050
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 106

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

0067366-12700

Electronic Northern for SEQ. ID NO.: 107

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0058	0.1055	0.0540	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

00673305-122700

Electronic Northern for SEQ. ID NO.: 108

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0038	1.3611	0.7347
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0030
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0310
		Uterus_n	0.0042

00673455-122700

Electronic Northern for SEQ. ID NO.: 109

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

0067305-122700

Electronic Northern for SEQ. ID NO.: 110

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1583	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

## Electronic Northern for SEQ. ID NO.: 111

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0051	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0052	0.0000	undef
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0022	0.0021	1.0799	0.9260
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0033	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0231
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0050
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

00673305-122700



Electronic Northern for SEQ. ID NO.: 112

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0017	0.0000	undef	0.0000
Brain	0.0019	0.0000	undef	0.0000
Hematopoietic	0.0022	0.0010	2.1599	0.4630
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0012
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0125

00573395-122700

Electronic Northern for SEQ. ID NO.: 113

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0050	1.0189	0.9815
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0041	0.7621	1.3122
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		% frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0030
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0310
		Uterus_n	0.0042

00573305.122700

## Electronic Northern for SEQ. ID NO.: 114

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0156	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0093	0.4142	2.4143
Brain	0.0022	0.0021	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0031	0.0164	0.1905	5.2490
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0180	0.3807	2.6265
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0064	0.3412	2.9308
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0204	0.0000	undef
Uterus-general	0.0032	0.0000	undef	0.0000
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.1595
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0087
Hepatic	Gastrointestinal 0.0244
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0356
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0164
Placenta	Nerves 0.0010
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0250

00673395-12700

Electronic Northern for SEQ. ID NO.: 115

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673355-122700

Electronic Northern for SEQ. ID NO.: 116

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0128	0.0000	undef	0.0000
Ovary	0.0061	0.0165	0.3707	2.6973
Endocrine tissue	0.0060	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0050	1.3585	0.7361
Brain	0.0038	0.0046	0.8283	1.2072
Hematopoietic	0.0037	0.0051	0.7200	1.3890
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0042	0.0137	0.3084	3.2426
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0000	undef	0.0000
Pancreas	0.0054	0.0068	0.7930	1.2610
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0118			
Cervix	0.0061			
	0.0106			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0051
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0076
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0228
Lung	Skin-muscle	0.0227
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0000
Placenta	Nerves	0.0060
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0155
	Uterus_n	0.0083

00573305.122700



Electronic Northern for SEQ. ID NO.: 118

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0026	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
% frequency	% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

0067355-122700

Electronic Northern for SEQ. ID NO.: 119

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0007	0.0041	0.1800	5.5559
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0026			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0110
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0155
		Uterus_n	0.0000

00673395-132700



Electronic Northern for SEQ. ID NO.: 120

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0090	0.0075	1.1909	0.8397
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0078	0.7675	1.3029
Endocrine tissue	0.0068	0.0125	0.5434	1.8403
Gastrointestinal	0.0038	0.0093	0.4142	2.4145
Brain	0.0059	0.0031	1.9199	0.5209
Hematopoietic	0.0027	0.0758	0.0353	28.3379
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0041	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0043			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0228
Lung	0.0145	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673305-122700

Electronic Northern for SEQ. ID NO.: 121

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
	% frequency	
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0000
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0010
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0000
	Uterus_n	

0057305.122700

## Electronic Northern for SEQ. ID NO.: 122

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0234	0.0230	1.0170	0.9833
Breast	0.0269	0.0207	1.2992	0.7697
Small intestine	0.0061	0.0662	0.0927	10.7893
Ovary	0.0150	0.0572	0.2616	3.8219
Endocrine tissue	0.0085	0.0100	0.8491	1.1778
Gastrointestinal	0.0134	0.0463	0.2899	3.4492
Brain	0.0015	0.0092	0.1600	6.2504
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0551	0.0000	undef	0.0000
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0073	0.0286	0.2540	3.9367
Stomach-esophagus	0.0966	0.0077	12.6053	0.0793
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0066	0.7930	1.2610
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0329	0.1600	0.2059	4.8565
Prostate	0.0087	0.0043	2.0473	0.4885
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0128	0.0000	undef	undef
Breast hyperplasia	0.0149			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0532			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0136
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0101
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0146
Hepatic	Gastrointestinal	0.0366
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0032
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0573
Placenta	Nerves	0.0040
Prostate	Prostate	0.0205
Sensory organs	Sensory Organs	0.0077
	Uterus_n	0.0000

09673305.122700

Electronic Northern for SEQ. ID NO.: 123

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0007	0.0031	0.2400	4.1669
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.1583	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00573305.122700

Electronic Northern for SEQ. ID NO.: 124

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0026	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0036	0.0000	undef	0.0000
Brain	0.0037	0.0010	3.5998	0.2778
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0035	0.0065	1.4706	0.6800
Heart	0.0035	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0062	Nerves	0.0100
Prostate	0.0000	Nerves	0.0000
Sensory organs	0.0000	Prostate	0.0077
	0.0126	Sensory Organs	0.0042
		Uterus_n	

00673305-122700

## Electronic Northern for SEQ. ID NO.: 125

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0153	0.0226	0.6792	1.4722
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0081	0.0092	0.8800	1.1364
Hematopoietic	0.0067	0.0379	0.1764	5.6676
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0134	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0103	0.0180	0.5711	1.7510
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0329	0.0000	undef	0.0000
Prostate	0.0153	0.0064	2.3885	0.4187
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0053			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0069			
Cervix	0.0106			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0121	Nerves	0.0060
Prostate	0.0249	Prostate	0.0342
Sensory organs	0.0000	Sensory Organs	0.0387
		Uterus_n	0.0250

00673395-122700

Electronic Northern for SEQ. ID NO.: 126

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0021	0.0000	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	
% frequency	% frequency	
0.0000	Breast	0.0000
0.0000	Ovary_n	0.0000
0.0000	Ovary_t	0.0000
0.0000	Endocrine tissue	0.0000
0.0000	Fetal	0.0006
0.0000	Gastrointestinal	0.0000
0.0000	Hematopoietic	0.0000
0.0000	Skin-muscle	0.0032
0.0000	Testicles	0.0000
0.0000	Lung	0.0000
0.0000	Nerves	0.0000
0.0000	Prostate	0.0000
0.0000	Sensory Organs	0.0000
	Uterus_n	

00673395.122700

Electronic Northern for SEQ. ID NO.: 127

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0312	0.0486	0.6423	1.5569
Breast	0.0192	0.0282	0.6805	1.4694
Small intestine	0.0399	0.0000	undef	0.0000
Ovary	0.0210	0.0364	0.5756	1.7372
Endocrine tissue	0.0290	0.0326	0.8892	1.1258
Gastrointestinal	0.0460	0.0231	1.9880	0.5030
Brain	0.0532	0.0575	0.9257	1.0803
Hematopoietic	0.0348	0.0379	0.9175	1.0899
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0048	0.0647	0.0735	13.5999
Heart	0.0699	0.0412	1.6961	0.5896
Testicles	0.0288	0.4210	0.0683	14.6349
Lung	0.0343	0.0368	0.9314	1.0737
Stomach-esophagus	0.0773	0.0230	3.3614	0.2975
Muscle-skeleton	0.0497	0.0660	0.7528	1.3283
Kidney	0.0353	0.1575	0.2241	4.4619
Pancreas	0.0165	0.0939	0.1760	5.6828
Penis	0.0299	0.0267	1.1232	0.8903
Prostate	0.0196	0.0298	0.6580	1.5197
Uterus-endometrium	0.0270	0.1583	0.1707	5.8579
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0890			
Sensory organs	0.0353			
White blood cells	0.0399			
Cervix	0.0319			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0417	Breast	0.0000
Gastrointestinal	0.0333	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0152
Hematopoietic	0.0197	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Fetal	0.0244
Heart-blood vessels	0.0783	Gastrointestinal	0.0057
Lung	0.0217	Hematopoietic	0.0032
Suprarenal gland	0.0507	Skin-muscle	0.0077
Kidney	0.0309	Testicles	0.0082
Placenta	0.0727	Lung	0.0141
Prostate	0.0997	Nerves	0.0000
Sensory organs	0.0000	Prostate	0.0310
		Sensory Organs	0.0125
		Uterus_n	

09573355-122700



Electronic Northern for SEQ. ID NO.: 128

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0038	0.0000	undef	0.0000
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0000	undef	0.0000
Gastrointestinal	0.0068	0.0025	2.7170	0.3681
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0007	0.0031	0.2400	4.1669
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0173	0.0117	1.4759	0.6775
Stomach-esophagus	0.0021	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0086	0.0000	undef	0.0000
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0135	0.1055	0.1280	7.8106
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0089			
White blood cells	0.0235			
Cervix	0.0026			
	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0204
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0152
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

00673305-122700

Electronic Northern for SEQ. ID NO.: 129

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0000
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0000
Hematopoietic	Endocrine tissue	0.0000
Skin	Fetal	0.0006
Hepatic	Gastrointestinal	0.0000
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0000
Suprarenal gland	Testicles	0.0077
Kidney	Lung	0.0000
Placenta	Nerves	0.0010
Prostate	Prostate	0.0068
Sensory organs	Sensory Organs	0.0000
	Uterus_n	0.0000

09673095.122700

Electronic Northern for SEQ. ID NO.: 130

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0013	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

00673395-122700

## Electronic Northern for SEQ. ID NO.: 131

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0115	0.0169	0.6805	1.4694
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0153	0.0176	0.8733	1.1451
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0074	0.0092	0.8000	1.2501
Hematopoietic	0.0080	0.0758	0.1059	9.4460
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0114	0.0164	0.6985	1.4315
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0051	0.0120	0.4283	2.3347
Kidney	0.0136	0.0137	0.9913	1.0088
Pancreas	0.0066	0.0110	0.5983	1.6714
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0068	0.1055	0.0640	15.6211
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0118			
Sensory organs	0.0009			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0099
Hepatic	0.0260	Gastrointestinal	0.0244
Heart-blood vessels	0.0107	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0259
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0062	Lung	0.0082
Placenta	0.0424	Nerves	0.0090
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

00573365.123700

Electronic Northern for SEQ. ID NO.: 132

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0011	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0017	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0022	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

09573395.122700

## Electronic Northern for SEQ. ID NO.: 133

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0141	0.0150	0.9357	1.0687
Ovary	0.0194	0.0000	undef	0.0000
Endocrine tissue	0.0120	0.0104	1.1513	0.8686
Gastrointestinal	0.0102	0.0176	0.5822	1.7176
Brain	0.0057	0.0139	0.4142	2.4145
Hematopoietic	0.0052	0.0072	0.7200	1.3890
Skin	0.0174	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0064	0.0000	undef	0.0000
Lung	0.0058	0.0234	0.2460	4.0652
Stomach-esophagus	0.0104	0.0204	0.5080	1.9684
Muscle-skeleton	0.0193	0.0153	1.2605	0.7933
Kidney	0.0096	0.0240	0.3569	2.8016
Pancreas	0.0244	0.0000	undef	0.0000
Penis	0.0066	0.0110	0.5983	1.6714
Prostate	0.0120	0.0267	0.4493	2.2259
Uterus-endometrium	0.0153	0.0149	1.0236	0.9769
Uterus-myometrium	0.0270	0.2111	0.1280	7.8106
Uterus-general	0.0305	0.0136	2.2445	0.4455
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0192			
Seminal vesicle	0.0327			
Sensory organs	0.0178			
White blood cells	0.0235			
Cervix	0.0000			
	0.0319			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0305	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.0253
Hematopoietic	0.0039	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0093
Hepatic	0.0520	Gastrointestinal	0.0122
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0253	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0309	Lung	0.0246
Placenta	0.0061	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

0067305-122700

Electronic Northern for SEQ. ID NO.: 134

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0273	0.0383	0.7119	1.4047
Small intestine	0.0141	0.0244	0.5758	1.7366
Ovary	0.0245	0.0331	0.7415	1.3487
Endocrine tissue	0.0120	0.0312	0.3838	2.6058
Gastrointestinal	0.0290	0.0201	1.4434	0.6928
Brain	0.0287	0.0278	1.0354	0.9658
Hematopoietic	0.0133	0.0298	0.4469	2.2378
Skin	0.0281	0.0379	0.7411	1.3494
Hepatic	0.0073	0.0847	0.0866	11.5419
Heart	0.0381	0.0259	1.4706	0.6800
Testicles	0.0191	0.1512	0.1262	7.9265
Lung	0.0173	0.0702	0.2460	4.0652
Stomach-esophagus	0.0447	0.0470	0.9498	1.0528
Muscle-skeleton	0.0773	0.0153	5.0421	0.1983
Kidney	0.0668	0.0420	1.5909	0.6286
Pancreas	0.0190	0.0342	0.5551	1.8014
Penis	0.0066	0.0331	0.1994	5.0142
Prostate	0.0150	0.1600	0.0936	10.6842
Uterus-endometrium	0.0196	0.0149	1.3161	0.7598
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0229	0.0204	1.1223	0.8911
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.1240			
	0.0213			

FETUS	STANDARDIZED/SUBTRACTED	
% frequency	LIBRARIES	% frequency
Development	Breast	0.0408
Gastrointestinal	Ovary_n	0.0000
Brain	Ovary_t	0.0253
Hematopoietic	Endocrine tissue	0.0245
Skin	Fetal	0.0169
Hepatic	Gastrointestinal	0.0244
Heart-blood vessels	Hematopoietic	0.0000
Lung	Skin-muscle	0.0454
Suprarenal gland	Testicles	0.0000
Kidney	Lung	0.0164
Placenta	Nerves	0.0000
Prostate	Prostate	0.0000
Sensory organs	Sensory Organs	0.0042
	Uterus_n	

00573305.122700

## Electronic Northern for SEQ. ID NO.: 135

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0390	0.0383	1.0170	0.9833
Small intestine	0.0102	0.0301	0.3403	2.9389
Ovary	0.0429	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0156	0.1919	5.2117
Gastrointestinal	0.0358	0.0351	1.0189	0.9815
Brain	0.0113	0.0278	0.4142	2.4145
Hematopoietic	0.0148	0.0226	0.6545	1.5279
Skin	0.0227	0.2273	0.1000	10.0016
Hepatic	0.0367	0.1695	0.2166	4.6168
Heart	0.0285	0.0582	0.4902	2.0400
Testicles	0.0445	0.0587	0.6476	1.5441
Lung	0.0173	0.0234	0.7380	1.3551
Stomach-esophagus	0.0291	0.0470	0.6185	1.6169
Muscle-skeleton	0.0580	0.0153	3.7816	0.2644
Kidney	0.0685	0.0840	0.8159	1.2257
Pancreas	0.0244	0.0685	0.3569	2.8022
Penis	0.0116	0.0607	0.1904	5.2530
Prostate	0.0180	0.0000	undef	0.0000
Uterus-endometrium	0.0131	0.0064	2.0473	0.4885
Uterus-myometrium	0.0135	0.6332	0.0213	46.8633
Uterus-general	0.0076	0.0408	0.1870	5.3463
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0128			
Seminal vesicle	0.0149			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0867			
	0.0639			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0068
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0236	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0030
Placenta	0.0182	Nerves	0.0000
Prostate	0.0997	Prostate	0.0464
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

0067395.122700



Electronic Northern for SEQ. ID NO.: 136

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000	undef
Small intestine	0.0102	0.0038	2.7221	0.3674
Ovary	0.0092	0.0165	0.5561	1.7982
Endocrine tissue	0.0090	0.0078	1.1513	0.8686
Gastrointestinal	0.0000	0.0150	0.0000	undef
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0059	0.0031	1.9199	0.5209
Skin	0.0040	0.0379	0.1059	9.4460
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0114	0.0041	2.7942	0.3579
Muscle-skeleton	0.0097	0.0153	0.6303	1.5866
Kidney	0.0103	0.0120	0.8567	1.1673
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0050	0.0000	undef	0.0000
Prostate	0.0060	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0064	0.0000	undef
Uterus-myometrium	0.0068	0.1055	0.0640	15.6211
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0104			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal		Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0056	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0079	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0142	Testicles	0.0000
Kidney	0.0108	Lung	0.0164
Placenta	0.0254	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0061	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0125
	0.0126		

00673395.122700

Electronic Northern for SEQ. ID NO.: 137

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.1055	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

00673395-122700

Electronic Northern for SEQ. ID NO.: 138

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0156	0.0051	3.0509	0.3278
Small intestine	0.0000	0.0038	0.0000	undef
Ovary	0.0000	0.0331	0.0000	undef
Endocrine tissue	0.0000	0.0052	0.0000	undef
Gastrointestinal	0.0051	0.0050	1.0189	0.9815
Brain	0.0077	0.0139	0.5522	1.8109
Hematopoietic	0.0059	0.0062	0.9599	1.0417
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0048	0.0065	0.7353	1.3600
Testicles	0.0085	0.0275	0.3084	3.2426
Lung	0.0000	0.0234	0.0000	undef
Stomach-esophagus	0.0062	0.0143	0.4355	2.2964
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0137	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0033	0.0276	0.1197	8.3571
Prostate	0.0120	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0064	0.0000	undef
Uterus-myometrium	0.0000	0.1055	0.0000	undef
Uterus-general	0.0152	0.0068	2.2445	0.4455
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0064			
Seminal vesicle	0.0030			
Sensory organs	0.0000			
White blood cells	0.0087			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	
Gastrointestinal	0.0028	Ovary_n	0.0272
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0118	Endocrine tissue	0.0253
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0151
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0057
Suprarenal gland	0.0000	Testicles	0.0356
Kidney	0.0000	Lung	0.0000
Placenta	0.0242	Nerves	0.0000
Prostate	0.0249	Prostate	0.0090
Sensory organs	0.0000	Sensory Organs	0.0068
		Uterus_n	0.0077
			0.0042

00673305.122700

## Electronic Northern for SEQ. ID NO.: 139

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef undef	
Small intestine	0.0013	0.0056	0.2268 4.4083	
Ovary	0.0061	0.0165	0.3707 2.6973	
Endocrine tissue	0.0120	0.0052	2.3025 0.4343	
Gastrointestinal	0.0017	0.0025	0.6792 1.4722	
Brain	0.0077	0.0046	1.6567 0.6036	
Hematopoietic	0.0000	0.0021	0.0000 undef	
Skin	0.0067	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0275	0.0000 undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0000	0.0041	0.0000 undef	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0017	0.0060	0.2856 3.5020	
Kidney	0.0054	0.0000	undef 0.0000	
Pancreas	0.0017	0.0000	undef 0.0000	
Penis	0.0060	0.0000	undef 0.0000	
Prostate	0.0044	0.0064	0.6824 1.4654	
Uterus-endometrium	0.0000	0.1055	0.0000 undef	
Uterus-myometrium	0.0076	0.0000	undef 0.0000	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0000

00673365-122700

## Electronic Northern for SEQ. ID NO.: 140

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0090	0.0000	undef	0.0000
Endocrine tissue	0.0085	0.0100	0.8491	1.1778
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0137	0.0771	12.9706
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0042	0.0020	2.0321	0.4921
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0000	0.0000	undef	undef
Prostate	0.0044	0.0043	1.0236	0.9769
Uterus-endometrium	0.0000	0.1055	0.0000	undef
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0026			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
% frequency	% frequency

Development	0.0000	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0061	Nerves	0.0060
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

00673395.122700

Electronic Northern for SEQ. ID NO.: 141

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N

Bladder				
Breast	0.0000	0.0051	0.0000	undef
Small intestine	0.0064	0.0150	0.4253	2.3511
Ovary	0.0000	0.0496	0.0000	undef
Endocrine tissue	0.0060	0.0025	2.3025	0.4343
Gastrointestinal	0.0068	0.0050	1.3585	0.7361
Brain	0.0096	0.0046	2.0708	0.4829
Hematopoietic	0.0052	0.0051	1.0079	0.9921
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0053	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0093	0.0061	1.3548	0.7381
Muscle-skeleton	0.0000	0.0153	0.0000	undef
Kidney	0.0103	0.0000	undef	0.0000
Pancreas	0.0027	0.0068	0.3965	2.5219
Penis	0.0033	0.0055	0.5983	1.6714
Prostate	0.0120	0.0267	0.4493	2.2259
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0068	0.1055	0.0540	15.6211
Uterus-general	0.0076	0.0000	undef	0.0000
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0087			
Cervix	0.0000			

FETUS	STANDARDIZED/SUBTRACTED
% frequency	LIBRARIES
	% frequency

Development	0.0000	Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0082
Placenta	0.0061	Nerves	0.0040
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

09673305.122700

## 2.2. Fisher Test

In order to decide whether a partial sequence *S* of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to *S*. If the null hypothesis can be rejected with high enough certainty, the gene belonging to *S* is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence *S* is completed in three steps:

1. Determination of all sequences homologous to *S* from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence *C* from the assembled sequences.

Consensus sequence *C* will generally be longer than initial sequence *S*. Its electronic Northern Blot will accordingly

09573308.122700

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  (i: iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from uterus tumor tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

09673395-122700



**Example 4****Mapping of Nucleic Acid Sequences on the Human Genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

09673395.122700

the results were evaluated with the above-mentioned software and  
the software of the Whitehead Institute

(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

09673395.122700

## References to the modules:

Pfam: Protein families database of alignments and HMMs  
(pfam@sanger.ac.uk)

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 (<http://www.expasy.ch/sprot/prosite.html>)

## TABLE I

Col. 1 - Sequence ID No.:  
Col. 2 - Expression in the endometrial tumor:  
Col. 3 - Function  
Col. 4 - Modules  
Col. 5 - Length of the applied sequence in bases  
Col. 6 - Cytogenetic localization  
Col. 7 - Next marker

[Key to Table I:]

[Col. 2:]  
[Seq. ID Nos. 1-62] erhöht = elevated

[Col. 3:]  
[Seq. ID Nos.: 1, 7-15, 78-126, 136] unbekannt = unknown  
[Seq. ID Nos.: 3, 4, 38, 67-72] Homolog zu... = homologous  
to...

[Seq. ID Nos.: 531-555] Verlängerung von Seq. ID No. ... =  
Lengthening of Seq. ID No. ...

00673305-122700

5 TABELLE I

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cylogenetische Lokalisation	nächster Marker
1	erhöht			1046	2p24-2p21	D2S174-D2S390
2	erhöht	Mouse mammary tumor virus proviral envelope gene Polymerase protein	2x "CSD"	373		
3	erhöht	Homolog zu Human protein kinase C-binding protein RACK17		1571	1q32.1	D1S477-D1S504
4	erhöht	Homolog zu Human mRNA for KIA0079		1789	10q21.3-q22.2	D10S537-D10S718
5	erhöht	Caenorhabditis elegans cosmid T23812	"BTB"	2361		D20S100-D20S173
6	erhöht	Caenorhabditis elegans cosmid C01A2		1638	20q13.32-q13.33	D12S1589-D12S85
7	erhöht	unbekannt		1034	12q12	
8	erhöht	unbekannt		947	17p11.2-p12	AFMa126yds
9	erhöht	unbekannt		497		
10	erhöht	unbekannt		269		
11	erhöht	unbekannt		1717		
12	erhöht	unbekannt	"zf-C3HC4"	1419		
13	erhöht	unbekannt		671	2q37.3	D2S2704
14	erhöht	unbekannt		524		
15	erhöht	unbekannt		345		
16	erhöht	IGSTK1-1=glutathione S-transferase subunit 13		1060	7q33-7q36.1	WI-9363
17	erhöht	Rattus norvegicus neuritin		1721	6p23-p25.1	D6S1617-D6S1674
18	erhöht	Rattus norvegicus cytosolic NADP-dependent isocitrate dehydrogenase	"isodh"	2367	2q34	WI-1247
19	erhöht	Rat unr mRNA for unr protein with unknown function		1321	1p13.3-1q11	D1S418-D1S252
20	erhöht	Rat prostatic binding protein polypeptide c1	2x "CSD"	384		
21	erhöht	Rat GTP-binding protein (ralB)		367		
22	erhöht	R norvegicus mRNA for TRAP-complex gamma subunit		2821	3q24-q25.2	D3S1570
23	erhöht	P salivum mRNA for Cop1 protein	2x "G-beta"	2019	1q23.3-q24.3	D1S242-D1S416
24	erhöht	P falciparum pfmdr1 gene		1866	18q12.1-q12.3	AFM164y99
25	erhöht	ORF 5' of ECLF2...ECRF3-G protein-coupled receptor homolog		1189		

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
26	erhöht	O cuticularis lambda-crystallin mRNA	"3HCDH"	814		
27	erhöht	Mus musculus follit		1418		
28	erhöht	Mouse glycerol-3-phosphate acyltransferase		3039	10q25.1-q25.2	D10S1465
29	erhöht	Mouse cblatin-associated protein (AP47)	"Adap_comp sub"	1448		
30	erhöht	Lycopersicon esculentum biotin-containing subunit of methylcrotonyl-CoA carboxylase	"CPSase L-chain" "biotin_req_enzy"	1394		
31	erhöht	Leucine aminopeptidase, bovine	"Peptidase_M17"	734		
32	erhöht	Klebsiella pneumoniae possible RNA helicase (dead)	2x "DEAD"	692		
33	erhöht	Human mammaglobin Homolog	"Uteroglobin"	517		
34	erhöht	Human DNA sequence from PAC 138A5 on chromosome X		322		
35	erhöht	Human DNA sequence from clone 230G1		1559		
36	erhöht	Human DNA sequence from clone 217C2		1072		
37	erhöht	Human Cosmid Clone 26a1	"RhoGAP"	454	22 q11.21-q11.23 3p21.1	D22S420-D22S446
38	erhöht	Homolog zu Human chromosome 3p21.1 gene sequence		700		
39	erhöht	Human DNA sequence from chromosome 19-cosmid 121246		914		
40	erhöht	H sapiens mRNA for Plg-1 protein		1669	17q21.31-q21.33	D17S791-D17S797
41	erhöht	H sapiens (T15) DNA genomic MseI fragment		355		
42	erhöht	H sapiens Cpg Island DNA genomic MseI fragment		2628	3q24	D3S3413
43	erhöht	H sapiens (T15) mRNA from LNCaP cell line		2535	9q34.11-q34.13 1q21.2	D9S179-D9S164 D1S305-D1S506
44	erhöht	Genomic sequence from Human 9q34	"MYB_3"	805		
45	erhöht	Drosophila melanogaster mlsato gene		1279		
46	erhöht	Chicken mRNA for vitellogenin I		1923		
47	erhöht	Caenorhabditis elegans DNA from clone F31D4		706		
48	erhöht	Caenorhabditis elegans cosmid ZK863		749		
49	erhöht	Caenorhabditis elegans cosmid ZK863		857	10q26.13	D10S212
50	erhöht	Caenorhabditis elegans cosmid ZK596		268		
51	erhöht	Caenorhabditis elegans cosmid T26A5		297		
52	erhöht	Caenorhabditis elegans cosmid T21G5		297		
53	erhöht	Caenorhabditis elegans cosmid F56D5		590		
54	erhöht	Caenorhabditis elegans cosmid F25D7		1714		
55	erhöht	Caenorhabditis elegans cosmid F08C6		1340		
		C.botulinum bont (partial) and nttn genes		765	3q24-q23	D3S3409

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cyogenetische Lokalisation	nächster Marker
56	erhöht	Bovine mRNA fragment for 49 kDa subunit of mitochondrial NADH:ubiquinone oxidoreductase (EC 1.6.5.3)	"complex 1_4 9kD"	1647		
57	erhöht	Bos taurus (clone pTKD7) dopamine and cyclic AMP-regulated neuronal phosphoprotein (DARPP-32)		1166		
58	erhöht	A. italiana mRNA for RNA helicase		487		
59	erhöht	A. italiana glycine-rich protein (clone aIGRP-4)		1630	5q23.3-q31.1	D5S398-D5S2119
60	erhöht	Saccharomyces cerevisiae Grd19p (GRD19)	2x "PX"; "BEM DOM AIN"	1272	6q21	AFMa191wd1
61	erhöht	Saccharomyces cerevisiae chromosome XII cosmid 9328	2x "DEAD"; "Helicase_C"	1914	7p12.3-p13	D7S667-D7S2427
62	erhöht	Spombe chromosome I cosmid c13D6		608		
63	erhöht	Rattus norvegicus RNA helicase with arginine-serine-rich domain		2674	17q21.31-q22	D17S797-D17S788
64		Rattus norvegicus matrilysin (MMP-7) mRNA		326		
65		Rattus norvegicus Diphtheria toxin receptor (GCR)	2x "PD2"	888	1q12	D1S2669-D1S488
66		Human herpesvirus-7 (HHV7) J1, G protein-coupled receptor (GCR)		202		
67		Homolog zu Human synapsin I (SYN1)		1225	1p22.3-p31.1	WI-3099
68		Homolog zu Human PAX3 gene		1093		
69		Homolog zu Human multiple exostosis 2 (EXT2)		309	1p21.3-p22.1	D1S2166
70		Homolog zu Homo sapiens integrin variant beta4E (ITGB4)		380		
71		Homolog zu Homo sapiens ICPE-R mRNA for CPE-receptor		1253		
72		Homolog zu H.sapiens mRNA for deoxyguanosine kinase		439		
73		Caenorhabditis elegans cosmid Y48E1B	"WW DO-MAIN_2"	1252	4p11-q12	D4S1619-D4S1600
74		Caenorhabditis elegans cosmid T21D12		695		
75		Caenorhabditis elegans cosmid R107		2514	13q33.3-q34	D13S261-D13S293
76		Caenorhabditis elegans cosmid M04C9		274		
77		Bovine opsin	"7Im_1"	449		
78		unbekannt		346		
79		unbekannt		1329		
80		unbekannt		805		

Sequenz- ID No.	Expression im Endometrium- Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
81		unbekannt		420		
82		unbekannt		2143	9q21.32-q22.1	D9S264-D9S257
83		unbekannt		450		
84		unbekannt		408	17q23.1-q23.2	D17S1680
85		unbekannt		311		
86		unbekannt		487		
87		unbekannt		1902	11p12-p13	WI-6150
88		unbekannt		1048	1q42.11-q43	WI-9317
89		unbekannt		804		
90		unbekannt		581		
91		unbekannt		2042		
92		unbekannt		430		
93		unbekannt		592		
94		unbekannt		674		
95		unbekannt		324		
96		unbekannt		709	5p15.33	D5S1954
97		unbekannt		562		
98		unbekannt		1948	16p13.2-p12.3	D16S499
99		unbekannt		483		
100		unbekannt		437		
101		unbekannt		359		
102		unbekannt		501		
103		unbekannt		1102	1q23.1-q23.2	D1S445-D1S431
104		unbekannt		306		
105		unbekannt		2042		
106		unbekannt		320		
107		unbekannt		506		
108		unbekannt		1276		
109		unbekannt		373		
110		unbekannt	TPR RE- PEAT*	492		
111		unbekannt		1678	6q21	D6S278-D6S302
112		unbekannt		866	9q22.1-q22.2	D9S1841-D9S196
113		unbekannt		1434	18q12.1-q12.3	D18S1124-D18S468
114		unbekannt		914	7q32.3	D7S686-D7S530
115		unbekannt		685	8p12-p11.23	D8S1821-D8S255

Sequenz ID No.:	Expression im Endometrium-Tumor:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
116		unbekannt		2646		
117		unbekannt		2667		
118		unbekannt		544		
119		unbekannt		1340	18p11.21	D18S471-D18S464
120		unbekannt		2376		
121		unbekannt		225		
122		unbekannt		1967	6q22.33-q23.1	D6S292-D6S1699
123		unbekannt		612		
124		unbekannt		1183	2q32.3-q34	D2S315-D2S2237
125		unbekannt		891	4q28.1-q31.1	
126		unbekannt		482		
127		Human triosephosphate isomerase mRNA		610		
128		Human ras inhibitor mRNA		2072	9q33.3-q34.11	
129		Human R kappa B		980		
130		Human putative interferon-related protein (SM15)		792		
131		Human protein trafficking protein (S3.11125)	2x "EMP24_GP251"	1092	14q32.2-14q32.33	WI-9179
132		Human protein kinase C-binding protein RACK7	"linker-histone"	1523	20q13.13-q13.2	D20S957
133		Human gene for histone H1(0)		2241	22q13.1	
134		Human cathepsin B proteinase	"Cys-protease"	631		
135		Homo sapiens cathepsin B mRNA	"Cys-protease"	980		
136		unbekannt		2238	14q24.1-14q24.3	D14S277
137		H.sapiens XG mRNA		398		
138		H.sapiens mRNA for RAB7 protein	ras	1084	7q21.3-q22.1	D7S652
139		H.sapiens mRNA for pyroline 5-carboxylate synthetase		1259		
140		H.sapiens mRNA for beta-1,4-galactosyltransferase		1938	1q22-q23.1	
141		H.sapiens IL-13Ra		1874	Xq23	
531		Verlängerung von Seq. ID No. 19	2x "CSD"	1708	1p13.3-1q11	D1S418-D1S252
532		Verlängerung von Seq. ID No. 23	2x "G-beta"	2128	1q23.3-q24.3	D1S242-D1S416
533		Verlängerung von Seq. ID No. 25		2640		
534		Verlängerung von Seq. ID No. 32	2x "DEAD"	1245		
535		Verlängerung von Seq. ID No. 34		822		



Sequenz ID No.:	Expression im Endometrium- Tumor.	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
536		Verlängerung von Seq. ID No. 43		2703	9q34.11-q34.13	D9S179-D9S164
537		Verlängerung von Seq. ID No. 44	"MYB_3"	2664	1q21.2	D1S305-D1S506
538		Verlängerung von Seq. ID No. 52		3888		
539		Verlängerung von Seq. ID No. 54		3304		
540		Verlängerung von Seq. ID No. 55		863	3q24-q23	D3S3409
541		Verlängerung von Seq. ID No. 59		1982	5q23.3-q31.1	D5S396-D5S2119
542		Verlängerung von Seq. ID No. 60	2x "PX"; "BEM_DOM AIN"	1772	6q21	AFMa191wd1
543		Verlängerung von Seq. ID No. 65		1009	1q12	D1S2669-D1S498
544		Verlängerung von Seq. ID No. 69	2x "PDZ"	2834	1p21.3-p22.1	D1S2166
545		Verlängerung von Seq. ID No. 82		2319	9q21.32-q22.1	D9S264-D9S257
546		Verlängerung von Seq. ID No. 84		2456	17q23.1-q23.2	D17S1680
547		Verlängerung von Seq. ID No. 87		2218	11p12-p13	WI-6150
548		Verlängerung von Seq. ID No. 88		2196	1q42.11-q43	WI-9317
549		Verlängerung von Seq. ID No. 93		701		
550		Verlängerung von Seq. ID No. 98		2214	16p13.2-p12.3	D16S499
551		Verlängerung von Seq. ID No. 108		1434		
552		Verlängerung von Seq. ID No. 111		2434	6q21	D6S278-D6S302
554		Verlängerung von Seq. ID No. 114		1457	7q32.3	D7S686-D7S530
555		Verlängerung von Seq. ID No. 126		741		

TABLE II

DNA Sequences  
Seq. ID. No.

Peptide Sequences (ORF's)  
Seq. ID. No.

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
1	142
	143
	144
2	145
	146
	147
3	148
	149
	150
4	151
	152
	153
5	154
	155
	156
6	157
	158
	159
7	160
	161
	162
8	163
	164
	165
9	166
	167
	168
10	169
	170
	171
11	172
	173
	174
12	175

00/22T-5682/960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
12	176
	177
13	178
	179
	180
14	181
	182
	183
15	184
	185
	186
	187
16	188
	189
	190
17	191
	192
	193
18	194
	195
	196
19	197
	198
	199
20	200
	201
	202
21	203
	204
22	205
	206
	207
23	208
	209
	210
24	211

002227-5622960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
24	212
	213
25	214
	215
	216
26	217
	218
	219
27	220
	221
	222
28	223
	224
	225
29	226
	227
	228
30	229
	230
	231
31	232
	233
	234
32	235
	236
	237
33	238
	239
	240
34	241
	242
	243
35	244
	245
	246

00673395.12700

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	247
36	248
	249
37	250
	251
	252
38	253
	254
	255
39	256
	257
	258
40	259
	260
	261
41	262
	263
	264
42	265
	266
	267
43	268
	269
	270
44	271
	272
	273
45	274
	275
	276
46	277
	278
	279
47	280
	281
	282

00673395.122700

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	283
48	284
	285
49	286
	287
	288
50	289
	290
	291
	292
51	293
	294
	295
52	296
	297
	298
53	299
	300
	301
54	302
	303
	304
55	305
	306
	307
56	308
	309
	310
57	311
	312
	313
58	314
	315
	316
59	317
	318

002227.5682960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	319
60	320
	321
	322
61	323
	324
	325
62	326
	327
	328
63	329
	330
	331
64	332
	333
	334
	335
65	336
	337
	338
66	339
	340
	341
67	342
	343
	344
68	345
	346
	347
69	348
	349
	350
70	351
	352
	353
71	354

09673395.122700

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	355
	356
72	357
	358
	359
	360
73	361
	362
	363
74	364
	365
	366
75	367
	368
	369
76	370
	371
	372
77	373
	374
	375
78	376
	377
	378
79	379
	380
	380
	381
80	382
	383
	384
81	385
	386
	387
82	388
	389

09673395-122700



DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	390
83	391
	392
	393
84	394
	395
85	396
	397
	398
86	399
	400
	401
	402
87	403
	404
	405
	406
88	407
	408
	409
89	410
	411
	412
90	413
	414
	415
91	416
	417
	418
92	419
	420
	421
	422
93	423
	424
	425

00/227.5667960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	426
94	427
	428
95	429
	430
	431
	432
96	433
	434
	435
97	436
	437
	438
98	439
	440
	441
99	442
	443
	444
100	445
	446
	447
101	448
	449
	450
102	451
	452
	453
103	454
	455
	456
104	457
	458
	459
	460
105	461

09673395-122700

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	462
	463
106	464
	465
107	466
	467
	468
	469
108	470
	471
	472
109	473
	474
	475
110	476
	477
	478
111	479
	480
	481
112	482
	483
	484
	485
113	486
	487
	488
114	489
	490
	491
115	492
	493
	494
	495
116	496
	497

004221-5622960

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	498
117	499
	500
	501
118	502
	503
	504
119	505
	506
	507
120	508
	509
	510
121	511
	512
	513
122	514
	515
	516
123	517
	518
	519
124	520
	521
	522
125	523
	524
	525
126	526
	527
	528
531	561
	562
	563
532	564
	565

00673305.122700

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
	566
533	567
	568
	569
534	570
	571
	572
535	573
	574
	575
536	577
	578
537	579
	580
	581
538	582
	583
	584
539	585
	586
	587
540	588
	589
	590
541	591
	592
	593
542	594
	595
	596
543	597
	598
	599
544	600
	601
	602

09673395.122700

DNA-Sequenzen Seq. ID. No.	Peptid-Sequenzen (ORF's) Seq. ID. No.
545	603
	604
	605
546	606
	607
	608
547	609
	610
	611
548	612
	613
	614
549	615
	616
	617
550	618
	619
	620
551	621
	622
	623
552	624
	625
554	630
	631
	632
555	633
	634
	635

00673395.122700

The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 142-528 are described in the following sequence protocol.

### Sequence Protocol

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: metaGen - Gesellschaft für Genomforschung  
mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from  
Uterus Tumor Tissue

(iii) Number of sequences: 622

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25  
(EPO)

09673035-122700

## (2) INFORMATION ON SEQ ID NO. 1:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1046 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

tcggaacgag ggatcactaa tcaacaaacc agcttttcggg gtctgacggc atccttgcc 60  
 caggcctctc gaggttcaga cagccgccca gcccgctctg cgacgcagca gtgaatagt 120  
 tggtaacctc ttgtctcggt tcagggtccag acctccccgt ctcccgctg cctggaacct 180  
 caggcgacct caggacctg tgattggcgc ctgcccgggc ggaccgtgac cgaggaaacc 240  
 cctggaggga cttgggcatt ccttgggcct cgtgcctggt ctctgctgc ctttcggggc 300  
 aaggatcca cattatcagt ctttgaccga cacagaatgc ctggcatttg ataaatg 360  
 gttgaacttg aagagacata tggacaatga atctgcaaag atactgggga gagataccaa 420  
 tatcatcaag ccagaccaac agaagtctct tcgatttgct ccacgggag ttccgtctgg 480  
 tgggaagtcca tgaccacacc ctgcaccaac cctcagccaa caagccgaag cccccacta 540  
 tgctggacat cccctcagag ccatgtagtc tcaccatcca tacgattcag ttgattcagc 600  
 acaaccgacg tcttcgcaac cttattgcca cagctcaggc ccagaatcag cagcagacag 660  
 aagggtgtaa aactgaagag agtgaacctc ttccctcgtg ccctgggtca cctcctctcc 720  
 ctgatgacct cctgccttta gattgtaaga atcccaatgc accattccag atccgggcaca 780  
 gtgaccagga gagtgacttt tatcgtggga aaggggaacc tgtgactgaa ctacagctggc 840  
 actcctgtgc gcagctctcc taccgaaggca gtggcacaaa tcttggccaa cggcgggctt 900  
 ttgactgtgc taatgagagt gtccctggaag accctaactt gatgttgcca catgagtatt 960  
 ggccttaaa tttaccaaa tttgctgcgt ttttgcgttt gagcgggaag cccgggtggg 1020  
 agagacttcc ttttgccgaa tgtgat 1046

## (2) INFORMATION ON SEQ ID NO. 2:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 373 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

0967395-122700



(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

cgaaggcaga gttcaacagg gatcttttgt aaatgttcaa caagggccac aggagccatt 60  
tattgaattt atccatcagt taacccaggc aattaagagc acacatggaa catcgaccat120  
tccacgggta tctcgtataa cctccaagga caagccatag tggaaacgttg cccattccac180  
gcttaaaaaat atgcttttaa aaaaggggga atatgaataa ggaccctaca acactactag240  
cacaagtgtt attcaccctt aatttcttaa atttagataa ttaaatttcc aatcagccct300  
agaaaagcac ttttgcttaa aacctcccca ggtagcaagg ctttcagtgt tttgggaagg360  
tgtaaatagt atc 373

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1571 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00673305 12700 007221 999999

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

ctgctctggc aaccaataga agctaggaga gggcggggac aactgggtct tttgcggctg 60
cagcgggctt gtaggtgtcc ggctttgctg gcccgagcaag cctgataaac atgaagctct 120
tatctttggt ggctgtggtc ggggtgtttgc tgggtgcccc agctgaagcc aacaagattt 180
ctgaagatcat ccggtgccaa tgcattctgtc cactttatag aaacatcagt gggcacattt 240
acacaccagaa tgtatcccgag aaggactgca actgcctgca cgtgggtggag cccatgccag 300
tgcttgccca tgacgtggag gcctactgct tgctgtgcga gtgcaggtac gaggagcgca 360
gaccacaccac atcaaggtca tcattgtcat ctacctgtcc gtgggtgggtg cctgtgtgct 420
ctacatggcc ttccatgatc tgggtggacc tctgatccga aagccggatg catacactga 480
gcaactgcac aatgaggagg agaattgagg tgctcgctct atggcagcag ctgctgcac 540
cctcggggga ccccgagcaa acacagtcct ggagcgtgtg gaaggtgcc agcagcggtg 600
gaagctgcag gtgcaggagc agcggaagac agtcttcgat cggcacaaga tgctcagcta 660
gatgggctgg tgtgggtggg tcaaggcccc aacaccatgg ctgccagctt ccaggctgga 720
caagcagggg ggtacttctt ccttccctc ggttccagtc ttccctttaa aagcctgtgg 780
catttttctt ccttctcctt aactttagaa atgttgtact tggctatttt gattagggaa 840
gagggatgtg gtctctgctc tccgtgttct tcttgggtct ttggggttga agggaggggg 900
aaggcagggc agaagggaat ggagacattc gaggcggcct caggagtgtg tgcgactctg 960
ctctctctgg tcacactctt cgccttccca gctctgagtc ttgggaatgt tgttaccctt 1020
ggaagataaa cgtgggtctt caggaactca gtgtctggga ggaagacatg gccagcattt 1080
cagcatgtgt tcttttctgc agtgggtctt tatcaccacc tccctcccag ccccgagcc 1140
tcagcccccag ccccgagctc agccctgagg acagctctga tgggagagct gggccccctg 1200
agccacactg gtcttcaggg tgcactggaa gctgtgtgtc gctgtccctt gtgcactt 1260
cgactctggg catggagtgc ccatgcatac tctgctgccc gtccctccac ctgcacttga 1320
gggactctgg cagtcctctc tctccccagt gtccacagtc actgagccag acggtcggtt 1380
ggaacatgag actcgagcgt gagcgtggat ctgaacacca cagccctgtg acttgggttg 1440
cctctgtgct ctgaactctg ttgtaccagt gcacggagag aaaattttgt cctctgtgct 1500
tagagtgtgt tgtaaatcaa ggaagccatc attaaattgt tttatttctc tccaaaaaaa 1560
aaaaaaaaa a

```

1571

## (2) INFORMATION ON SEQ ID NO. 4:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1789 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

0067395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

agaccatgct ggaaaaaatt ccaagggaag agcaagaaga gacgtctgca attcgagtgg 60  
 gttttatcac atataacaaa gtctccattt tctttaatgt gaagagtaat ctggccccagc 120  
 ctccagatgat gggggtgact gatgttggag aagctcttgt tcctttgttg gatgggtttcc 180  
 ttgtcaacta tcaagaatcc caatctgtga ttcataattt gttggaccag attccagaca 240  
 tgtttgcaga ctctaataa aatgagactg tctttgtccc tgtcatccag gctggcatgg 300  
 aagcaactaaa ggcagcgagac tgtcctggga agctgttcat cttccattct tccttgcaca 360  
 ctgtcgaagc accaggggaag ctcaaaaaa gagatgacaa aaaactgggtt aatacagaca 420  
 aagagaagat acttttccag ccccaaaaa atgtctatga ctccattggc aaggactgcg 480  
 tggctcacccg gctgctctgt gacactcttc ctctttccta gtccagtatgt ggacgtggcc 540  
 tcgctggggc tggttcctca gctcactgga ggaacccctt acaaatacaa caatttccag 600  
 atgcacttgg atagacaaca atttttgaac gacctcagaa atgatattga aaagaaaata 660  
 ggctttgatg ctattatgag ggttcgtacc agcacagggt tcagagccac tgatttcttt 720  
 ggtggaatct tgatgaacaa caccaccgat gtagaatagg ctgccaatga ttgtgacaag 780  
 gcagtgcaccg tggagtccaa gcacgatgac aaactcagtg aagacagtgg agccttaatc 840  
 cagtggtgctg tgccttacac gacaatcagt ggtcaagaa gacttcggat tcacaatctt 900  
 ggcttaaaact gcagctctca gctagctgat ctttaataa gctgtgagac agatgctctt 960  
 atcaactctt ttgccaaagt agcttttaaa gcagttctcc accagccctt gaaggctcatc 1020  
 cgggaaattc tagttaatca gactgcacct atgttggcat gttaccggaa gaattgtgca 1080  
 agtccctctg cagcaagcca gctttatcta ccagattcca tgaaagtatt gccagtgtacl 1140  
 atgaattgct tggttgaaaa ctgtgtacta ctcagcgagac cagagatctt aactgatgaal 1200  
 cgagcatacc agagacagct ggtcatgacc atgggtgttg ctgactctca gcttttcttcl 1260  
 taccacaac tctgcacct acacacgtta gatgtcaaga gtacaatggt acctgctgcc 1320  
 gttcgttctg ctgagctccc tctttcagaa gaaggaatat tcttactggc taatggtcta 1380  
 cacatgtccc tgggttggg agtaagcagc ccaccagaac tgatccaag aatatttaat 1440  
 gtgccatctt ttgcacatat caacacagat atgacattgc tgcctgaagt gggaaaccca 1500  
 tactctcaac aactcagaat gataatgggt attatccaac aaaagaggcc atattcaatg 1560  
 aagctcacia ttgtaagca gcgagaaaca ccagaaatgg ttttccgaca gttcctggta 1620  
 gaagacaaag gactttacgg aggcctctct tatgtggatt tcctttgttg tgttcaacaag 1680  
 gagatctgtc agctgcttaa ttaattggaa actccccgg caatggagggt tgccttgcca 1740  
 gggggggaaa agcccccttt tggggcccaa atttgccagg gggaaaaag 1789

## (2) INFORMATION ON SEQ ID NO. 5:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 2361 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
- (A) ORGANISM: HUMAN
  - (C) ORGAN:

00673395.132700

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

gggccagcgg gctcgcgccgg gggccatggc agcagcggct actgcagcgg aggggggtccc 60  
cagtcggggg cctcccgggg aagtcacoca totgaatgtg ggaggcaaga gattcagttac 120  
ctctcgccag actctcacct ggatcccaaga ctctctcttc tccagtcttc tgagcgggacg 180  
catctcgacg ctgaaagatg agaccggagc aatcttcacg gacaggggacc ctacagttctt 240  
cgcccccatc ctcaacttcc tgcgcaccaa agagtgtgat cccagggttg tccacggttc 300  
cagcctctcc catgaagccc agttctatgt gctcactctc ctggttcgtc gcttcgagct 360  
tcgagaggag ttggatcgat cttcttctgg aaacgtctct tccaatgggt acctgcccgc 420  
accagtgttc ccagtgaaagc ggcggaaacc gcacagcta gtgggggctc agcagctagg 480  
aggacggcca gccctctgct gacggagcaa cactgatccc cccaaacctg gcaatgcagg 540  
cgctgctggg cgaatgctgg atgagaaaac cctccctcca ccttcaggac aactgcagg 600  
gcccggggat gtgcgcctgg tgtgtggaca ccaataattg atcgctgttg cctataccca 660  
gtttctagtc tgcatacagg tgaaggaaag ctctggcggg cagctgggtg tttccagccc 720  
ccgcctggac tggcccatgc gaacgactgg cgtctcaacg cccgggtgca ttggtggggct 780  
ttgggtgaac atgacaagat ggtggcagca gccaccggca gcgagatcct gctatgggct 840  
ctgcaggcgg aaggcggg-gg ctccagataa ggggtctctt atctgggggt gccctgggag 900  
ggcttgttct tgcgtcgggaa ccagctcatt gctacaagcc acacaggggc catcggggtg 960  
tggaaatgcc tcaccaagca ctggcaggtc caggagggtgc agcccatcac cagtatatga 1020  
ggggcaggct ccttctctct cctgggctgc aacaacggct ccaattacta cgtggatgtg 1080  
cagaagtctc ccttgcgcct gaaagacaac gaacctcttg tcagcgagct ctatcgggac 1140  
ccagcggagg atgggggtcac gcgcctcagt gtctacatca cccccaagac cagtgcaggt 1200  
gggaactgga tcgagatgca ctatggcacc agctcagggg cgtgctgggt catcgtgcag 1260  
caccocgaga ctgtgggtctc ggggcctcag ctcttcacaga ccttcactgt gcaccgcagc 1320  
cctgtcacca agatcatgct gtccgagaag cactctatct cagtctgtgc cgacaacaac 1380  
cacgtcgga catggctctg gactcgcttc cgcgcctaga tttccaccca gcccgctctc 1440  
accocactcg ctctctttaa gatcctggct ctggagtggc cagatgggca tggcggtctc 1500  
agtgcgtgga atgacattgg cccctacggt gagcgggacg accagcaagt gtctccagc 1560  
aagggtgtgc ccagtgcagg ccagctcttc ttgcgtctct catctacttg cagcgggtg 1620  
tgctcgtgct gctcctgtga cggctcacc cagacagcct tcacagtgtc ggagtgcgag 1680  
ggctcccgcc ggctcgtgct tcggcccccg cgtacctctc tcacttgcca ccccaacggc 1740  
agcttggcca tgtgggacac aaccacggc atggacggc tcggccaggc gcttcaggt 1800  
ggctcagcgg agcaagagct gatggaacag ctggaacact gtgagctggc cccgcgggtc 1860  
ccttcagctc cctcatgggg ctgtctctcc agccctcac ccccatctc cctaccagc 1920  
ctccactcag cctccagcaa cactctcttg tctggccacc gtgggagccc aagcccccg 1980  
cagctcgagg ccgcgcggcg agcttctggc aacgtctgca ggaactggtg 2040  
cggaagtggg cagacctccg accgcccacc acaccaagccc cgtggcctc cagcgtctct 2100  
ggcaactccc tcacacctcc caagatgaag ctccatgaaa ctctcttttg aacaacggc 2160  
gctccatgat gccctgggat gccctggctc ttgggggact aggtgcctcc ctgattcct 2220  
tgggaacccc ggggtcaggg ccaggggctc ctctggaata atggttatgt ttactagct 2280  
cccacctctc ctcttttctg gaagccaaag tcacctctcc caataaagtc ctactgcac 2340  
aaaaaaaaa aaaaaaaccc g 2361

09673395.12700

## (2) INFORMATION ON SEQ ID NO. 6:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1638 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

ggctcgccgat ttccgcggaa atcccggaag tgacagcctt ggggggtttgc tgctggctct 60
gactcccgtc ctgcgatggg ttgcgcaggg ggaacaatcc ccaagaggca tgaactgggt 120
aagggggccga agaaggttga gaaggtcgac aaagatgctg aattagtggc ccaatggaa 180
tattgtactc taagtcagga aatattaaga cgaccaatag ttgcctgtga acttggcaga 240
ctttataaca aagatgcgct cattgaattt ctcttggaca aatctgcaga aaaggctctt 300
gggaaggcag catctcacat taaagcatt aagaatgtga cagagctgaa gctttctgat 360
aatctcgctt gggaagggga taaaggaaac actaaagggt acaagcacga tgacctccag 420
cgggcgcggt tcatctgccc cgttgtgggc ctggagatga acggccgaca caggttctgc 480
tcccttcggt gctcgggctg tgtgttttct gagcgagcct tgaagaagat aaaagcgaaa 540
gtttgccaca cgttgggggc tgccctccag gaggatgat tcatcgtgct caatggcacc 600
aaggaggatg tggacgtgct gaagacaagg atggaggaga gaaggctgag agcgaattgg 660
aaaagaaaac aaagaaaccc aagcgagcag agtctgtttc aaaccagat gtcagtgaag 720
aagccccagg gccatcaaaa gttaagacag ggaagcctga agaagccagc ctgtattcta 780
gagagaagaa aaccaacttg gctcccaaaa gcacagcaat gaatgagagc tcttctggaa 840
aagctgggaa gcctcgtgtt ggagcccaa agaggtccat cgtgcagat gaagaatcgg 900
aggcctacaa gtccctcttt accactcaca gctccgccaa gcgctccaag gaggagtctg 960
ccactgggtt caccacacgc tctactgct tctgaagccc gcactgccac cgctctgtcc1020
ccagaagggt gtttatgttc cacgtaggca ggtcgcttgg tgccctctgag tgcgctgtgt1080
tgtgttctct ctatagttct gtgcataaaa gctgtcctgg ccagccttca agctggtgtgt1140
gccactcttg atgtgaggcg tctcggttcc agggggggaca tggggggggc tgcacagtgg1200
ccagaggcca tgctgtcttc cactgcaggt tgcatttggc ccttctccatg gccaggaaagc1260
cctgtgggct gcaactttta tgcttgagct aacaagagac tccagagctcc tcacccggtgc1320
agagtgtgca catatttaatt aactaaaatt ctaatgatct tgctaccagc aataaatcaal380
gtaggccaag tgaactcggg ctttaaaaag gatggatttc aaatcacactg tgcacctag1440
aagcttcgaa gggcctcgct cctctgctac agccctggga ggaagcagga tctctgttgg1500
tctagctaaa tactgttagg ggagtgtgcc ccatctcctc atttccaaga tagcagagtc1560
atagtgggc acccggtgat tgggttcaaa aataaagctg gtctgcctct tcaaaaaaaal620
aaaaaaaaa aaaaaaaa
1638

```

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

cgccctgcgcg ctgagtgcggt gccgctccgc cgaccgaaga ggctggacat gacaccagtg 60  
 gcataatcacg gccatgggggt ctccagcattc cgctgctgct cgccctctct cctgcaggcg 120  
 aaagcaagaa gatgacaggg acggttttgt ggctgaacga gacgagggaag aagccattgc 180  
 tcagttccca tatgtggaat tcacccgggag agatagcatc acctgtctca cgtgccaggg 240  
 gacaggctac attccaacag agcaagtaaa tgagttgggt gctttgatcc cacacagtga 300  
 tcagagattg cgccctcagc gaactaagca atatgtctct ctgtccatcc tgctttgtct 360  
 cctggcatct ggtttgggtg tttttctctt gtttcgcgat tcagtccttg tggatgatga 420  
 cgggcatcaa gtggtgaaag tcacatttaa taagcaagac tccttgtaa ttctcccat 480  
 catggccacc ctgaaaatca ggaactccaa ctctcacacg gtggcagtga ccagcctgtc 540  
 cagccagatt cagtacatga acacagtgtt gaattttacc ggggaaggcg agatgggagg 600  
 accgttttcc tatgtgtact tcttctgcac ggtacctgag atccctgggtg acaacatagt 660  
 gatcttcatg cgaacttcag tgaagatttc atacattggc ctcatgaccc agagctctct 720  
 ggagacacat cactatgtgg attgtggagg aaattccaca gctattttaac aactgtctatt 780  
 ggttcttcca cacagcgctt gtagaagaga gcacagcata tgttcccaag gcctgagttc 840  
 tgggacctac ccccacgtgg gtgttaaggc agagggaagg aattggttca ctttaacttc 900  
 ccaggcaaac attcctcctg gccacttagg gagggaaaca ccttccctat gggttaccat 960  
 ttgtgttttg ttcaggaacc aggcggattc agttgcctag gcgtgtgtgc ccagcaattal020  
 gtttgggcat tgca 1034

## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 947 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09673395.122700

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

cgagggccctg gcatgtgcaa agagtactga gtgggattcc cagcaggata ccatcaagta 60
ctacaccatg cacctgacca cattgtgcaa cagctgattg gacaacccaa cccagagaa120
caaggatcag ctgatccggg cagccgtgaa gtttctggac accgacacca tctgtacag180
ggtggaggag cccgagacat tagtggaaact tcaaaaggaat gagtgggac caatcatcga240
atgggctgag aaaagatacg gcgtggagat cagctctccc accagcataa tgggacccag300
catccctgcc aaaactcggg aggtgctcgt cagccacctg gcattcttaca acacatgggc360
tttacaaggg attgagtttg tagctgccca gtcgaagtc atggtgctaa ccttgggcct420
gattgacctg cgctcgacag tggagcaggc cgtgctgctg tcacgccttg aggaggagta480
ccagatccag aagtggggca acattgagtg ggcccatgac tatgagctgc aggagctcgc540
ggcccgacc gccgcgggca cctcttcat ccactctgac tccgagagca ccacagtcaa600
gcacaagctc ctgaaggagt gaggcctggg cagagcacac tcagcaggat agaggcagtg660
cagccacagc tcccgcggcc ttcagggtcc ccagcctgt ggggctggct tcottggct720
ttggggactc ggctcagcg tcacccctgag attccccccg agacacagtg cgctagtagc780
gctgtccgga ggtcagcctg atttcaaccc aggtgccctt ggccctggcca gcagtgaatg840
taggagatga attgtgcaag tgactttctc togactctga ttttattaaa tatttctcca900
ccctggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 947

```

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 497 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

00673795.1.22700

- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```
ctcgtggcga gagactgaga taaaagagca actcactgaa cacctttgta cgaatcaca 60
gcacaaatgag ctccgaagag ccaagaagtt ggaggagtgg atgcaacaac tagatgtaga120
agccgatgaa gagactttgg agcttgaggt ggaggctgag agattgctac acgaacaaga180
agtgaatca aggaagaccag tgggtcgttt agagaggcca ttccagcctg cggaggagag240
tgtgacatta gaaattgcta aagagaacag aaagtgtcaa gaacaagctg ttcccccaaa300
ggtagatgac cagtgtggaa attccagtag catccccctt cttagtccaa actgccccaa360
tcaagaaggt aatgacattt cagctgcttt ggccacatga agttctggtt ttcttttgag420
ctaataatggt attgagttaa gtatactttt tgcagtagat catgcccctg cctccaataa480
aaacctcttt aaaaaca 497
```

- (2) INFORMATION ON SEQ ID NO. 10:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 269 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
cggggagagg tgggctgggc tgcaggtcct ggcggttgtc tggatcatcg cgcccgact 60
ctgaagtttt ctccgtggcg ctccctgaga ggggttcctc ctgcatcttg agaataattt120
gcatttcggc tcccttctct tctcgtcggc atcggatgcc ccaaataggt cctgtcccct180
cggtgaatca gacttcggaa accgcctcgc ttcaggggtca gagtccaagt acagatgagc240
ttgagaggga ttctgaaatg caacggccc 269
```

- (2) INFORMATION ON SEQ ID NO. 11:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 1717 base pairs

09873395.122700



(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

attctaggac caacactcct gtggagacgt gaaaagggtc caaaggcaaa cagtcctata 60  
cctacatcat tgaggagaaac actaccaacga gcttcacctg ggccttccag aggaccactt 120  
ttcatgaggc aagcaggaag tacaccaatg acgttgccaa gatctactcc atcaatgtca 180  
ccaatgttat gaatggcgtg gcctcctact gccttccctg tgccctagaa gcctctgatg 240  
tgggctcctc ctgcacctct tgtcctgctg gttactatat tgaccgagat tcaggaacct 300  
gccaactcctg cccccctaac acaattctga aagcccccca gccttatggg gtccaggcct 360  
gtgtgcccctg tgggtccagg accaagaaca acaagatcca ctctctgtgc tacaatgatc 420  
gcacctcttc acgcaacact ccaaccagga ctttcaacta caacttctcc gctttggcaa 480  
acaccgtcac tctttgctgga gggccaaagt tcaacttcaa aggggttgaat tacttccatc 540  
actttacctc cagtctctgt ggaaaccagg gttaggaaaa gtctgtgtgc accgacaatg 600  
tcaactgacct ccggattcct gaggggtgagt cagggtttctc caaatctatc acagcctacg 660  
tctgccaggc agtcatcatc cccccagagg tgacaggcta caaggccggg gtttccctac 720  
agcctgtcag ccttgcctgat cgacttattg ggggtgacaa agatattgact ctggatggaa 780  
tcacctcccc agctgaactt ttccacctgg agtccttggg aataccggac gtgatcttct 840  
tttataggtc caatgatgtg acccagtcct gcagttctgg gagatcaacc accatcccg 900  
tcagggtcag tccacagaaa actgtccctg gaagtttgct gctgccagga acgtgctcag 960  
atgggacctg tgatggctgc aacttccact tctgttggga gaggccggct gcttgcccg 1020  
tctgtctcagt ggctgactac catgctatcg tcacgacgtg tgttgcttgg atccagaaga 1080  
ctacttaactg ggggggagaa ccaagcttat gctctggtgg catttctctg cctgagcaga 1140  
gagtcacact ctgcaaaaac atagatttct ggctgaaaat gggcatctct gcaggcacct 1200  
gtactgcatc cctgctcacc gtcttgacct gctacttttg gaaaaagaa caaaaactag 1260  
agtacaagta ccccaagctg gtgatgaatg ctactctcaa ggactgtgac ctgccagcag 1320  
ctgacagctg cgccatcatg gaaggcgagg atgtagagga cgacctcaatc ttaccagca 1380  
agaagtcaact ctttgggaa atcaaatcat ttacctcaa gaggaactct gatggatttg 1440  
actcagtgcc gctgaagaca tctccaggag gccacagacat ggacctgtga gaggcactgc 1500  
ctgcctcacc tgccctccca ccttgcatag caacctttga agcctgcggc gatttgggtg 1560  
ccagcatcct gcaacaccca ctgctggaaa tctcttcatt gtggccttat cagatgtttg 1620  
aatttcagat ctttttttat agagtaccca aacctctct tctgcttgcc tcaaaacctgc 1680  
caaatatacc cacactttgt ttgtaaatta aaaaaaa 1717

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 12:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1419 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ggcagaggta ttacctgaaa acttaaaaga aggcctgaag gaattctcct ggagttcatt 60  
 accatgtaact aaaaaacagac cttttgattt toatttcagt atggaagagt ctcagttctct 120  
 caatgaacct agcccaaaagc agagtgaaga aataccagag gtccacttcag agcctgtcaa 180  
 aggaagctta aaccgtgttc agtcagcaca gtctataaat tcaacagaaa tgcctgccag 240  
 agaggactgt ttgaaaaaaag agtgccctca gaacctgttc tgtcagttca agaaaaaggt 300  
 gttctgtctga aaagaaagtgt gtctctttta gaacaggatg tgattgtaaa tgaagatgga 360  
 agaaataagc tgaaaaaaaca aggagaaact cccaatgaag tctgtatgtt ttcccttagct 420  
 tatggtgata ttccagaaga attaatcgat gtctcagatt tcgagtggtc tctctgcagt 480  
 aggttctctt ttgagccagt aacaacccct tgcggacatt cgttctgtaa gaattgtctt 540  
 gagcgttgtt tagatcatgc accatatgtt cctcttttga aagaaagcct aaaaagatgt 600  
 ctagcagata gagggtactg tgtcacacag ctgttggaag gaattaatag tgaagtatct 660  
 gcctgatgaa ctgtctgaga gaaaaaaaat atatgatgaa gaaactgtct aactctcaca 720  
 cttgaccaag aatgtttccaa tattttgttg cactatggcc tccccactgt tgccttgccc 780  
 tctccatgta tttagagcaa gatacagatt gatgattcga agaagtatat agactggaac 840  
 caaacagttt ggcattgttg tcagtgatac acaaaatagt ttbgcagatt atggttgtat 900  
 gttcacaatt agaaacgtgc atttcttacc ggacggaagg tctgtggttg atacagtggg 960  
 aggaagacgg tttaggtgtt taataagagg aatgaagat ggatattgca ctgccgacat1020  
 tgaatatctg gaagatgtta aggttgagaa tgaagatgat attaagaatc tcagagagct1080  
 tcatgatttg gtttactctc aagcctgcag ctggtttcag aatttaagag acagatttcg1140  
 aagccaaaat cctcagcatt tcggatcaat gccagagagg agggaaaaac ttcaagcagc1200  
 cctaatagga cctgcattgt gttgtgtggt tcttgcaagt ctccctgtag acccagcata1260  
 ccagctgtcg gttttgtcaa tgaagtcttt gaaagaaagg ttgaccaaga tcaagcata1320  
 actgacctat ttttctagag accaattcta agtaactaac tctttgggat cttccctttg1380  
 aaagttagac cctaattctt gggctgccat ttggttggg 1419

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 13:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 671 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

agcgcggtga agcgggggtg ggatctgaac atggcggcgg tggtagctgc tacggcgctg 60
aagggccggg gggcgagaaa tgcccgcgtc ctccggggga ttctgcgag agccacagct120
aacaaggctt ctcataacag gacccggggc ctgcaaaagg acagctcccc agagggcgaag180
gaggaacctg aacccctatc ccgcgagctg gaatacatc ccagaaaagg gggcaagaac240
cccatgaaag ctgtgggact ggccctgggc atcggtcttc cttgtggtat cctcctcttc300
atcctcacca agcgggaagt ggacaaggac cgtgtgaagc agatgaaggc tcggcgaaac360
atgcggtgtt ccaacacggg cgagtatgag agccagaggt tcagggtctc ctcccagagt420
gccccgtccc ctgatgttgg gtctgggggtg cagacctgag gagcgctgcg accctcctag480
gctattgact gttaaagtct caggcttggc ccagattcca gttcgtgcct ctgaggtcca540
ccagagggcg catgaagccc aggcgtgtgc caaacctac cctgccccac accaaggagc600
ccaccaaagg caaataaagt tattgagtgt ttagttagaa ggaaaaaaaaa aaaaaaaaaa660
aaaagtgcag c                                     671

```

## (2) INFORMATION ON SEQ ID NO. 14:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 524 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

09673795.122700

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

aagtgttttc agatgctgat gtttgaagc tccgggtggg gccatgagga agaagaggag 60
ctgaaggtaa gagactcata aacaagatga ctctttgatg catgaacaa atttgaaat120
ctcaagcctg taaagaatac cctgctatt taaataaagc tcataccaa aggtaacatt180
ttgccccggg ccaaattcag ggggtctagt cctgcattc ctttgaggca aaaaaataat240
gggctatgac tggttaaatg tccaaaaggc gaattctcat ttcattcaaa caaagacaga300
tttgcgcatc cactcaagca gaatgtggcc atgaatatc agccctgca tacatacaaa360
gatgtacgca tgattccccc caccaagcac acacacagtc acacacgcac acacacacac420
atgcacacac gcgcgtgcac acacggacac atgcacacac acacgcacac gtaaacacat480
gcacacatgc acacacgtgc acacatgcac acacggacac actt 524

```

(2) INFORMATION ON SEQ ID NO. 15:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

aaactttctt tctacaaaa atcaaaagct tagctgatag atcatgaaaa tagattatga 60
acagtgaatt tcttgagaag gctgaaagtg cggggaacca aagcagggga gattagccct120
agtcocggagg aggggagaagc agatggaagt caggagcctg ccttgtttt acgtgtaata180
tttaaatatt caaatgtgat tacaggaggg cctactttct gttttatca agagtttttc240
ttttgttcaa agacactggt tatgggaata ttttgaaagg gtaagaaacg ctgggtataaa300
aaggtgttgc agattaaatt tgaaggctct tacggaacca gtccc 345

```

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ggcgggtccca ggcaggccca gaagctgggc agcctctgcc ggggtccggg aaaagagact 60
cctgctgccca ctgctcttcc ggagcctgca gcatggggcc cctgcccgcc accgtggagc 120
tcttctatga cgtgctgtcc cctactcctt ggtgtgggctt cgagatcctg tgcgggtatc 180
agaatatctg gaacatcaac ctgcagtctg ggcacagcct cataacaggg atcatgaaag 240
acagtggaaa caagcctcca ggtctgtctc cccgcaagg actatacatg gcaaatgact 300
taagctctct gagacaccat ctccagatcc ccatccaact ccccaaggat ttcttgtctg 360
tgatgcttga aaaaggaagt ttgtctgcc tgcgtttcct caccgccgtg aacttggagc 420
atccagagat gctggagaaa gcgtcccggt agctgtggat gcgcgtctgg tcaaggaaatg 480
aagacatcac cyagccgcag agcatcctgg cggctgcaga gaaggctggt atgtctgcag 540
aacaagccca gggacttctg gaaaagatcg caacgccaaa ggtgaagaac cagctcaagg 600
agaccactga ggcagcctgc agatacggag cctttgggct gcccatcacc gtggcccatg 660
tggatggcca aaccacatg ttatttggct ctgaccgat ggagctgctg gcgcacctgc 720
tgggagagaa gtggatgggc cctatacctc cagccgtgaa tgccagactt taagattgcc 780
cggaggaagc aaactctctg tataaaaaaa cgaggccatc tgcttaacc ttggctccac 840
cataaggcac tgggactcgg attctctat ctgatagagg tattttctgt ggccttgagg 900
gctgtctgtc ttccctcac cccaaggat gccaggaaga cgtccacct tagccatgtg 960
gcaaccttta cttctatgcc tcacaagtgc ctttcagaga gccccaattc tgctttcccal020
caaaataaac ctaatgccat caggcaaaaa aaaaaaaaaa 1060

```

## (2) INFORMATION ON SEQ ID NO. 17:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1721 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09673395.122700

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

00673495.122700

```

ctctctctct  ttctgtctct  tctctgtctc  ctctctttct  ctctctctct  tgccttcccc  60
gtgctataaa  ttctgtctgc  tcccggaaact  tgttggcaat  gcctattttt  tggctttccc  120
ccgcgtcttc  taacttaact  atttaaaggt  ctgcggtcgc  aaatggtttg  actaaacgta  180
ggatgggact  taagtgaac  gccagatata  ttctactgat  cctcgcgggt  caaatagcgt  240
atctggtgca  gccggtgaga  gccgcgggca  agtgcgatgc  ggtcttcaag  ggcttttcgg  300
actgtttgct  caagctgggc  gacacatggc  caactacccg  caggcctgga  cgaacaagac  360
aacatcaaga  ccgtgtgcac  atactgggag  gatttccaca  gctgcacggt  cacagccctt  420
acggattgcc  aggaaggggc  gaaagataat  tgggataaac  tgagaaaaga  atccaaaaac  480
ctcaacatcc  aaggcagctt  attcgaactc  tgcggcagcg  gcaacggggc  ggccgggttc  540
ctgctccccc  cgttcccggt  gctcctgggt  tctcctcctg  cagcttttag  gacctggctt  600
tctctctgag  cgtggggcca  gctccccccc  cgcgcgccac  cacactcaat  ccaatgctcc  660

ggaaatcgag  aggaagatcc  attagttctt  tggggacggt  gtgattctct  gtgagtctga  720
aaacactcat  ataggattgt  gggaaatcct  gattctcttt  tttatttcgt  ttgatttctt  780
gtgttttatt  tgccaaatgt  taccaatcag  tgagcaagca  agcacagcca  aaatcggaac  840
tcagctttag  tccgtcttca  cacacaaata  agaaaaagcg  aaacccaccc  cattttttaa  900
ttttattatt  attaattttt  tttgttgcca  aaagaatctc  aggaacggcc  ctggggccac  960
tactatatta  atcatgctag  taacatgaaa  aatgatgggc  tcctcctaat  aggaaggcca  1020
ggagaggaga  agggcagggg  aatgaattca  agagagatgt  ccacggacga  aacatacgtt  1080
gaataattca  cgctcacgtc  gttcttcac  agtatcttgt  tttgatcatt  tccactgcac  1140
atttctctcc  aagaaaaagc  aaaggacaga  ctgttggcct  tgtgtttgga  ggataggagg  1200
gagagagggg  aggggctgag  gaaatctctg  gggtaagagt  aaaggcttcc  agaagacatg  1260
ctgctatggt  cactgagggg  ttacgtttat  ctgctgttgt  tgatgcaccc  gtccaagttc  1320
actgccttta  ttttccctcc  tccctcttgt  tttagctgtt  acacacacag  taataacctg  1380
atatcccaag  gtatagatca  caaggggggg  atgttaaatg  ttaattctaa  atatagctaa  1440
aaaaagattt  tgacataaaa  gagccttgat  tttaaaaaaa  aaagagagag  agatgtaatt  1500
taaaaaagtt  attataaatt  aaattcagca  aaaaaagatt  tgctacaaag  tatagagaag  1560
tataaaaaaa  aagttattgt  ttgaaaaaaa  agtgcgtttt  gtttccctac  ccaacctgct  1620
ttcttgacc  agttctcagg  gaacctgaag  ggacacagga  tgccggtgat  aagctcacct  1680
cttcagggaag  ccgtctcaag  cagacctgac  acctcaagc  a
1721

```

## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

accctgtggg cccgggtttc tgcagagtcct acctcagaag cggaggcact ggggactccg 60
tttgggattg ccaggctgtg gttgtgagtc tgagcttggt agcggctgtg gcgcctcaac 120
tcttcgccag catatcatcc cggcaggcga taaactacat tcagttgagc ctgcgaagact 180
gggaggaaact ggggtgataa gaaatctatt cactgtcaag gtttattgaa gtcaaaatgt 240
ccaaaaaaat cagtgggcgt tctgtggcag agatgcgaag agatgaaatg acacgaatca 300
tttgggaatt gtgtaaaag aactcatttt ttccctacgt ggaattggat ctacatagct 360
atgatttagg catagagaat cgtgatgcc aacacgacca agtcaccaag gatgctgcag 420
aagctataaa gaagcataat gttggcgctc aatgtgccac tatcactcct gatgagaaga 480
gggttgaggg gttcaaatgt aaacaaatgt ggaatcacc aaatggcacc atacgaataa 540
ttctgggtgg cagggtcttc agagaagcca ttatctgcaa aaatatcccc cggctgtgtga 600
gtggatgggt aaaaacctat atcataggtc gtcatgctta tggggatcaa tacagagcaa 660
ctgattttgt tgtctctggg cctggaaaag tagagataac ctacacacca atgacggaag 720
cccaaaaggt gacataacct gtacataact ttgaagaagg tgggtgtgtt gccatgggga 780
tgtataatca aqataaqtca attgaagatt ttgcacacag ttccctccaa atgqctctgt 840

```

```

ctaaggggtg gccctttgat ctgagcacca aaaaacatat tctgaagaaa tatgatgggc 900
gttttaaaag catctttccag gagatatatg acaagcagta caagctccag tttgaagctc 960
aaaaagatct gtatgagcat aggtctcatg acgacatggt gcgccaaagt atgaaaatcag1020
agggaggctt catctgggccc tgaaaaaact atgatgggtg cctgcagctg gactctgtgg1080
cccaagggtg tggctctctc ggcatgatga ccagcgtgct ggtttgtcca gatggcaag1140
cagtagaagc agaggtcgtcc cagcggactg taaccctgtc ctaccgcagt taccagaaa1200
gacaggagac gtccaccaat cccattgctt ccatttttgc ctggaccaga gggtagcc1260
acagagcaaa gotttgataa aataaagagc ttgccttctt tgcaaaatgt ttggaagaag1320
tctctattga gacaattgag gctggcttca tgaccaagga cttggctgtg tgcattaaag1380
gtttacccaa tgtgcaactg tctgactact tgaatacatt tgaattctatg tgagctaaag1440
gagaaaaact gaagatcaaa ctgactcagg ccaaacctta agttcatacc tgagctaaga1500
aggataattg tcttttggtg actagggtca cagggtttaca tttttctgtg ttacactcaa1560
ggataaaagg aaaaatcaatt ttgtaatttg tttagaagcc agagtttatc ttttctataa1620
ttttcacagg tttttcttat atatacagtt attgccacct ttgtgaacat ggcaaggga1680
ttttttacaa tttttttatt attttctagt accagcctag gaattcgggt atactcatt1740
tgtattcaat gtcaactttt ctcatgtttt aattataaat gaccaaaatc aagattgctc1800
aaaaagggtg atgataagtc cagtattgct ccttaaaaaa tgcataaagt agaaattcac1860
tgctttcccc tctgttccat gaccttgggc acaggggaag tctggtgtca tagataatcc1920
gttttggtag gttagagctg gcattaaact tgcacatgac ttggaacgaag tatgagtgc1980
actcaaatgt gttgaagata ctgcagtcac tttgttaaa accottgtctg acttttcca2040
tagactaaat actgttttag ccgcaggaga gttttggaat ccgaataaat actactcga2100
ggtttgtctt ctccattttt ctctttctcc tctgtgctgt gcctgaatat tatactactc2160
taaatagcat atttctacca agtgaataaa tgtaagctga atctttttt gactttctgtc2220
ggcctgtttt atttctttta tataaaatgt atttctcaga aacttgatatt aaacactatc2280
ttatcttttc ctgaactgtt gatcttaatt aaaattaaat gctaattacc attaaaaaaa2340
aaaaaaaaa aaaaaaaaaa aaaaaaa 2367

```

09673305.122700

## (2) INFORMATION ON SEQ ID NO. 19:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1321 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

0057305-13200

```

cctggaaaca agatccaaac ccaagtgacc ccgcccggaaa gtgacccagt cagggtttaaa 60
aattccaaaca aaccgacgtg aacaaataga ccgaccaacc aaatatacaa tccgtcaaaa 120
tacattcact tccactacga aaccccaaca aaggggtgtga atgcccccgc aggagagacg 180
gttttgggtt catcaagtgt gtggatcgtg atgttcgtat gttcttccac tcagtgaaa 240
ttctggatgg gaaccagctc catattgcag atgaagtaga gtttactgtg gttcctgata 300
tgctctctgc tcaaagaaat catgctatta ggattaaaaa acttcccaag gccacgggtt 360

catttoattc ccatttcagat caccgttttc tgggcacggt agaaaaagaa gccacttttt 420
ccaatcctaa aaccactagc ccaataaaag gcaaaagaaa ggaggctgag gatggcatta 480
ttgcttatga tgactgtggg gtgaaactga ctattgcctt tcaagccaaag gatgtggaag 540
gatctacttc tctccaaata ggagataaag ttgaatttag tattagtgaac aaacagaggg 600
ctggcacagca ggttgcaact tgtgtgcgac ttttaggtcg taattctaac tccaaagagg 660
tcttgggtta tgtggcaact ctgaaggata attttggatt tattgaaaaa gccaatcatg 720
ataaagaaat ctttttccat tacagtgaat tctctgggtg tgttgatagc ctggaacttg 780
gggacatggt cgagtatagc ttgtccaaag gcaaaaggcaa caaagtcaat gcagaaaaag 840
tgaaacaaac acactcagtg aatggcatta ctgaggaagc tgatccacc atttactctg 900
gcaaaagtaat tcgccccctg aggagtggtt atccaacaca gactgagtac caaggaatga 960
ttgagattgt ggaggagggc gatatgaaag gtgaggtcta tccatttggc atcggtggga 1020
tgcccaacaa aggggattgc ctgcagaaag gggagagcgt caagttccaa ttgtgttcc 1080
tgggccaaaa tgacaaact atggcttaca acatcacacc cctgcgcagg gccacagtg 1140
aatgtgtgaa agatcagttt gccttcatta actatgaagt aggagatagc aagaagctct 1200
tttccatgtg gaaagaagtt caggatggca ttgagctaca gccagagagt gagggtgagt 1260
tctcagtgat tcttaagagt tcaggcggac tggcagggtc aggcgcctgt agatgtttt 1320
g
1321

```



## (2) INFORMATION ON SEQ ID NO. 20:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 384 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ggtcgaatcc aaatcactca ttgtgaaagc tgagctcaca gccgaataag ccaccatgag 60  
 gctgtcagtg tgtctctcga tgggtctcgtc ggcctcttgc tgctaccagg cccatgctct120  
 tgctctgccca gctgttgcct ctgagatcac agtctcttcta ttcttaagtg acgctgagggt180  
 aaacctccaa gttgccaaac ttaatccacc tccagaagct cttgcagcca agttggaagt240  
 gaagcactgc accgatcaga tatcttttaa gaaacggctt ctcatcttgaa aaagtccctgg300  
 gtgggaatag tgaaaaaatg tgggtgtgtg acatgtaaaa atgctcaacc tgggtttcca360  
 aagtccttttc aacggcaacc tgat 384

## (2) INFORMATION ON SEQ ID NO. 21:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 367 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

00673305.122700

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gggcactggg  ggtccgggtc  ctcaccaaac  gattcatcgg  tgactatgaa  agaaatgcag  60
gtaatctcta  tactagacaa  gttcagatag  aagggtgaaac  cctggctctt  cagggtcaag120
acactccagg  tattcagggtc  catgagaaca  gcctgagctg  cagtgaacag  ctgaatagg180
gcattcgctg  ggcagatgct  gtggtgatcg  ttttctccat  cactgactac  aagagctatg240
aactcatcag  ccagctccac  cagcacgtgc  agcagctaca  ccttggggcac  cgggctgcct300
gtgggtgggc  gtggggccaac  aaaagtgacc  tgttgccat  caaacagggt  gaccctcagc360
ttggact

```

367

(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2621 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

gggcctttgc ccgcctttgc ggcgggctct acgttccctg tcttcgcctg cagctccggc 60
atggcttccta aaggcgagctc caaacagcag tctgaggagg accctgcctc gcaggatttc 120
agccgcaatc tctcggccaa gtccctccgcg ctctctcttcg gaaacgcggt catcgtgtct 180
gccatcccca tctggttata ctggcgaaata tggcatatgg atcttattca gtctgctgtc 240
ttgtatagtg tgatgacctc agtaagcaca tatctggtag cctttgcata caagaatgtg 300
aaatttgttc tcaagcacia agtagcacag aagaggaggag atgctgtttc caaagaatgtg 360
acctgaaaac ttctcgaagc tgataataga aagatgtctc ggaaggagaa agatgaaaga 420
atcttgttga agaagaatga agttgctgat tatgaagcta caacattttc catcttctat 480
aacaacactc tgttctcgtt cgtggctcatt gttgcttctc tcttcataat gaagaaattc 540
aaccctcacg tgaactacat attgtccata agtgcttcat caggactcat cgcctcctcg 600
tctactggct ccaaatagac catgtcagct tcaccccctg gctttgtgtc tatgggttgc 660
ctgtgtgata tgggaaaagta gcagggtggg cagggttggga gacacaagat gtttttatag 720
tctagagcct ttaaaaaacc cagcagaatg taattcagta ttgtttatt ggctgttttt 780
tgacagattg ttgaaattaa atgaattgaa agggaaaactc agagtactag gacgtttatt 840
aaaaaggaaaa aaatgtcttg caatgtgctg taatcacaag aggagaaaaa aacttgtttc 900
cttgatctgt cagagggtcac agtaacctgg gccagagctg tattatttat tatataatag 960
tagtaggaag ttaataactg gttctctgtg ttccaaagcac aatattacaa ctctttttga 1020
accgtaaaaa tcagaattgaa tctctctccc aggggagtga acagaagctt aatgttttca 1080
cactgtttgaa ttgtgtatct gaaataaacac aaaattaaaa acatgatttc tctaatcttc 1140
caactagagg aagagaaact tgtggaagg ttcttttttt ttcttttttt ttcttttttt 1200
aaggcgagcc aaggttgatga cctaaaaata gtgccacggc atatgagagt tgtcctacga 1260
gggttaaaaga cacactgttc cactgtatgg ctttggccctc gagtggccag ggaggtcaac 1320
ttgacctgc catgttgttt tgacttacta agacacagga atcattgttt tcttggacct 1380
gggtctcaca cctcggagga atgttaagta agagaaaaga cctcttctct gaatatgac 1440
atgtaaaaa ccaaaatgat ttttctgaac ttctgcaatt ctgagaactc tccaaggaa 1500
ttacagtgat tttagtgctt tgcagcattt ttocatgagg actttcatatc atttgactc 1560
ttagttcaca ggttcccatc gattgtgagc aagatattta tctcttttagc ccttggggat 1620
ccagctgaga gcaatctctt gcattttttt acccgtgtat gtacagatat catttttgt 1680
gtatgcatag acttgaaaaa gtttgggaag ctcttttagc atatcacgta aagagtatg 1740
aaatcacagg tctagcaggt tgtcattcac taatttctca caagcagcac cccaaggaa 1800
atatgtrctt aatctttact atccacttct aaatttaagt tgaatttcat acatgttat 1860
agttgttttc ttataaattt tataaaaaatt attcatcggt aggttaaact ccacttcat 1920
gctatcggtt gtgtttggctt ccatgcaaga acttggaaga aaaacaggca ggaatgcatt 1980
tgcaataatg cccagatcat cattttctgc aactgagaat tatatttcat cattgtctc 2040
aagaagtctg caatctttac ttttctttgg tgcattatta tctaggtgac atcacggat 2100
aatgtggagt gactagagaa gtcacatcac actgtaaggt acagttaagg taacacttt 2160
gaggttttat atttttaaaa aacttttctt gaactctcgg ccaacatggt gaaaccccg 2220
ctctactaaa aataccaaaa ttagccaggc gtgatgggtg gtgctgttaa tctcagctac 2280
ttggggaggt gaagcaggag aactgcctga acccaggagg cagaggttgc agtgagtga 2340
gatcgtgcta ctactgcctt ggtggcgaag ctgcagactcc actcaaaaa agaaaaaaaa 2400
aaacccaaaa agttttctct actgttgggt aaaaaaaaaa gccagacctt agtttgactg 2460
gtggcatgga atttgtgtat caaataaaat catttgctta ttgacaaac aaaaagtgtc 2520
cactatttgg gacgcaggtg gggccgtttt ttgaaaattg ggggggaaat ttgcccgtg 2580
gtggggaggg ctttgtgggg ggggaaaaat tqcccccctg g 2621

```

00673305.122700

## (2) INFORMATION ON SEQ ID NO. 23:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2019 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ctgtatccta attctttggt gaatgaacac attcttaaag agaagcaaa atttgaggaa 60  
 aagaggttca aattggacca ctccagtgtg agcaccaatg gccacaggtg gcagatatatt 120  
 caagatttgt tgggaactga ccaagataac ctgtattttg ccaatgtcaa tcttatgttg 180  
 gagtctactg tgcagaagaa gaaacaaact gaagcagaat cacatgcagc ccaactacag 240  
 attctctatg aattccctca ggttgcaaga agaataaga gagagcaact ggaacagatc 300  
 cagaaggagc taagtgtttt ggaagaggtt attaagagag tggagaagaa gagtggctta 360  
 tactctcttg tcagtggaga tagcacagtg cctcaatttg aagctctctc tccatcacac 420  
 agtagtatta ttgattccac agaatacagc caacctccag gtcttcagtg cagtctctac 480  
 acaaagaaac agccttggtt taatagcacg tttagcatca gacgaaaaag acttactgct 540  
 cattttgaag acttggagca gtgttacttt tctacaagga tgtctcgtat ctccagatgac 600  
 agtcgaactg caagccagtt ggaatgaatt caggaaatgct tgtccaagtt tactcgatat 660  
 aattcagtat gaccttttag cacattgtca tatgctagtgt atctctataa tggttccagt 720  
 atagtctcta gtattgaatt tgaccgggat ttgactactt ttgcgattgc tggagttaca 780  
 aagaagatta aagctatga atagacacat gtcatccagg atgcagtgga tattcattac 840  
 cctgagaatg aaatgcaccc caattcgaaa atcagctgta tcagttggag tagttaacct 900  
 aagaacctct tagctagcac tgattatgaa ggcactgtta ttttatggga tggattcaac 960  
 ggacagaggt caaaggctca tcaggagcat gagaagaggt gtgtgaggtg tgcatttaatl1020  
 ttgatggatc ctaaaactct ggcttcaggt tctgatgatg caaaagtga gctgtggtct1080  
 accaatctag acaatcagtg ggcaacgact gaggcaaaag ctaatgtgtg ctgtgttaaal140  
 ttccagccct ctccagatga ccattttggc ttccgctgtg cagatcactg tgtccaactcl200  
 tatgatcttc gtaacactaa acagccaatc atggattatca aaggacacccg taagcagctcl260  
 tcttatgcaa agttttgtgag tggtagggaa attgtctctg cctcaacaga cagtcagctcl320  
 aaactgtgga atgtaggggaa accatactgc ctacgtttcct tcaaggggtca tatcaatgaal380  
 aaaaactttg taggccttgc ttccaatgga gattatatag cttgtgggag tgaaaaataac1440  
 tctctctacc tgtactataa aggaactttc aagactttgc taacttttaa gtttgatacal500  
 gtcaaaaagt ttctcgacaa agaccgaaaa gaagatgata caaatgaatt tgttagtgtcl560  
 gttgtgctgga gggcaactac agatggggag tccaatgtgc tgattgtctg taacagtcagcl620  
 ggtacaatta aggtgctaga attggtatga aggggttaact caagtcataa tgtactttgat1680  
 gctgctgaaa tacactctgca gctgacaatg agagaagaaa cagaaaaatgt cagtgtgatcl740  
 ctctcccccac agtcatcatg ggttttggat ttgttttgaa tatttttttc tttttttctcl800  
 ttccctccct tatgactctt gggacattgg gaataccagc ccaactctcc accatcaatcl860  
 taactccatg gacattgtct ctcttgggtg ttgttatctaa tttttgtgat agggaaacaa1920  
 attcttttga ataaaaataa atacaaaaac aataaaaagt tattgagcca caaaaaaaaal980  
 aaaaaaaaaa aaaaaagaaa agaagggagg agggaaaagg 2019

09573395.1.22700

## (2) INFORMATION ON SEQ ID NO. 24:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

gtgggttgctg tgacaggcac tatttgaagt gctttatcat ggattaactc ttaatcctca 60
gctaccgttat aaagttaggac ataaccocat ctacactgag accttgcctcc 120
tctcccccac cattgaagat gttctttttt cataactata tactattcca ttgcattgaat 180
attctgtaatt ttatttaact cccatgggat tgataaattag gtccattata gatagaagtg 240
taattaacat tctctgtacat gtattttgct acctgtgtgg gtatttctgt aggatgaata 300
actagaaatt tattggatca ggtttcacat ttgcagtttt gaaaactact accaaaaaga 360
tttcaccaat ttacaactcc atcattagta agaatgcctg ttgacctata gtctgccaac 420
cctgaatcct taaaaatttt tggcaatctg gtaggcaaaa ttctcttttt ttctttgaa 480
attaatgagg aggaacatct ttccatgttt cttggccatt tgcatttctt attatgaatt 540
gcttttggcc attttccttt tttaattat gaaagtctaa tgactacctt ctcatgttat 600
aaaaaacaca gttctttgaa tagagagacc cttttctcca atgctaccaa tcacattcca 660
cttaccacag tttaacatac atcctctagt cacttttccg tacgaatata catcacata 720
aaaaaccttt ttacataaac aggatctcat attctgtagc tttttaaaaa ttgtgtctca 780
aaaaaagata acaggtcttt aaatttcttt aatggttgaa tatgattaaa tactatgaaa 840
atgccattat ttattccctt aaattttttt ctctcgctat tacattgccca aagtaaacat 900
cctattcaga tgtcttttgg catgtgtgtg aatattttct tagtctggag tccagtaagg 960
tggatttttg gatcaaaagg ttgtttctct gtccaccttc agtcttccca aaggccctca 1020
taactgtatt ttacaccaag gtatggagaa ttgttcattc cccatataac cataccacal 1080
cttgatagtc ttattctgtt gggcgaaaaa gaaccttttc ttattttgca ttccctctgat 1140
tataaaaaaa aatggttgaga ttggggttat ttccatgttt attggccatt tatatttacl 1200
tttggtattg ttgtatccct taacctgttt ctattggggt atgtgtggat atattgtttt 1260
tatttgctca gcatctccct ccccatcttc tggtaacaca accttttatt atttggggg 1320
aacctactcc ctgtggctta ggtgagcatg tgaccaggcc tggcctctgt agtccacag 1380
cttcttagcc acagtgtata aagaatgggt atataactta agccaggcta aggaagccc 1440
ttaacagaac ttctgtctga actactggaa agaaggtctt atggagatcc caggaaacaa 1500
ggaccatgta agcctgaatt tgtgcatgtg ggagagagtc tgtctgagga gaaactcgga 1560
ctgtagcaga aatggaaaga gaactaagtt ctgatgtcat ttttctggag gccctagatc 1620
cagctgtgco taaagcctgc cctacctccg gactttaaag ttttctgagc caataaagtc 1680
cctttcttgt ttaagataat tgaattgagt ttctgtttctg attaatatag gttatttgtal 1740
ttttcttatt gatttgtaga aaacctttgt aatttttaaa tctagacctt atgcactata 1800
taagttaata aaatttagcat ggctttccat gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1866
aaaaaa

```

00573305.122700

## (2) INFORMATION ON SEQ ID NO. 25:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1189 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ctagcaagca ggtaaacgag ctttgtacaa acacacacag accaacacat ccgggggatgg 60  
 ctgtgtgttg ctagagcaga ggctgattaa acactcagtg tgttggtctt ctgtgccact 120  
 cctggaaaat aatgaattgg gtaaggaaaca gtttaataaga aaatgtgcct tgctaaactgt 180  
 gcacattaca acaaaagagct ggcagctcctt gaaggaaaag ggctttgtgcc gctgccgttc 240  
 aaacttgtca gtcaactcat gccagcagcc tcagcggtctg cctccccagc acacccctcat 300  
 tacatgtgtc tgtctggcct gatctgtgca tctgctcgga gacgtcctg acaagtgggg 360  
 aatttctcta tttctccact ggtgcaaaaga gcggatttct cctgtctctt cttctgtcac 420  
 ccccgctcct ctcccccagg aggcctccttg atttatggta gctttggact tgcttccccg 480  
 tctgactgtc cttgacttct agaattggaag aagctgagct ggtgaaggga agactccagg 540  
 ccatacacaga taaaagaaaa atacagggaag aaatctcaca gaagcgtctg aaaatagagg 600  
 aaagcaaaact aaagcaccag catttgaaga aaaaggcctt gagggagaaa tggcttctag 660  
 atggaaatcag cagcgggaaaa gaacagggaag agatgaagaa gcaaaatcaa caagaccagc 720  
 accagatcca ggttctagaa caaagtatcc tcaggcttga gaaagagatc caagatcttg 780  
 aaaaagctga actgcaaatc tcaacgaagg aagaggcca: tttaaagaaa ctaaatgtcaa 840  
 ttgagcggagc aacagaagac attataagat ctgtgaaagt ggaagagagaa gaaagagcag 900  
 aagagtcaat tgaggacatc tatgtcaata tccctgacct tccaaagtcc tacataacct 960  
 ctagggttaa ggaaggagata aatgaggaaa aagaagatga tgacacaaat aggaaaagctt1020  
 tatatgccat ggaaattaaa gttgaaaaag acttgaggac tggagaaaagt acagttctgt1080  
 cttcaatacc tctgccatca gatgacttta aaaggtccag gagtaaaagt ttatgatgat1140  
 ggggcaaaagt ccagtgtatt cagtaaaagt ctaatcacia gttggagg 1189

## (2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1418 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

09573395.122700

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

gagctcgag ctcgcgcggc gccctggctccc agcgcgcgcg gcgcgcgcgc cccgggccaa 60  
ccatggcgct ctcgcgcggc ggctgcgctgg tgatcgctgg cagtgaggctc attggggcga 120  
gtggggccatg ctgttttgcca gtggaggcctt ccaggtgaaa ctctatgaca ttgagcaaca 180  
gcagataagg aacgcgcctgg aaaacatcag aaaggagatg aagttgctgg agcaggcagg 240  
ttctctgaaa ggctccctga gtgtggaaga gcagctgtca ctcatcagtg gttgtcccaa 300  
tatccaaaga gcagtagagg gtgccatgca cattcaggaa tgtgtccag aagatctaga 360  
actgaagaag aagatttttg ctcatgttag ttccatcatt gatgatcgag tgatcttaag 420  
cagttccact tctgtctcca tgcccttccaa gttgtttgct ggcttggtcc atgtgaagca 480  
atgcctcgtg gctcctcctg tgaatccgcc atactacatc ccgctgggtg agctgggtccc 540  
ccaccgcggg acggccccccta cgacagtggg cagaacccac gccctgatga agaagattgg 600  
acagtgcctc atgcgagctcc agaaggaggt ggccggcttc gttctgaacc gccctgaata 660  
tgcaatcctc agcgaggcctt ggccggctagt ggagggaagg atcgtgtctc ctagtgcctt 720  
ggacccctgtc atgtcagaag ggttggggcat gcggtatgca ttcattggac ccctggaaac 780  
catgcctctc aatgcagaag gtatgttaag ctactgcgac agatacacg agggcataaa 840  
acatgtccta cagacttttg gaccattccc agagttttcc agggccactg ctgagaaggt 900  
taaccaggac atgtgcctga aggtccctga tgaccgggag cacttaagctg ccaggaggca 960  
gtggaggggc gagtgcctca tgagactcgc caagtgaag agtcaagtgc agccccagtg 1020  
aatttcttgt aatgcagctt ccactcctct cattggaggc cctatttggtg aacactgcaa 1080  
gcccttaatc agccctctgt gacataggtg gcagccacg gagatcccaa gctggctgtc 1140  
ttgtgtgcag cctgagtggtg gtgtgtgcagg ccggtagctt gcccgctcact ttggatcata 1200  
gccctggggc tggcgggcaca gcagcaacttg cgttctcggg gctgtcgatt tcttgcaccc 1260  
tgggcagata acctggagat ttccaccttt tctttttcag cttgattgca tttgagtatg 1320  
atttcacagg cagtgattgt agttttcact ttaaatatgt ggcaaaaata ttttgaattt 1380  
atttttgtaa tccctttctg agtaactctg gggctcctt 1418

(2) INFORMATION ON SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 814 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

09673395.122700

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

gcagcaacgg ggtgcggcag ggtggggaac gcgggagggg gccagctccc aggaaagctg 60  
gtctgcgagc ggcccttgcc cggctcccaag gtccctgcgc gaccccgccc ttcccagagc120

cccagccggg ctgcccggcg cgtcccggaa gctccagcct gaaccatgtt ttccacttgt180  
ggcccaaatg aggccatggt ggtctccggg ttctgcogaa gcccoccagt catggtggct240  
ggaggggcgtg tctttgtcct gccctgcctc caacagatcc agaggatctc tctcaacaca300  
ctgaccctca atgtcaagag tgaagaagtt tacactcgcc atggggctcc catctcagtc360  
actggcattg cccaggtgaa gctttcagag ccttttcccc acagtccact tccccatcac420  
cctctctccc agacattaa acatcttctg gccacagtct tctcaaccct tgcctgcaga480  
gaagtctctc tgctagtctc atcttttcca ggcaccccaa ggcacttgcc tctctctcct540  
ttctttccct gaaatgggaag aagcatttct gagagggtct tcccttctct cctctgtttt600  
cctctgactt catgagaccc ccaccacacc ttctctacc ctaactctggc tacaggtaaa660  
aatccagggg cagaacaagg agatgtttgc ggcgcctctg cagatgttgc tggggaagac720  
ggaggctgag attgccaca ttgccctgga gacgttagag ggccaccaga gggccatcat780  
ggccacatg acttctggga ggggtgggct taga 814

## (2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 3039 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

0057305-102700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

gaactgagat attgtaataca aataggttaac atcaggaagt taattttgctt ggcaaaattc 60
tagggaaact tggccagaaa actggtgttg aaggcttttg ctcatataaa caagtgccat 120
tgagtttcaa atgaccagca aataatatta gaacccttcc tgttttatgt ctgtacctcg 180
tccacccttc aggttaatacc tgccctccac aggtacagct gtttctttga aatcctccaa 240
ccaaaatgca gtttctctaa ctgtattagc ttgagctgac agactgttag atatacaggtt 300
tctggccaca gctgtagagg gctttctgtc ctgcacacag attgtgtact gcaccccaag 360
ccaggtgact gttaccocat cgagttgtgc cgtgcacaa cctgtccagta tatgcattgt 420
tgggccctac tgactggtaa tgggttagag cacttatgga ttttaagctt tagggaaaaa 480
ccatgacctt taacaaattt ttatgggtta tatgcctaaa cctttatgcc acatagtggg 540
aaataaatat gaaaaatggt ctgttcaata ttggtaggtg ccttttttga gcagggaaga 600
taattatttg tttattatgg taattatggg gattttttaa atatcatgta atgttaaaac 660
gttttctaac agtttactgt tgcttacttc caagatatta tgggaattaag aatttttcca 720
gatgagtgtt acatagattc ttggaattta gtataaaagt actgagaatt aagtttgtac 780
ttcataagc ttggatttta aacactgata gtatctcatg agtaagtgtt gttttgggag 840
agggagggat gctgattgat atttccacatt gtaagaaata ccatgtttga aactcatagc 900
aataatgcta tgctgtttgt atccctctca agtcttgcac ttaaaatata ttttttcttt 960
ataggaattg atgtatacca tgaagtcatt tgcagtttga gtatgcttga ttttgaatgal 1020
gatatacagt tttagcattc cattttactg actagggtag aagaacattt tcttgcctal 1080
catttgaggg ataccagggg agtcttgggt gttccttatac tggggaagca aacatttccal 1140

tagtctcttt ttttcatctt ttaaattgta aattaaggat tactcaagct caccattatt 1200
caagatgtgg actgctctcc cagtgcacac tctgccctgc ctgtcattgc tgcacaaagc 1260
tgctgtcttt ccaaccttaag caaagaaaaa acggtctctc ttgcatttgc tctccctttg 1320
gttggtttgt tttctagaagc tacgttcaag tgctttgggg aatgcaatgt atgattttgt 1380
agctctctca ccatcttaact cactgtgagg ataaatatgc atgtcttttg taattaaact 1440
tgcttttgaa aatctttttt aaggggagaaa aatctcaaac aaagtattgc tcatccagac 1500
aagctgacct ttgagttaat ttcagcaaaa ctcatcttcc agtgccctat gactgaaaaa 1560
aaaaaaacaa aaaacgaagc catcttcaca gatgaagctc cagatagcac cgttttgtal 1620
aaagatacat tctcattgtt tcccaacagt gatggcttcc acataaggtt aaaaaactal 1680
ggtgtcttta aataatttat tacagtttac tctatgcatt tctgttaaca tgaatgtcat 1740
ggccttcttc aggggaagac tgtgttcaag ttaaaaaaaa aaaaacaat taacacaaact 1800
gaactgcag tctgtttttt aaaaatgagaa tgtcctaagt gattcagaag agagggggal 1860
agttgtgac tctgaaaaat catgaaaaaa aaggccaata actagtggga aatgtgtaga 1920
actgttaact gagacggctt cgagtcttcc tcttggaatc tgttaaatc taataagtc 1980
tgagggtaaa tgggagaaaa atttctggga ttacaatgaa tgaatgcccc aattgtggaa 2040
ttgccagtaa cctggatggg gaaaaacatt tcccatagca ctccatgtaa tatgagtgtc 2100
ctgtgagatg ttcatcagtg ttttatagaa atggtgttgc tgggaaacca agtttgcacc 2160
tggaaaacta caatgcactt tagcgagta agggcttggc atccggttag tatgaaactg 2220
ctaacccagc attgcccacaa ctattttgac accaggacct ttttctctt tgggatactt 2280
atgaaactct cactaatgct ctgtggagaa cattttggga aacactatgt tagatagttc 2340
tttaagcaga caaaacggtt atgaacagat agcaactggg cagaatatgc atgcaatttg 2400
taacgtccag tgtggcgttg aatagatgtg tatttctccc cctgcagaaa atagcacag 2460
aaaattataa tgtaggtgat cggagctctt tcttttgata gagagaacag cccaactgat 2520
cctggctttt tcaactgaacg tatcagaata ctggatgaa ttggggttaa ataggtttt 2580
attcagatct agaagaaaag attgtacgtt tgaatgcaag ttttatccca caagatttat 2640
tagtgtttat acatgacagc acctatcgtt gaggtttcta agacttacta tgggctgtaa 2700
acctgttttt taataactatt ttgagaaacct gagacttgcc gtctggcatt ttagtttaat 2760
acaaactaat gatgcattt gaaagagatt ctgacactta tttctaaaag ctatagagct 2820
tgaaaatctt tgaatgagct tatataaact ttatgcctgt ttacaaaaga atgttaagac 2880
tcgtgaaaag aattactata aggtactgtg aataaactgc gattttgtga gcaaaacata 2940
cttggaaatg ctgattgatt tttatgcctt ttatgttat gcaagaaaca cagaaaaatg 3000
agttttgttt taataaacca aaaaattgaa ataaaaaac

```

3039

## (2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1448 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

09673395.122700

```

taccgaatctg aagggggaag cggcgccggc atcgccctccc ggcgctccct ccccgactcc 60
taagtccttc ggccgcgaac atgtccgcct cggctgtctt cattctggac gtaagggca 120
agccattgat cagccgcaac tacaagggcg atgtggccat gagcaagatt gagcacttca 180
tgcctttgct ggtacacggg gaggaggaa ggcgcctggc ccgcctgctg agccacggcc 240
aggctccact cctatggatc aaacacagca acctctactt ggtggccacc acatcgaaga 300
atgccaatgc ctccctcggt tactcctccc tgtataagac aatagaggta ttctgcgaat 360
acttcaagga gctggaggag gagagcatcc gggacaactt tgtcatcgtc tacgagttgc 420
tggacgagct catggacttt ggcttccccc agaccaccga cagcaagatc ctgcaggagt 480
acatcactca gcagagcaac aagctggaga cgggcaagtc acgggtgccca cccactgtca 540
ccaacgctgt gtcttggcgc tcgcagggtta tcaagtataa gaagaacagag gtcttcatatg 600
atgtcataga gtctgtcaac ctgctgttca atgccaacgg cagcgtctct ctgagcgaaa 660
tcgtcggtac caacaagctc aagggtgtttc tgtcaggaaat gccagagctg cggctgggcc 720
tcaatgaccg cgtgctcttc gagctcaact gccgcagcaa gaacaaatca gttagctggc 780
aggatgtaaa attccaccag tgcgtgcggc tctctcgctt tgacaacagc cgcaccatct 840
ccttcacccc gcttgatggt gactttgagc tcatgtcata ccgcctcagc acccagggtca 900
agccactgat ctggattgag tctgtcattg agaagttctc ccacagccgc gttggagatca 960
tggtcaaggc caaggggcag tttaaagaac agtcagtggt caacggtgtg gagtatctctg 1020
tgctgttacc cagcgatgcc gactcccccga gattcaagac cagtgtgggc aggcaccaagt 1080
atgtgcggga gagaacagct gtgatttggg gtattaaagt tttccggggc ggcaggaggt 1140
acttgatgag agcccacttt ggcttcccca gtgtggaaaa ggaagaggtg gagggccggc 1200
cccccatcgg ggtcaagttt gagatccctt acttcaccgt ctctgggagc caggtccgat 1260
acatgaagat cattgagaaa agtggtttac agggccctgc cttgggggtt cgtacattc 1320
accagagatg ggcgattacc aactttcgtt accagctagg aaggggagaa gagatggggg 1380
ggttttaaca cgggggtttgc ttacagccc cggatgcaga tttttagaag ggagggcagg 1440
tgccgggtt
1448

```

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1394 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

atgaatacaa ggctgcaagt ggaacatcct gttactgaga tgatcacagg aactgacttg 60  
 gtggagtggc agcttagaat tgcagcagga gagaagattc ctttgagcca ggaagaaata 120  
 actctgcagg gccatgcctt cgaagctaga atatatgcag aagatcctag caataacttc 180  
 atgcctgtgg cagggccatt agtgcacctc ttactctctc gagcagacc ttccaccagg 240  
 attgaaactg gagtacggca aggagacgaa gtttccgtgc attatgacc catgatggcg 300  
  
 aagtgggtcg tgtgggcagc agatcgccag gcggcattga caaaactgag gtacagcctt 360  
 cgtcagatca atattgttgg actgcccacc aacattgact tcttactcaa cctgtctggc 420  
 caccagagat ttgaagctgg gaactgtcac actgatttca tccctcaaca ccacaacacg 480  
 ttgttgctca gtccgaaggc tgcagccaaa gagtctttat gccaggcagc cctgggtctc 540  
 atcctcaagg agaaaagcat gaccgacact ttactctctc aggcacatga tcaattctct 600  
 ccattttcgt ctgacagtgg aagaagactg aatatctcgt ataccagaaa catgactctt 660  
 aaagatggta aaaacaatgt agccatagct gtaacgtata accatgatgg gctcttatagc 720  
 atgcagattg aagataaaac ttccaagtgc cttggtaatc ttacagcga gggagactgc 780  
 acttacctga aatgttctgt taatggagtt gctagtaaa ggaagtgtat atcctggaaa 840  
 acactattta cctattttcc aaggaaggaa gtatttgat tgacattcca gtccccaata 900  
 acttatcttc tgtgagctca caagaaactc agggcgcccc cttagctcct atgactggaa 960  
 ccattgaaaa ggtgtttgtc aaagctggag acaaaagtga agcgggagat tccctcatgg 1020  
 ttatgatcgc catgaagatg gagcatacca taaagtctcc aaaggatggc acagtaaaag 1080  
 aagtgttctc cagagaaggt gctcaggcca acagacacac tcccttagtc gagtttgagg 1140  
 aggaagaatc agacaaaagg gaatcggaat aaactccagc aaggaatagg ccagttaagt 1200  
 agtgtctctt ctctccaccca aaaagaggaa gtgcctccag cttttctggg ggtctcataa 1260  
 agagcagttt tactaaatga ttgtatgct atgtctgaac cctttcatat tggagaatca 1320  
 tgcaattggg tcaactaatc tctcaaaata tttcatacta ataaagttag attatttttt 1380  
 attggaagcc aaaa  
 1394

0967305.122700

## (2) INFORMATION ON SEQ ID NO. 31:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 734 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

gcgcacaaga tgtctcttgc gccctcttcg gctgcggggc gagtagtcgt ccgacgtctg 60  
 gccgtgagac gtttcgggag ccggagtcct tccaccgcag acatgacgaa gggccttggtt120  
 ttaggaaatc attccaaaaga aaaagaagat gatgtgccac agttcacaaq tgcaggagagi80  
 aattttgata aattgttagc tggaaaagctg agagagactt tgaacatatt tggaccacct240  
 ctgaaggcag ggaagactcg aaccttttat ggtctgcata aggacttccc cagcgtgggtg300  
 ctagttagcc tcggcaaaaaa ggcagctgga atcgacgaac aggaaaaactg gcattgaaggc360  
 aaagaaaaaca tcagagctgc tgttcgacgc ggtgcaggc agattcaaga cctggagctc420  
 tcgtctgtgg aggtggatcc ctgtggagac gctcaggctg ctgcggaggg agcgggtgctt480  
 ggtctctatg aatacgtatg cctaaaagcaa aaaaagaaga tggctgtgtc ggcaaaagctc540  
 tatggaaagt gggatcagga ggcctggcag aaaggagctc tgtttgcttc tgggcaagaa600  
 cttgggcacg ccaatttgcg gggagacgcc agccaattga gattgacgcc aaccagattt660  
 tgccgaattt atttgagaag attttcaaaa ttgtagtcta gttaaaaccg aggtcctttt720  
 cagaccccaa tttt

734

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 692 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

00673395.122700

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

tgcagcgcgt gcgtgctgcg ctactgagca ggcgcattga ggactctgaa gcactgggct 60  
tcgaacacat gggcctcgat ccccggtccc ttacggctgt caccgatctg ggctggctcgc120  
gacctacgct gatccaggag aaggccatcc cactggccct agaagggaag gacctcctgg180  
ctcgggcccc caccggctcc gggaagacgg ccgcttatgc tattccgatg ctgcagctgt240  
tgctccatag gaaggcgaca ggtccgggtg tagaacaggc agtgagaggc cttgtctcttg300  
ttcctaccaa ggagctggca cggcaagcac agtccatgat tcagcagctg gctacctact360  
gtgctcggga tgcctcagtg gccaatgtct cagctgctga agactcagtc tctcagagag420  
ctgtgctgat ggagaagcca gatgtggtag tagggacccc atctcgcata ttaagccact480  
tgcagcaaga cagcctgaaa cttcgtgact ccctggagct tttggtggtg gacgaagctg540  
acctctcttt ttcctcttgg ctttgaagaa gagctcaaga agtctctctc tggctcacttt600  
gcccccggt ttttaacaagg ctttctctcat gtcagctact ttttaacgagg acgtacaagc660  
actcaaggag ctgatattac ataagccggt at 692

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 571 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ctgccacgca cgactgaaca cagacagcag ccgcctcgcc atgaagctgc tgatggctct 60  
catgctggcg gccctcctcc tgcactgcta tgcagattct ggctgcaaac tcttggaggal20  
catgggtgaa aagaccatca attccgacat atctatacct gaatacaaaag agcttcttca180  
agagtccata gacagtgaat ccgctgcaga ggctatgggg aaattcaaacg agtgtttctc240  
caaccagtca catagaactc tgaaaaactt tggactgatg atgcatacac tgtacgacag300  
catttgggtg aatatgaaga gtaattaaact ttacccaagg cggttggctc agagggctac360  
agactatgac cagaactcat ctggtgatgt ctagaaacca cttttctttc ttgtgtgtgc420  
tttttatgtg gaaactgcta gacaactgtt gaaacctcaa attcatttcc atttcaataa480  
actaaactgca aatcacaaaa aaaaaaaaaa gtcgacg 517

09673305.122700

## (2) INFORMATION ON SEQ ID NO. 34:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 322 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

tcaagctgtg ggtgagaagc tctctagcag ggactctgac cttatggagg atcgctgttt 60  
 cccccatttt tcccttttcac ccaaaaaaagt cctgcttctg tcaccttca aacagcctgtl20  
 gagcctaaat ttttgtggcc atgggacaga caaggacccc gtcttcagct gaactaaggal80  
 aaagtccctgc gacatctttg gccatcaaac tccaacccag tcacccaacc agagcctctg240  
 aggaatggcc ccttcttgcg gggaaaccctt tacaatgggc ctcttgactg atgtttcccc300  
 aaaacagctgc cctgttcacg ag 322

## (2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1559 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

0067306-12700

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gcacgagtggt agagtgcagt tgtgtgtgtg cgtgtgcacg tgcacacatg tgcacggttg 60  
 tatgtatggg aataaaactt ataaatgggg acgtattgga gaaggaaata catagacctt 120  
 caactttgag caaatagcag tgatgtttta ggaactgaaa tgtcacactt aaagcttcta 180  
 gccacgctac tccctattt ttggcgggga gaagagggcc tgattagaac tgtctgtggt 240  
 gtgtttggcg ggaggggaat aattttttgt cagtcctctt tagtgaccaa accttaattt 300  
 ttaagaataa tatattgact tactgaactg aagcattctg agttgaaagg agctccagag 360  
 gagtggagtt ctgtgttgct cacatgttaa aagcttgctc acctccagag cagaggggaat 420  
 acctatcttc agatatccgc ccattttcat ctcttcatta tagtcaaaac gtgtgacttg 480  
 agagtgttgc tctgtgtgtt gtatttttgc ttatgaagat tatttgaaaa agaactctta 540  
 ctacattgaa atgcagactt ttaaaaaattt aaatattgga ttaggcagtc aaaaaaccaa 600  
 acaagcataa aaggtcaata agttgtaact ttaaaagtaa aggtggaata ctattataa 660  
 atgggaagaaa agtttttgat tccctttttt tttgatggcg agtatgccat attatccca 720  
 aagttctttt aaaaaactt tccatcaacc atttttattt aaaaataaca tttgagggaa 780  
 gttaccgaag cagctttttt cctcaaaagt aacctgttcc tctttggaat agcacattt 840  
 aggggcagtg ttaataacctg agattttttac tcagttaaat ctgattggta ctgtgtgtaa 900  
 aatatcttta agtaggattg aaggcctctg tgggggaata aaatattacc aaagtctata 960  
 aaaaataatt ttacatgttc tcttttatga cagagagcag cactggttct gttattttta 1020  
 aaatgaatca ttgatttctt gatagggtgt taatatcttc tccctcactg ctgattctta 1080  
 gatagaacc attctttata ttgatagac tgccttcaga aaacccttat caacaagtg 1140  
 acaatactta tctaaaacta tacatttaga atggagcagt ttaatactag atctcagaag 1200  
 ttttgaaaaa tagcaagaaa gactggattt ggaaagcagt gtctcaaat gggtgttaaa 1260  
 tctgaagct atgaagataa aatgtttcaa ctttgatta tgaaccacca tttatgatt 1320  
 ttttaataca cttgaataaa aaatgattaa actaaatttt ggtccagtg cattactttg 1380  
 cactgcataa tccattatag gttgtacgac tttttttttt ggtttgaatt aataactgag 1440  
 agttttgtgt gaagctacgg catattcaac cggagaattt cggatgcctt atacggtgat 1500  
 tatattatat gggggcattt gtatgtcagc ggaagacgga atttatgcct ttgggaaac 1559

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

09673395.122700

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

cacacgtgct gacggcgggg acattcacat ccataagaag aaatctcagc aagtgttcgc 60  
 gtccccccagt aaacacccca tggacagcaa gggggaggag tccaagatca gctaccccaa 120  
 catcttcttc atgattgaca gcttcgagga ggtgttcagc gacatgaccg taggggaagga 180  
 gagatgggtct gtgtggagct ggtggctagt gacaaaacca acacgttcca ggggggtcatc 240  
 tttcagggtct ccattccgcta cgaggcgctc aagaagggtgt atgacaaccg ggtgagcgctg 300  
 gccgcccgca tggcacagaa gatgtcgttt ggcttctaca agtacagcaa catggagtatt 360  
 gtgcgcatga agggccccc gggcaaggcg cagcccgaga tggcggtcag ccgagtgtct 420  
 acaggtgaca cagccccctg tgggactgaa gaggactcca gccagcttc gcccatgcac 480  
 gagcgggtga cctccttcag cagaccccc accccagaac ggaacaaccg gcctgccttc 540  
 ttctccccat ccctcaagag gaagggtccc cggaaccgga tcgctgagat gaagaagtgc 600  
 cactcggcca acgacagcga ggaattcttc cgggaggacg acgggtgagc cgaactgcac 660  
 aatgcaacca acctcgcgct tcggtccctg tcgggcacag gacggtccct ggtcgggtcc 720  
 ttgctgaagc tgaacagagc agatggaaac ttcttctct atgcacactt aacctacgct 780  
 acgttgcgcg tgcattcgat ttaacagac atcctggaa gtcggcagaa gcccatcctg 840  
 atgacctagc cgcgtgcgga gcctgcgca gaccccgccc gggcccgccc ctcggaagtgc 900  
 ttgccaagtgc ctacctgtcc accgccaccg gggtctcgga tggcacgcca gtgttggagc 960  
 cgcagccagc cgaggccaact cgactgcggg ggcggggccc gactgcacga acaccagccc1020  
 aaactgaagt gcctctgacg ggccctgctg gcgctgcttc cgcctgtgctc cc 1072

## (2) INFORMATION ON SEQ ID NO. 37:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 454 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
 (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

gtgctgcatg gagtgaagtgg cggcatccac cgtgaggagg agaggagctc tgataccctc 60  
 aggaccggcc aggaggggca tcacggaggc ttctggagca cttggagctg tgccttgggg120  
 agaaaaccgc tctgtgtgtg gccctgagtg ctgaggagga agctgccatg cacttttccc180  
 ttggcattttt cctgcattgt tcgtctgttt ttttgcataa aacatgttgt catgaatttt240  
 tatgcattgag gcatatttca tcaatgtctgt atgctgaagt ccccttcac ctttcaattg300  
 gtttggtggag aggagagaga ggtccaaggt gccctacatc gtgcgccagt gccgtgggag360  
 gagatcgagc gccgaggcac ggaggagggt ggcatctacc gcattgtctg ggtggccgca420  
 gacatccagc cactgaaggc agccttcaac gtca 454

09673305-122700



## (2) INFORMATION ON SEQ ID NO. 38:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 700 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

cttctcggag ccctaaccag gggtaacctt gagcctgggt ggatccccgg agcgtcacat 60  
 cactttccga tcacttcaaaa gtggttaaaa actaatattt atatgacaga agaaaaagat120  
 gtcattccgt aaagtaaaaa tcatcatctt ggtcctgggt gttgctctct tcttactcgt180  
 tttgcacctt aacttctctca gcttgagcag tttgttaaag aatgaggtta cagattcagg240  
 aattgtaggg cctcaacctta tagactttgt cccaatgtct ctccgacatg cagttagatg300  
 gagacaagag gagattcctg tggctcatgc tgcattctgaa gacaggcttg ggggggccat360  
 tgcagctata aacagcattc agcacaacac tcgctccaat gtgattttct acattgttac420  
 tctcaacaat acagcagacc atctccggtc ctggctcaac agtgattccc tgaaaagcat480  
 cagatacaaa attgtcaatt ttgaccttaa acttttggaa ggaaaagtaa agggagatcc540  
 tgaccagggg gaatccatga aacctttaac ctttgcaagg ttctacttgc caattctcgg600  
 ttcccagcgg caaagggaag cccgtttaca tggggttgat gatgttattt gtggcagggt660  
 ggattttttg ccctttacat tacagcagtg aggcgggggc 700

## (2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 914 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

00673505 122700

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ccggccctgcg gtgggcagca gctcagggtc tccaaatcat tgcgtagtgc cgaataccct 60  
cgggccacacc tggccttctc catgctcggg ataacttccg gcagcgacca acaggctaaal20  
gaggggggaag ggatccagca ccggctcctc ctccgggaac caggggggga gcggcggagg180  
aaatggacat aaaccgggt gtgaaaagcc agggaatgaa gccgcggga gcgggaaatc240  
tgggattcag ggcttcagag gacagggagt tccagcaaac atgagggaaa taagcaaga300  
gggcaatcgc ctccctggag gctctggaga caattatcgg gggcaagggt cgaactgggg360  
cagtgaggga ggtgacgctg ttggtggagt caatactgtg aactctgaga cgtctcctgg420  
gatgtttaac ttgacactt tctggaagaa ttttaaatcc aagctgggtt tcatcaactg480  
ggatgccata aacaagaacc aggtcccggc ccccgacc cagccctcc tctacttcag540  
ccgactctcg gaggatttca aacagaacac tcccttccct aactggaaag caattattga600  
gggtgcggac gcgtcatcac tgcagaaacg tgcaggcaga gccaggtcag aactacaatt660  
acaaccagca tgcgtatccc actgcctatg gtgggaagta ctcaagtcaag acccctgcaa720  
agggggggag tctcaccttc tccctcggt tccgggtgc aactgggccc tgcttgag780  
tgggtgaagt ttgtgaag caatttcttg caaccaacca ccgaaggccc cggaaaaagc840  
actgggttcg tcaagggaag ctcccttccc ctctggggcc ccagacctg tggcaggccc900  
ctgggcccgg gttg 914

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1669 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

gagctgcagc agagcaggta acagctcttg cacctgtttc tcttgccact gacgtgcagc 60
tgctctcacc caccctctctt ggctgagcct tgcctgatac agcagcccg aggcaccact 120
tgcttcccca gctctcacctt cccaggcagc tctctacact aactgcttct ctaggaaaag 180
tctcaccctcc agcctcgaggc agtctgggatt acagaaaagcc ccatcctcttg cttaggggagc 240
gccatgacga ctgaaattgg ttgggtggaag ctgaccttcc tccggaaaaaa gaaatccact 300
ccccaaagtgc tctatgagat cctctgacacc tatgccccaa cagaggggaga tgcagaacct 360
ccgaggcctg acgctggagg ccccaacagc gactttaaca cccgcctgga gaagattgtg 420
gacaagagca caaaggggcaa gcacgtcaag gtctccaact caggacgctt caaggagaag 480
aagaaagtga gagccacgct ggcagagaac cctaacctct ttgatgatca cagggaagga 540
cggctcatcaa agtgaagggc tgaggagggt gctagcactt cttggctccc tgcctcagc 600
cagatctgag acaggacott gccacgctgg cctctttggc catagctgaa gctgtggggc 660
cagttgatac ctgctggcag gaaatggctg ttttttaggt ttgtatttat gtgcgccac 720
ttttgtaagg cctgggagat cccaggggtcc tccacccctcc ccttgaccac atacaaaggc 780
actctagttc aagagtga aaagtctccc aggggaaca gccctccttg aagcaatggc 840
agggccagca gggaggtggg catggcaggg aatggagaga gtgagccaga cagaacttcc 900
ctccttactg gacacagggt caagggcgag ttccaattgc tgcctccctt accttctcta 960
cctgtgacta ctccctggac caatcctgag gagggcacat tttccagaag ccacgtgata 1020
ggggctgggt tctgtggagc cagaggcaga gacactgaac ttgagctcac ctctaacac 1080
cggcagtaaa cttcctggaa ctt-gccctc aggtgcggag gggacagagg accctggcac 1140
tctgttaggg tgctgtagaa gactagattg atggtagttt ggctctgtac ttctgttttt 1200
ggccatgat tttgcagatg gcaagtacac caccctcaaa ggggaagctac accggccaaa 1260
tcgggggagt ggggtggggaa tttctcctc tccctttcct actataatag tatttaagac 1320
atatcagctc cagagatgag tcttggaacc ttgaattttt ttaacaaaaa taattgtagg 1380
ttctctctcg taataacaac gctggaaaag cagagaacct cttttatgct catgtcttgc 1440
atttattgag atgactgttt cctatgcctt tatgttctct catgtaagt aagtggacct 1500
ttgtgctcaa aaaaaaaatt tcaagcttca ggaaggggtt cccaaggtgt gacaatgtag 1560
gaacctgggt cactaatatt taccatcaaa cctagcctta gtatgggat ggggcaagca 1620
gaaggagcta gttacacctc agtgggtcagt tctctccagt caacagaga 1669

```

## (2) INFORMATION ON SEQ ID NO. 41:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 355 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

0067395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ccggccctccc ctcgctctga ggctcggggg cccagctcc gcgtaaacty cagcatttcg 60
ccctctgctc agctccctc tgccctctc ttccaagaga gacttcaga toccacattt120
tcttgactga ttttgaagct gtctgtttgc attctgattg ggaacactgg gatcattttc180
atcatgccga cagtgggtgt aatggatgta tccctttcca tgaccggacc tgtgtctatt240
gaggggtccg aggaatacca gcgtaagacc tagcagccca tggtttaacg atgcttgttt300
tgagcacatg gccacaaatt acaagcttga atttacagca cttgtggttt ttcca 355

```

## (2) INFORMATION ON SEQ ID NO. 42:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673295.12700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

gggtgcgcct gctttcgcgc tccctctcca gcgggagggg gcgggacttc gcggggggcg 60
agtcgcgtcta gtgcgtgacgt tggcagccga acccaaaagta gatcgagggcg gcggggtcga 120
cattcccgctt gttgcgtttgc gtttccctcc tctttcaactc gcgcgtccagc gcggcgccga 180
aagcggcgccg gacggcgggcg cgagaaacgac ccggcgccga gttctcttcc tccctgcgcac 240
ctgcgcctgct cggtcagtcga gtccggcgccg gccgcggcgcc ttgtgctcag acctcgcgct 300
tgccgcgcctc aggcgccagcg gccgtagcta gcgctctggcc tgagaaacctc ggcgcctccgg 360
cgccgcggggc accacgagcc gagcctcgca gcgggtccagc aggagggcagg cgagtgcggcg 420
agtcggagggg gtcggcggggg caggctgggtg ccgcgcgaag atggtcgcca agcaaaagat 480
ccgtatggccc aacgagaaagc acagcaagaa catcacccag ccggcgcaacg tcgccaaagac 540
ctcgagaaat gcccccgaag agaaggcgctc tgtaggaccc tggttattgg ctctcttcac 600
ttttgtttgtc tgtggtttctg caattttcca gattattcaa agtatcagga tgggcatgtg 660
aagtgcactga ccttaagatg ttctcattct cctgtgaatt ttaaactgaa ctcatctctg 720
atggtttgata cctctggtga aaacaattca gtaaaagcatc ctgcctcaga atgactttcc 780
tatcatgctt catgtgtcat tccaaggctt cttcatgagt cattccaagt tttctagtcc 840

ataccacagt gccttgcaaa aaacaccaca tgaataaagc aataaaattt gattgttaag 900
atcacagtgt ggaccctact tattcagtcga attaagagta agttttttta tgtggttatt 960
aaaacagtat gaacaatttag tctaactctg catagacagg gctagattt tgttaaccata 1020
aatgtataat tgcagtttagc ttaaaattaca atttgaagtc ttgtgggttt tatatagcta 1080
ggcactttat tactcttttg aactgaaagc acactccctc atagggttcat gtaactgtccc 1140
tgttaataag tgcttataaa tggaaacaact acacagccca gttttgccac aaccttttagc 1200
atctaaaaag ttttaaaaagc ttctaaatgt ctaataataa gggagatgct tatagccaca 1260
acatctattt taccattatt gtttccatta cactaccctg gattttgcat gagtgcagta 1320
agtaacccaa gatgccataa aaaaaaactt gatcgttttc tgacttaatc agttactgtg 1380
gtttccactaa aagctcacgt ggtggagtga agtcagtcag ggaaggtttg tttatgttac 1440
atttatttca ccagaactcat ttaatatat caaagggttt tactatgcca acaaaaattc 1500
tagggaaaaa tactgtcaaa aatggatgcc tcaatcagaac atgctgttga gtccaatgtg 1560
ccataagaca tttttagcat ttaaatagca cttttaatag caaaaaaagg cacatcaact 1620
gcgaagttat ccttagtttg caaatgcttt ttctagatta atgacttttc aatcattagg 1680
gtactagaca catcagocca aagtggcatc tggaaattga tggatttact gataacgatc 1740
agtctttagt ctccctcttg ttatatgact ttataggtta tgattgatca aatttcagtt 1800
ttactaatgg taagggtgag ggtcataggg caggtttttg gttttcttgc atctgtgaaa 1860
actgcaagta ttggctattt gtatacttag ccaataacttg gtgaaaaaaa acctgagcac 1920
tgtctatgta ttaattgcgtt ggaaagaaaag ctgcttgtgt ttgcttttgt aattgcctca 1980
ggatatcttc tttaaaaagc cgtgttttaa gaggaacaga aggggaaatct gctaccagta 2040
ctatacacag cgtgaacctc acagggggct tctgataacc tcaaacatgg agaacagtaa 2100
gggagcagag tggttaagga ctttcaggaa cttaaactat ctggaataag gaatgaatca 2160
actgaccttg ggcacagcag tttttaacta aattgttact tgcctttctc acccagttaa 2220
tcagctctcg tactctgttc cctttttgaa acaagtgtct tgggttaacta attctgttt 2280
atggtttgtg taaattgcata gcaggtgcct tattcttttg ttttagtcaa accattccat 2340
atcagaattt tctctgggtt actatagata ttggggttta agttgttgtt tgtgttttt 2400
aattgatacat gttctgataa atttgactgt taaattgtcta tagctagcaa tcattttaca 2460
tatgtaaaaa tgcattccct ttgatttcaa tgttataaag accaatttag tgcagtttat 2520
attcaggttg gattatgcac gtttaggtta acgaaagctg tgtcttaact gattttatct 2580
ttaaaaaata agtctccctga atatttgaaa aaaaaaataa aaaaaaaa 2628

```

09673365-122700

## (2) INFORMATION ON SEQ ID NO. 43:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2535 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

agttcgccac aggggggagga accctggccct gggaggaggc tgttgctgtgc tccacagaaa 60
tcccgctctcg aaggggaaagc catgttttgcg ggcgttcccca ccattgcgtga gaactccccc 120

aaacagtcaca ttgcagctcgg aggcagggtc ttgctgttgc tgaatgttcat gacctctcct 180
cacttttgagc ccagctttctt ttctattgtc cagaacatcg tgggcaacagc tctgatgatt 240
ttagtgtccca ttgggttttaa aaccaagctg gctgttttga ctctgtttgt ttggcctctt 300
ggcatcaacg tatatttcaa cgccttctgg accattccag tctacaagcc catgcatgac 360
ttcctgaaat acgacttctt ccagaccatg tcggtgattg ggggcttggt cctgggtggct 420
ggcctggggcc ctgggggtgt ctccatggat gagaagaaga aggagtggtt acagtcacag 480
atccctacct ggcctggctaa gaccctgggc cgtcaaggac tggttcgggg tggattcaac 540
aaaaactgccg gcttttatgt atocctcttc ctcccccctc cttggttaaa gcaacagatg 600
tttgagaact ttatttgcag agacacctga gaattcgatg ctcagctctg tctggagcca 660
cagttctggcg tctgacctt cagtgcaagg cagcctggca gctgggaagc tccccacgc 720
cgaggtcttg gagtgaacag cccgcttgcc tgtggcatct cagtcctatt ttgagtttt 780
tttgtggggg tacaggaggg ggccttcaag ctgtaactgt agcagacgca ttggtattat 840
cattcaaaag agtctccctc ttatttgcata gtttacatt tttagcgaaa ctactaaatt 900
attttgggtg gttcagccaa accctcaaaa agttaatctc cctggtttaa aatcacacca 960
gtggcctttga tgttgtttct gcccgcgatt gtattttata ggaatagatga aaacattttag 1020
ggacacccaaa agaattgatgc agtattaaag ggggtggtaga agctgctgtt tatgataaaa 1080
gtcactggtc agaaaatcag cttggattgg tgccaagtgt tttattgggt aacacctggg 1140
gagtttttag agcttgaggc aaggtggagg ggcaagaagt ccttggggaa gctgctggct 1200
tgggtgtcga ttggcctcaa gctggcagtg ggaagggtca gtgagaccac acaggggtag 1260
cccagcagc agcacacctg aagccagcct ggccagctgc tcagacaccg cttgagagcc 1320
gcagccgctg tgggcagggg gtgtggcagg agctcccagc actggagacc caaggactca 1380
accaggttac ctacataggg gctttttctg agcaaggctc cgaaagcgca ggcgcgcctg 1440
gctgagcagc accgcctctt cccagctgca ctgcgcctgt ggacagcccc gacacaccac 1500
tttctcgagg ctgtcgctca ctacagattt ccgtttgcata tggcgaatgc agccaaaatt 1560
cctcttttaca atttgtgatg ccttaccgat ttgattctaa tctgtattt aaagttttct 1620
aacactgctc tataactgtg ttctcttttt gggggagctt aactgcttgt tgcctcctgt 1680
cgtctgcacc atagtaaatg ccacaagggt agtcgaacac ctctctggcc cctagacct 1740
tctgggggaca ggctggctca gctgtctctc agggctgctg cggccacagc ccgagcctgc 1800
ctccctcttg gctctctatc cattggctct gcaggggcagg ggtgaggcag gttctgtctc 1860
ataaagctct ttggaagtca cctacctttt taacacagcc gaactagtc caacgcgttt 1920
gcaaaatttc cctgtgtagc ctacttctct acccccgaat attggttaaga tcgagcaatg 1980
tcttcaggagc atgggtttct ttctctgtg atcattcaa gtctcaactg atgaagactg 2040
ctgtgtctca tgttttcaac ctacaccagg ctgtctcttg gtccacacct cgctccctgt 2100
tagtgccgta tgacagcccc catcaaatga cctgcggctt ctctgtgtgtc 2160
aaggttgggt gggtgatagg tggaaaagtag ggtggaacaa aggaggccac gtgagcagtc 2220
agcaccagtt ctgcaccagc agcgctctcg tccctagtgg tgttctcgtt tctcctggcc 2280
ctgggtggcg tctgggctga ttggggaaga tgcctttgca ggggagggag gataagtggt 2340
atctaccaat tgatttctgc aaaaacaatt ctaagattct ttgtctttat gtgggaaaaa 2400
gatctaaatc tcatttttat ctgtatttta tatcttagtt gtgtttgata agcttttgat 2460
tttggaaac acatcaaaat aaataatggc gtttgttgta aaaaaaaaaa aaaaaaaaaa 2520
aaaaaaaaaa aaaaaa 2535

```

0967305-122700

## (2) INFORMATION ON SEQ ID NO. 44:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 805 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

ggcacgagcg gcacgagcca tctccatccc cggagcatct gtatgattca gaagtacaac 60  
 cacgatgggg aagcagggtcg gctggaggct tttagcccaag gggaaagtgt cctaaaggaal20  
 cccaagtacc aggaagagct ggaggacagg ctgcatttct acgtggagga atgtgactac180  
 ttgcagggct tccagatcct gtgtgacctg cacgatggct tctctgggggt aggcgcgaag240  
 gcggcagagc tgctacaaga tgaatattca gggcggggaa taataacctg gggcctgcta300  
 cctgggtccct accatcgtgg ggaggccagc agaaacatct atcgtctatt aaacacagct360  
 tttggtctcg tgcacctgac tgctcacagc tctctgttct gcccttctc cttgggtggg420  
 agcctgggccc tgcgacccga gccacctgtc agcttccctt acctgcatta tgatgccact480  
 ctgccccttcc actgcagtgc catcctggct acagccctgg acacagtcac tgttcctta540  
 cgcctgtgtt cctctccagt ttccatgggt catctggctg acatgtcgag cttctgtggg600  
 aaaaagggtg tgacagcagg agcaatcctc cctttccctt tggctccagg ccagtccctt660  
 cctgattccc tgatgcagtt tggaggagcc accccatgga ccccaactgt tgcattgtgg720  
 gaggccttctg gaacacgttg ctttggccag tcagtgtgtg tgagggggta tagacagagc780  
 atgccacaca agccacaagac ttaat 805

## (2) INFORMATION ON SEQ ID NO. 45:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

cggaagttagc	cgcaggcatg	gcgcgcgcta	tgcgctgttt	gctctgctcg	tcctgttgct	60
cctggggccc	ggcgctggt	gccttgca	acccccacgc	gacagcctgc	gggaggaact	120
tgteatcaacc	cgctgcctt	ccggggacgt	agccgcacac	ttccagttcc	gcacgcgctg	180
ggattcggag	cttcagcggg	aaggagtgct	ccattacagg	ctctttccca	aagccctggg	240
gcagctgatc	tcacaagtatt	ctctacggga	gctgcacctg	tcattcacac	aaggcttttg	300
gaggaccgca	tactgggggc	cacccttct	gcaggcccca	tcagggtcag	agctgtgggt	360
ctggttccaa	gacactgtca	ctgatgtgga	taaatcttgg	aaggagctca	gtaattgtcct	420
ctcagggatc	ttctgcgcct	ctctcaactt	catcgactcc	accaacacag	tcactcccac	480
tgccctcttc	aaacccctgg	gtctggccaa	tgacactgac	cactactttc	tcgctatgc	540
tgctgtgcgc	cgggagggtg	tctgcacga	aaacctcacc	ccctggaaga	agctcttgcc	600
ctgtagtctcc	aaggcaggcc	tctctgtgct	gctgaaggca	gatcgcttgt	tcacaccag	660
ctaccactcc	caggcagtcg	atatccgccc	tgtttgca	aatgcacgct	gtactagcat	720
ctctcgggag	ctgaggcgaga	ccctgtcagt	tgtatttgat	gccttcatca	cggggcaggg	780
aaagaagaac	tggtccctct	tcgggatggt	ctccgaac	ctcacggagc	cctgccccct	840
ggcttcagag	agccagatct	atgtggacat	caccacctac	aaccaggaca	acgagacatt	900
agagggtgcac	ccacccccga	ccactacata	tcaggacgtc	atcctaggca	ctcgggaagac	960
ctatgccatc	tatgacttgc	ttgacacgcg	catgatcaac	aactctcgaa	acctcaacat	1020
ccagctcaag	tggaagagac	ccccagagaa	tgaggccccc	ccagtgcctt	tcctgcatgc	1080
ccagcggtac	gtgagtggct	atgggctgca	gaagggggag	ctgagcacac	tgctgtaca	1140
cacccaccca	taccgggcct	tcccggtgct	gctgctggag	accgtacctt	ggatatctgc	1200
gctgttacct	ccactaccag	cctgcccagg	accggctgca	acccccctc	ctggagatgc	1260
tgattcagct	gccggccaa					1279

(2) INFORMATION ON SEQ ID NO. 46:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1923 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

0067395-12700

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cdna library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

gcgcaagaca caggaggccc aggcgggcag tcaggacatg gcggcgatt gcagattcca 50  
atctctctgt ttctgcggcg attgaacacc caacattggc gaccgggacg gcggaaaagt 120  
atggctgtcg tcccggcggtc tctctcagga caggacgtgg gatcatttgc atatcttaca 180  
attcaagaca gaataccaca gatcttaact aaggttattg atacattgca tcgacataaa 240  
agtgaatttt ttgagaaaca cggagaggaa ggcgaggaa ctgaaaagaa agctatctct 300  
ctctcttcta aattacggaa tgaattgcaa acagataaac catttatccc cttgggttag 360  
aaatttgttg atactgatat atggaatcag tacctagaat atcaacagag tcttttaaat 420  
gaaagtgatg gaaaatcaag atgggtctac tcaccgtggg tggttgtaga atgttacaatg 480  
tatcgaaaga ttcatgaagc aattatccag agtccaccaa tcgattactt tgatgtattt 540  
aaagaatcaa aagagcaaaa ttctatggg tcacaggaa ccatcattgc tttatgtact 600  
cacctgcaac aattgataag aactattgaa gacctagatg aaaatcagct gaaagatgag 660  
ttttttaaac ttctgcagat ttcaactgtg ggaaataagt gtgatctgtc tctctcaggt 720  
ggagaaagta gttctcagaa taccaatgta ctaaatctat tggaagacct aaaacacctt 780  
attttattga atgatattga acatctttgg tcattgtcta gcaattgcaa gaaaacaaga 840  
gaaaaagctt ctgctactag agtggtatatt gttctcgata attctggatt tgagctgtgt 900  
acagatttaa tattagccga cttctgtttg tctctggaac tggctactga ggttcaattt 960  
tatggaaaaa caattccatg gtttgtttct gatactacta tacatgattt taattgggta 1020  
attgaacagg taaaaacacg taatcataag tggatgtcca agtgtggggc tgactgggaa 1080  
gagtattatta aaatgggtaa atgggtttac cacaatcata tattttggac tctgcctcat 1140

gagtagctgt caatgctca ggttgcaact gacttatatg ctgaactaca gaaggcacat 1200  
ttaatttttt tcaaggggtga ttggaattac aggaagtgtg cagggtgacag aaaatgggag 1260  
ttttctgttc catttcacga ggcctcgaat ggcttccatc ctgcaccact ctgtaccata 1320  
agaacattaa aagctgaaat tcagggttgt ctgcagcctg ggcaagggga acagctcctg 1380  
gcctctgagc ccagctgggt gaccactgga aaatatggaa tatttcagta cgaatgggtccc 1440  
ctttgacttg attttaggag tctcagttgc atagaagaat ctggtgagca ccttttcatc 1500  
cccagaaaag gagcacgtga attgagtcgc ctggcgggtc tgtacgcgct cagggaagct 1560  
tagctctctg gtgcccactc acgtgcactg gatgattttt cttttgaaca ttttgcccca 1620  
ctacactgtt ttgggggata gctgggttaa gatatttaca tttatatggg 1680  
agatttttaa caactttttt ttcagggtga atatataaat tcaaatgtct tttaaatggg 1740  
ccttaatttt gaagtgggtg gggccaaaaa ataaagggag ggcctccttg aggtaggttac 1800  
ccttggcctt tcttaaaaaa cccctcaatg ggatttagat ccgggggggt ggggttattt 1860  
tccttgggtt ggccatgaaa atccttgga cggcttatg cccttttgaa aaggggggtt 1920  
ttt 1923

09573305.122700

(2) INFORMATION ON SEQ ID NO. 47:

- ```
(i) SEQUENCE CHARACTERISTIC:
    (A) LENGTH: 706 base pairs
    (B) TYPE: Nucleic acid
    (C) STRAND: individual
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
    ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
    (A) ORGANISM: HUMAN
    (C) ORGAN:

(vii) OTHER ORIGIN:
    (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
```

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| cattttacga  | caggcgggat  | tgttttgtg   | cgtcagctt   | tctccgtggt  | ctgagtttgt  | 60  |
| ggctgattct  | ttaattcttg  | tgtgctctgt  | acggcgggcg  | agaaattagg  | cagaagcggal | 120 |
| acgagatct   | cagccctcgt  | gagctgatga  | tctgactact  | aggagatggt  | attataaacac | 180 |
| tgtatgaagc  | ccacgagcag  | ggcaagaagca | tctgactaaa  | taaggtgaaa  | accaaagcag  | 240 |
| ctgcacaaata | tggcctttct  | gcccagcccc  | gctcgtgtga  | tatcatctgt  | ccgagctccct | 300 |
| ctcagtatcg  | caaggtcttg  | atgcccaact  | taaaaggcga  | accctacaga  | actcgtatagt | 360 |
| ggattgctgt  | cgtgctctgt  | atgtgcacac  | cccacagtag  | tccacacatc  | agttttacag  | 420 |
| gaaattctgt  | tgtatactgc  | cctggctggac | ctgattctga  | tttttgatat  | tccacccagat | 480 |
| ctctacactg  | cttagagcaac | cctccatagc  | agactattccg | tgcgcagatat | ggaccttttt  | 540 |
| ccttacaggga | caaggacaaa  | ggattaggaa  | cagttttaaa  | caagttgggt  | tcttagttgt  | 600 |
| gggttaagtg  | ggagtttgtt  | ctggaagcgg  | tgtggaaact  | tttggggcgc  | tccacaggaga | 660 |
| ttcacagagt  | attttttatt  | gggaagttaa  | ctgtatgggt  | ttttcc      |             | 700 |

(2) INFORMATION ON SEQ ID NO. 48:

- ```
(i) SEQUENCE CHARACTERISTIC:
    (A) LENGTH: 749 base pairs
    (B) TYPE: Nucleic acid
    (C) STRAND: individual
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
                   ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iiii) ANTI-SENSE: NO
```

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

gacccatccct catctgtgca aggaggagtg gcccaactctg gagcccaggc tgttgcttcc 60  
 tgggtctgggt gtgaatccct catagtctgg tgagtgtagt gcccaactct ggagcccagg120  
 atgttgcttc ccggtctgggt ggtgaatccct ccatagtctg gagatctcag ccctgctgag180  
 ctgatgatgc tgactatagg agatgttatt aaacaactga ttgaagccca cgaagcagg240  
 aaagacatcg atctaaataa ggtgaaaacc aagacagctg ccaaatatgg cctttctgcc300  
 cagccccgcc tgggtggatat cattgcttgc cgtccctcct cagtatcgca aggtcctgat360  
 gcccaagtta aaggcgaaac ccacacagac tgctagtggg attgctgtcg tggctgtgat420  
 gtgcaaaccc cacagatgtc cacacatcag ttttacagga aatatatgtg tatactgcc480  
 tgggtgggac ctgattctga ttttgagtat tccaccagct cttacactgg gctatgagcc540  
 aacctccatc aggaagctatt ccgtgccaga tatggaccct tttccttaca ggacaaggac600  
 accggattag gaacagttta aaacaagttg ggttcgtagt gtgggggttaa gtgggagttt660  
 gttttgtgat ggggtgggaa ctttttgggg ccgtccaga ggattacaga gttattttta720  
 tttcggaagt ttacgtgatg ggtttttccg 749

- (2) INFORMATION ON SEQ ID NO. 49:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 857 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

00675000-100700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

accttacc aa ggggagaaaa aaacccctcca ctttgggtca ctgtgggttt ggcactaaga 60
ggcacgatat ctgaaggagg tcattccagt tttaaaaagta cggacagtgct tgttgggaact120
gaccacaaaa atgtatttgtt aaaaaaaaaat tgaaaaaccag cagtgtatttg ggtcccccctg180
aaacctctgt gaatcggagg tgggcccgagg aggggtgcagg acgcagcaga aatgttccca240
gaaaggagag acgggttcagt cagcggggctt gtgctttttt gtgtgtgttt gtgtgtttta300
caccatacat ctccaaatga agtattttatt aacaattgta gtgtaagcct gtgataaaat360
agcacaaaagg ttcttttaagg aagttcactt ttaaggcatc agaaaagtta atgtggcaaa420
catttttaatt aaaacatcag aagtaaattt tattttaaac tttaggcctc tgaattttttc480
cagttaaacac agttcagcta tgtggcgaag tcaatgggtg gcatctaaaa tgaatttttta540
cattctacaa aaaaaataaaa taaaataaagg acacagcccc aaacgggtgtc acctcttcgc600
ggcggtccca catgcacaga atctactagg atttgtcacg gccgggtggc acccgatttg660
ttttgactat acaacaaact tttttttcaa aagattttgt tcaggataaac tttaaaaaata720
atataaaaaa aaacaatgga ttgactttt cctcaaaaat tgaaaaagaaa ggggtggggg780
gaggtgttaa ccattggcct tttttttttt ggagggggccc cattgggtatt gtaaggccct840
ggggttcagg cctttcc

```

857

## (2) INFORMATION ON SEQ ID NO. 50:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 268 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

ccgcgcgcgg cccccaggca attttaataa taaatcttaa tagatgggggt aagagctgcc 60
ttcatcccat acagagaata caatgggtgct agactaaagta gagattttat ttcagertaa120
agattctgtt tgatgtctga aattacatgt ttaggcgga tggggaacag gactgtttct180
tagcatcagt ttccacaatta ctttaactta ctaggtttca ttcaccttat aattctgaaa240
tttcatcagc agtgggggaa agaaaaagg

```

268

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 297 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

ctgatgtgca ctctaggtta gtaaccattt ttgtgaaaaa tttagagaaa ttctttgagc 60
agcttccact gaaacactaa aaccacaatag gcccaaaggc ccataacctg aggaaacctt120
atctattgct taatccaaca taggctatga aagttttgag ttctctcttg tgtattagaal80
tttcattcct atttgttgta gagagtatag tacggggaat cagtaaatta aatgaagtaa240
actaaagatt acacccttgc tgctggcact aagcgaaaag caaaaccagt ggctgtc 297

```

## (2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 590 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

00673395-162700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

acgggtcaaaa tgataactca tgtatTTTTat tccaacaaca ttgggtttat aaaggaatac 60
aaacaggcac aaaacatggt tcagaagatt tattaagtaa acttgctaaa atatggacag120
atacacttag cagtcaaaaca gttgaatatatt cattgctacc tcattaaaagt ttttgcatac180
gtattaccag gtccaaacat aaaaaccacc tctgttcaaa aaataaaagt tcagagagct240
gtatgttctt tgttctggta gtacatttt aaaaaaacac ctctttccag tcttgctaac300
caagaatatt agtcataataa aagaacttag aatTTTTttt cccaagtaca agctatctt360
tgctccaaaa cagttctgaa ggTTTTtatt atattttatc ttatccccgag ggaccaacag420
caggcatacc ttgtccaggc cttcttgtag aaagacacag agccgtaaag gcaaaaaataa480
aattgcaata aagtatatgg tattggggggc agggagaacc agaaaccctc aaggggacca540
atttttagca cgttctttt ttagggttta ccctgtggag taagaactag 590

```

## (2) INFORMATION ON SEQ ID NO. 53:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09573305.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ggaaggggaa gtttcgcctc agaaggctgc tctcgctggtc cgaattcggt ggcggccagt 60  
 ccgcgcgtct ccgccttctg catcgcggtc tggcgcggtt ccacctagac acctaacagt 120  
 cgcgagcccg gccgcgtcgt gaggggggtcg gcacggggag tggggcggtc ttgtgcatct 180  
 tggctacctg tgggtcgaa atgtcggaca tgggagactg gttcaggagc atcccggcga 240  
 tcacgcgcta ttgggtcgag gccacgctcg ccgtgccctt ggtcggcaaa ctcggcctca 300  
 tcagcccggc ctacctcttc ctctggcccg aagccttctt ttatcgcttt cagattttgga 360  
 ggccaatcac tgcacacctt tatttccctg tgggtccagg aactggattt ctttatttgg 420  
 tcaatttata tttcttata cagtattcta cggcacttga acaggagact ttgtatggga 480  
 ggccaacaga ctattttatc atgctctctt ttaactggat ttgcactgtg attactggct 540  
 tagcaatgga tatgcagttg ctgatgattc ctctgatcat gtcagtactt tatgtctggg 600  
 cccagctgaa cagagacatg attgtatcat ttgtgtttgg aacacgattt aaggcctgct 660  
 atttaccctg gggtatcctt ggattcaact atatcatcgg aggcctcggt atcaatgagc 720  
 ttattggaaa tctggttggga catctttatt ttttcttaat gttcagatag ccaatggact 780  
 tgggagggaag aaattttcta tccacacctc agtttttcta ccgctggctg cccagtagga 840  
 gagggaggat atcaggattt ggtgtgcccc ctgctagcat gaggcgagct gctgatcaga 900  
 tatggcgagg cgggagacac aactggggcg agggctttcg aactggagac cagtgaaggg 960  
 gcggcctcgg gcagccgctc ctctcaaagc acatttcttc ccagtgtcgg gtgcgcttaa1020  
 caactcgctt ctggctaaca ctggtggacc tgacccacac tgaatgtagt ctttcagtacl080  
 gagacaaaat ttcttaaatc ccgaagaaaa atataagttg tccacaagtt tcacgattct1140  
 cattcaagtc cttactgctg tgaagaacaa ataccaactg tgcaaattcg aaaactgact1200  
 acatttttgg gtgtcttttc ttctccctct tccgtctgaa taatgggttt tagcgggtctc1260  
 tagtctgctg gcaattgagct ggggtgggtt caccaaaacc ttcccaaaag gacccttatc1320  
 tctttcttgc acacatgctt ctctcccaact ttcccaaac cccacatttg caactgaag1380  
 aggttgccca taaaattgct ctgcccttga caggttctgt tattttatga cttttgcca1440  
 ggcttgggtc caacaatcat attcacgtaa ttttccccct ttggtggcag aactgttagca1500  
 atagggggag aagacaagca ggggatgaag cgttttctca gcttttggaa ttgcttcgac1560  
 ctgacatccg ttgtaaccgt ttgccacttc ttcagatatt ttataaaaa agtaccactg1620  
 agtcagtgag ggccacagat tggattaat gagatacag ggttgttgct ggggtgttgc1680  
 tccagtagaag tgagaaggtg agtggaattga ctac 1714

## (2) INFORMATION ON SEQ ID NO. 54:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

00673335.122700



(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

ctcgagccgc tcgagccgaa tcggctcgag ctgaaaaagg gctacctgac cctgtcagac 60
agtggggaca agtggccgt ggaatgggac aaagaccatg ggtccttgga gtcccacctg 120
gcggagaagg ggaaggagcat ggagctatcc gacctgattg ttttcaatgg gaaactctac 180
tccgtggatg accggacggg ggtcgtctac cagatcgaag gcagcaaagc cgtgccctgg 240
gtgattctgt ccgacggcga cggcaccgtg gaaaaaggct tcaaggccga atggctggca 300
tggaaggacg agcgtctgta cgtggcgccg ctgggcaagg agtggacgac cactacgggt 360
gatgtggtga acgagaaccc ggagtggtg aaggtgtgtg gctacaaggg cagcgtggac 420
cacgagaact ggggtgtccaa ctacaacgcc ctgcccgtg ctgccggcat ccagccgcca 480
ggtaacctca tccatgagtc tgccgtctgg agtgacacgc tgcagcgtg gttcttctg 540
ccgcgcgcgc ccagccaggga gcgtacacgc gaggaaaggac gacgagcgca agggcgccaa 600
cctgctgtg agcgcctccc ctgacttcgg cgacatcgct gtgagccacg tcggggcggt 660
ggtcccaact cacggcttct cgtccttcaa gtccatcccc aacaccgacg accagatcat 720
tgtggccctc aaatccgagg aggacagcgg cagagtgcgc tccatcatca tggccttcac 780
gctggacggg cgcttctgt tgccggagac caagatcgga agcgtgaaat acgaaggcat 840
cgagttcatt taactcaaaa cggaaacact gagcaaggcc atcaggactc agcttttata 900
aaaacaagag gagtgcact ttgtttgtt ttgtctttt tggaaactgt cctgggtgtg 960
aggtctggac agggagccca gtcccgggccc ccatagtgtg gcggggcactg gaaccccggg 1020
ccccacggag gccgcgtgtt gaactgcttt ccatgctgcc atctgtgtgt gatttcggct 1080
actcaggca ttgactcaag gcctgcctaa ctgggtgggt cgtttcttcc atccgacctc 1140
gtttcttttc tttctatgt tctttgttc agtgaatate ctatgagctc ctaccatgat 1200
tcaggcccta tgcctcacc tcgaaacgca gtaagcatga aggtggacct ggttctgtgt 1260

gaacccgagg gctaaacccc tttttcttcc caaatgtgtg gccttggaag aatcagggtcc 1320
agccctgaag atccttgggg

```

(2) INFORMATION ON SEQ ID NO. 55:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 765 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

caggattgaa acaagatggc gggttcgttg tgagaagccg tcaaggagta gaaattggta 60
tgcttagaag cagattctaa aagcagtttc tcttcagaac atcttttttc ataccacttg120
ataagcatct tgaaacacca tggctgtagc tgcagtaaaa tgggtgatgt caaagagaac180
tatcttgaaa cattttatct cagtcacaaa tggagcttta tattgtgttt gtcaataaac240
tacgtattct cctctaccag atgactataa ttgcaacgta gagcttgctc tgacttotga300
tggcaggaca atagtatgct accacccttc tgtggacatt ccataatgaac acacaaaacc360
tatccctcgg ccagatcctg tgcataataa tgaagaaaca catgatcaag tgctgaaaac420
cagattggaa gaaaaagttg aacaccctga ggaaggacct atgatagaac aacttagcaa480
aatgttcttt actactaagc accgttggta tcctcatgga cggtatcaca gatgtcgtaa540
gaatctgaat cctccaaaag acagatgatg cggaggttcc tgggggaatc aaagagaaat600
gtgcctcatt tgcatttga gaaaatgcag tctggtgtat tcagtaatat atagtaaat660
aataatgata aatatcttt tcatatatta gaatgtgtac ttttatataa agtaattctg720
gatttgacat tctcatttag ggggacctat tccttttttc gtttt 765

```

## (2) INFORMATION ON SEQ ID NO. 56:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673305.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

gcagccggag taagatggcg gcgctgaggg ctttctggcg cttccggggc gtccggggcc 60
agggtgctcg gcoctggggct ggagtcggat tgccagcaga ggtgttcggc 120
agtgccagcg agatgtggaa tgggcacagc agtttggggg agctgttatg taccacaagca 180
aagaaacagc ccactgggaag cctccacctt ggaatgatgt ggacccctcca aaggacacaa 240
ttgtgaagaa cattaccctg aactttgggc cccaacaccc agcagcgcat ggtgtcctgc 300
gactagtgtat ggaattgagt ggggagatgg tgcggaagtg tgatccctac atcgggctcc 360
tgcaccgagg caactgagaag ctcaattgat acaagaccta tcttcaggcc cttccatact 420
ttgaccgggt agactatgtg tccatgatgt gtaacgaaca ggccatttct ctagtctggg 480
aagaagttgct aaacatccgg cctccctctc gggcacagtg gatccgagtg ctgtttggag 540
aaatcacacg tttgttgaac cacatcatgt ctgtgaccac acatgcccctg gacctggggg 600
ccatgacccc tttctctctg ctgtttgaag aaaggagaaa gatgtttgag ttctacgagc 660
gagtgtcttg agcccgaaat catgctgtct atatccggcc aggaggagtg caccaggacc 720
tacccttggt gcttatggat gacatttato agttttctaa gaactttctt cttcggcttg 780
atgagtttga ggagttgctg accaacaata ggatctggcg aaatcggaca attgacattg 840
gggtttgtaac agcagaagaa gcacttaact atggttttag tggagtgatg cttcggggct 900
caggcatcca gtgggacctg cggaaagacc agccctatga tgtttacgac caggttgagt 960
ttgatgttcc tgttggttct cgaggggact gctatgatag gtacctgtgc cgggtggagg 1020
agatgcgcga gtccctcgaga attatcgcac agtgtctaaa caagatgcct cctggggagag 1080
tcaaggttga tgatgcacaa gtgtctccac ctaagcgagc agagatgaag acttccatgg 1140
agtcactgat tcatcacttt aagttgtata ctgaggcgta ccaagttcct ccaggagccal 1200
catatactgc catgagggct cccaagggag agtttggggg gtacctgggt tctgatggcal 1260
cgacgcgccc ttatcgatgc aagatcaagg ctccctgggt tgcccatctg gctggtttgg 1320
acaagatgtc taagggacac atgttggcag atgtcgttgc catcataggt acccaagatal 1380
ttgtatttgc agaaatgagt cggtgagcag gggagcagcg tttgatcccc cctgcctatcl 1440
agctttctct gtggagcctg ttccctactg gaaattggcc tctgtgtgtg tgtgtgtgtg 1500
tgtgtgtgtg tgtgtgtatg ttoatgtaca cttggctgtc aggcctttct tgcattgtac 1560
aaaaaggag aaattataat aaattagccg tcttgcgccc ctaggcctaa aaaaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaa 1647

```

## (2) INFORMATION ON SEQ ID NO. 57:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1166 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09672305.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

cgccgcctgc gccggggggga gccagacaca gaccgcgcgc gggaccocga gtcgcgcacc 60
ccagcccccac cccccacccc gcgcgcctag gaccocaaag accgcaagaa gatccagtgc 120
tcgggtccccc cgcgccctag ccagctcgac ccccgccagg tggagatgat ccggcgccagg 180
agaccacacgc ctgccatgct gttccggctc tcagagcact cctcaccaga ggaggaagacc 240
tccccccacc agagagcctc aggagagggg caccatctca agtcgaagag acccaacccc 300
tgtgcctaca caccaccttc gctgaaagct gtgcagcgca ttgctgagtc tcacctgcag 360
tctatcacga atttgaatga gaaccaggcc tcagaggagg aggatgagct gggggagctt 420
cgggagctgg gttatccaa agaggaagat gaggaggaag agggagatgc agccagagctg 480
aagtctgaa ggtcatcagg cagctctgctg gcaaaaagac aacctgtggc cagggtctgg 540
aaggccctg ggagcgccca cccctctggt atgagtcoga gagagatgga ggctctgagg 600
accaagtgga agaccctc ctaagtgagc ctggggagga acctcagcgc ccttccccct 660
ctgagcctgg cacaaccc cccagcctgc atctccagg aggaagtgga ggggacatcg 720
ctgttcccca gaaaccccc ctatcctcac cctgttttgt gctcttcccc tcgcctgcta 780
gggctgcggc ttctgaactc tagaagacta aggcctgtct gtgtttgctt gtttggccac 840
ctttggctga taccagaga acctggggcac ttgctgcctg atgcccccc ctgccagtca 900
ttctccatt caccagcgg gaggtgggat gtgagacagc ccacattgca aaatccagaa 960
aaccgggaac agggatttgc ccttcacaat tctactcccc agatcctctc cctctggcac1020
aggagaccca cagggcagga cctaagatc tggggaaaag aggtcctgag aacctgtagg1080
tacccttaga tctttttcta ccacttttc tatggaggat tccaaagtaa catttgtctg1140
aacggcttgt aacagggttc aggttg                                     1166

```

## (2) INFORMATION ON SEQ ID NO. 58:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 487 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ctcagatcgg tggacgtgct cgcctccact cggggccagg tctatgtccc ggtttcccg 60
agtccggggc agggcgccaa ggcggcagga ggagggtgag cggccaagag acctccagga120
agagcggctc tcggctgttt gcatcgccga tagaagaag aaaggatgca cgtcccagga180
gggaggaact acctcaactt ttctattca gaaacaaaga aaaaagatta ttcaagctgt240
gagggacaat tctattcctta ttgttactgg aaatacagga agtggttaaaa caactcaact300
cccaaaatat ctatatgaag cagggttttc acaacatggt atgattgggt taactcaacc360
acgaaaagta gctgctatct cagttgctca gagagtagct gaagaaatga aatgcacttt420
gggatccaaa gtaggatacc aagttcgttt tgatgattgc agttctaagg agacagcaat480
caaatat

```

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 59:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1630 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

aaactgtgta atgccccatg taatccataa aattttaact ttcccccccta acgtttttgc 60
tgaaaaaatgt tgggaaaaacc tcaacacgccc ttccctgaaaa caattaaaaat acttgaaaacc 120
tgtgaacctt tcataaaaaacc ctccagggttg gaaaagacccc ccaaacctctc ttttaaggat 180
catttgtctc gcccatcaca ggatcttggg aatgtttccc tagggtgtgt aaaaaataac 240
ccagggggga atgaagcaca tttttctggc aaccacaaact gagttctcca gagaacagat 300
gcagagagac ctgctcctgc ttgccccggt acagggggcca ctgtggagtc acactgaggg 360
tgtgacccgc cataagccca ggagagcccg tggcagctgt gccgaggcgc caggacctct 420
aagcgggaag ttcccaagct aggaatggag caacactgca atgaaatgtg tccaccaagc 480
tcattgttcc tcccggtgtg ttataaaagt cagatgtata gtgacgtatg gacaaataca 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gccctttctt ctccacaggca taagacacaa 600
attatatatt gttatgaagc actttttacc aacggtcagt ttttacattt tatagctgcg 660
tgcgaaagcg ttccagatgg gagaccctac tctcttggcg tccagacttc atcacaggct 720
gctttttatc aaaaagggga aaactccatg ctttcccttt taaaaaatgc tttttgtat 780
ttgtccatgc gtccactatc atctgagctt tataagcgcc cgggagggaac aatgagcttg 840
gtggacacat tccatttgca gtgtgtccca ttccctagctt ggggaagcttc cgcttagagg 900
tcctggcgcc tcggcacagc tgcccagggc tctcctgggc ttatggccgg tcacagcctc 960
agtgtgactc cacagtggcc cctgtagccg ggcaagcagg agcaggtctc tctgcactgt 1020
ttctctgagg aactcaagtt tggttgccag aaaaatgtgc ttcatctccc cctggttaatt 1080
ttttacacac cctaggaaac atttccaaga tccgtgtatg gcgagacaaa tgatccttaal 1140
agaaggtgtg gggctcttcc caacctgagg atttctgaaa ggttcacagg ttcaattatt 1200
aatgcttcag aagcatgtga ggttcccaac actgtcagca aaaaccttag gagaaaactt 1260

aaaaaaaaa gaatacatgc gcaatacaca gctacagaca cacattctgt tgacaagggg 1320
aaaccttcaa agcatgtttc ttccctcac cacaacagaa catgcagtag taaagcaata 1380
tatttgtgat tcccatgta attottcaat gttaaacagt gcagctctct ttcgaaagct 1440
aagatgacca tgcgcctttt cctctgtaca tataccctta agaacgcccc ctccacacac 1500
tgccccccag tatatgccgc attgtactgc tgtgttatat gctatgtaca tgtcagaaac 1560
cattagcatt gcatgcaggt ttcatattct ttctaagatg gaaagtaata aaatatattt 1620
gaaatgtacc
1630

```

09673305.122700

## (2) INFORMATION ON SEQ ID NO. 60:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

tgcgcgcgag cccgtgtccc caccggcgggc agcagcggcg gcggcggcgg ctgaacgcgg 60  
 aggggggcgga gggagcccg cgcggcgcca gcagctacag cgaatggcg gagaccgtgg 120  
 ctgacacccg gcggctgatc accaagccgc agaactgaa tgacgcctac ggacccccca 180  
 gcaacttctt cgagatcgat gtgagcaacc cgcaaacggg gggggtcggc cggggccgct 240  
 tcaccactta cgaatcagc gtcaagcaaa atcttcctat ttccaagctg aaagaatcta 300  
 ctgttagaag aagatacagt gactttgaat ggctgcgaag tgaattagaa agagagagca 360  
 aggtcgtagt tccccgctc cctgggaaag cgtttttgcg tcagttcctt ttgagaggaga 420  
 tgatggaata ttgatgaca attttattga ggaagaaaa caaggctcgg agcagtttat 480  
 aaacaaggct gctggtcatc ctctggcaca gaacgaacgt tgtcttcaca tgtttttaca 540  
 agatgaaata atagataaaa gctatacttc atctaaaaata agacatgcct gaaatttggc 600  
 aagaaggggc aaaaacgtga ctattaatga ttgataagca ccagtgaaga agttctaact 660  
 tttagcatgc tgcacagaaa ctgggtataac atgccttcag tatactaaca ctcatatgct 720  
 cagtttttgt ttgttttggc agttgacaag aagttaattt gcttttagtaa aaatccctca 780  
 ttccagcctt tctatataaa tagctctttc ttgctgtttt aatgtgggtg acactatagc 840  
 ctccaaaaac ttgtattcca gtgtaactcg cagtgtcgta actaaagtta ctggcttggg 900  
 cttatttgca cagtttttgc gtcttgtttg ctctctgcat ctgattaact agaataatcc 960  
 tctttccccc ttttaatttg tgatgtcact tgaccccat tttgtgtagg agcactacac1020  
 cattgggttc caatactgca cacataagat acatactttg gtgcagaaag tatcttctct1080  
 caggctttga atacccttat catggaagat taatgaggga aatctttata ttctgtataa1140  
 aaacaaaaagc aaattttat actaaaaatc tttgtctaaa aatttaagtt gttttcaaat1200  
 aaaaattaaa atgcatttct gatatgcaaa aaaaaaaaaa aagaaaaaga aaaaaagagg1260  
 ggcgccgct ct 1272

09573365.122700

## (2) INFORMATION ON SEQ ID NO. 61:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1914 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

tgcagcgcgt  gcgctgctcg  ctactgagca  ggcgcattga  ggactctgaa  gcactgggct  60
tcgaacacat  gggccctcgat  ccccggtctc  ttcaggctgt  caccgatctg  ggctgggtcg  120
gacctacgct  gatccaggag  aaggccatcc  cactggccct  agaagggaag  gacctctctg  180
ctcgggcccc  caccgggtcc  gggaagacgg  ccgttatgct  tattccgatg  ctgcagctgt  240
tgctccatag  gaaggcgaca  ggtccggtgg  tagaacagcg  agtgagagcg  cttgttcttg  300
ttcctaccaa  ggagctggca  cggcaagcac  agtccatgat  tcagcagctg  gctacctact  360
gtgctcggga  gtgccgagtg  gccaatgtct  cagctgctga  agactcagtc  tctcagagag  420
ctgtgctgat  ggagaagcca  gatgtggtag  tagggacccc  atctcgcata  ttaagccact  480
tgcaagcaag  cagcctgaaa  cttcgtgact  cccctggagct  ttgggtgggt  gacgaagctg  540
acctctcttt  ttccctttgg  tttgaagaag  agctcaagag  tctcctctgg  gaaggcagag  600
tcaacttgcc  cggattttacc  aggtctttct  catgtcagct  acttttaacg  aggacgtaca  660
agcaactcaag  gagctgatat  tacataaacc  ggttacccct  aagttacagg  agtcccagct  720
gctctggcca  gaccagttac  agcagtttca  ggtggtctgt  gagactgagg  aagacaaaat  780
ctctcctcgt  tatgccctgc  tcaagctgtc  attgattcgg  ggcaagtctc  tgctctttgt  840
caacactcta  gaacggaggt  accggtctac  cctgttcttg  gaacagttca  gcattccccac  900
ctgtgtcttc  aatggagagc  ttccactgct  ctccaggtgc  cacatcatct  cacagtccaa  960
ccaaggcttc  tacagctgtg  tcatagcaac  tgatgctgaa  gtctctgggg  ccccgagtcaa  1020
gggcaagcgt  cggggccgag  ggcccaagg  ggcaaggcc  tctgatccgg  aagcaggtgt  1080
ggccccgggg  atagacttcc  accatgtgtc  tgctgtgtct  aactttgact  ttcccccaac  1140
ccctgagggc  tacatccact  gagctggcag  gacagcagcg  gcttaacaa  caggcatagt  1200
cttaaccttt  gtgcttcccc  cggagcagtt  caacttagcg  aagattgagg  agcttctcag  1260
tggagagaac  agggggcccc  ttctgctccc  ctaccagttc  cggatggagg  agatcgaggg  1320
cttcgcgtat  cgcctgcagg  atgccatgct  ctacgtgact  aagcaggcca  ttcggggagg  1380
aagatttga  gagatcaagg  aagagcttct  gcatctcgag  aagcttaaga  catactttga  1440
agacaacctc  agggacctcc  agctgctgcg  gcatgacctc  cctttgcacc  ccgcagtggt  1500
gaagccccac  ctggggccat  ttccctgact  cctggttctc  cctgctctct  gtggcctgtg  1560
acgccctcag  aagaagcgga  agaagctgtc  ttctctctgt  aggaagccca  agagagccaa  1620
gtccccgaac  ccactgcgca  gcttcaagca  caaaggaaa  aaattcacag  cccagcccaa  1680
gccctcctga  ggttgtttgg  cctctctgga  gctgagacca  tctgtggaga  caggcttaca  1740
ccctctcgtg  acaggcgagg  ctctgggtct  tactgcacag  ctggaacaga  cagttctggg  1800
gocggcagtg  ctggggccct  tagctccttg  gcacttccaa  gctggcatct  tgccccttga  1860
caacagaata  aaaaattttag  ctgccccaaa  aaaaaaaaaa  aaaaaaaa  1914

```

09673305-122700

## (2) INFORMATION ON SEQ ID NO. 62:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 608 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

aatggaacca ggaattctta attaagcccg aagttcccaa gtctccttag cggaaaccgg 60  
 aaattgccca aggaaagcaa agagggagat gaccagtgat acctccagtg ccagaggtcal20  
 ctttgtggag ccataatcgt gacatgggca gtcgagactc ggcatcttct gtcccccgca180  
 ttaatgactc tcaggaaagga ggatgtaatt caaggcaagt ttctaattcc gaagctgcct240  
 gttcattgta acaggacttc tttttattcg tcaagatgta ctggttccct ggcaacctaa300  
 gggaaatcct gataaagga aacctgttga gccatttggc cccataggat ccaggaaccc360  
 aagtcctgtg ttctatcgtt actaccatgt gtcccgtagg ggagaactgg aaggtgcctg420  
 caggactgtg agtgatgtca gaattctgca aagctactac gatcaagaa actggtgtg480  
 gattcttcaa aaggcctgat tatttacctg aacacatcat atataagaa gaaatgctca540  
 cttaaaaaaa aaagagggga taaattaatt acccgtttaa ttaagagaa aacttgtggg600  
 gaagtacc 608

## (2) INFORMATION ON SEQ ID NO. 63:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2674 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN

0067395.122700



## (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

tgaagagaag ttaagggtgaa gagccgaaga gctgatgcg tgaatgagcgt ctaagaaagg 60  
 agaagcaaga gcagagaaga gagagagaaa gaacgggaga gagaagaggga agaaagagaa 120  
 aggaaaaagac gaagggaaga ggaagaaaaga gaaagagaaa gggctcgtga cagagaaaaga 180  
 agaaagagaa gtctgtccacg aagtagacac tcaagccgaa catcagacag aagatgcagc 240  
 aggtctcggg accacaaaag gtccagaaat agagaaagaa ggccgagcag aagtagagat 300  
 cgacgaagaa gcagaagcca tgatcgatca gaaagaaaac acagatctcg aagtcgggat 360  
 cgaaagaagt caaaaagccg ggatcgaaag tcataaagc acaggagcaa aagtcgggat 420  
 agagaacaa atagaaaatc caaggagaaa gaaaagaggg gatctgatga taaaaaaagt 480  
 agtgtgaagt ccggtagtcg agaaaagcag agtgaagaca caaacactga atcgaaaggaa 540  
 agtgatacta agaacgaggt caatgggacc agtgaagaca ttaaatctga aggtgacact 600  
 cagttccaatt aaaaactgac tgataagacc tcagatcaga cagaggttaac tgtattgttt 660  
 ctacatttga ttagggtctt ttgttactgt ttgacagctg acgctaagta tgcacagatg 720  
 aagatggaaac taagccgagt aagaagacat aaaaagacct ctctcgaaag aaaagacagt 780  
 gtgtctctgc aaaaacattt gaggtacatt gtttctctc agctattttg tagcagactc 840  
 gtgcccccat tagtgtgctt ctttggaatc tatcgccac attttgaata tagtcgccat 900  
 tgaaaagtta attatccttt ttttagggat ttgatgtca tttctttttt ttttttaata 960  
 aaaaagttga actgtttttt ttttctttt ttgtattaa tccatcttgt gttggatcat 1020  
 ttgcagagac atatgcttta aaaaacttaa tatttcggag gcacatgttg gactaatttg 1080  
 ttttaattaa actgtcagta tttctttgtc aagatgtttt ctatgttttt gctttattgc 1140  
 cttgcattct aatgcagttt gttctgtaac tcgagagcca gtacagactg atcgagaa 1200  
 gtgtagggtt tatgaattat tgcagctgac taccatacct cacacagcgt ttggtgtgtg 1260  
 agcggcccat gaaaagccaa attaaaaatc aaggatccag tcaaaactaa caggtactcc 1320  
 tgccaggtac tctctttctt acccacatcc atgtttgaat gctattgcct gtgactctta 1380  
 cgcttaacct ttgtgtatct ttttcttctc ttacaagaag tgcagagggg tttttgtgtg 1440  
 attgcgtgaa aacttataaa acaaatgtta acagaatgga attttttttc aactgtatgt 1500  
 agggctgcag tggctggccag aattagatat ctttaaaaga ttttaaatat aataaacact 1560  
 tcatattatt ccgtctgtta cactcaatgc aattctcaag tctataaag gtatgtgctt 1620  
 aatatttctt actgtgttag agaatttgca gtcagccata ggtatgtgag aatagtcact 1680  
 cactggctga tacattttaa gcagcagctg gaataagcaa gcagacaccc tcaattttgt 1740  
 gaaatcaaa aactgtatga cttatataga cgaatttggt tttttaaaga aatatataaa 1800  
 gttaggtact tcaagtgctt ttaaaacctg taaactctat tctgtgggt agtggtgtgtg 1860  
 gacaaaatat tctaatagaa aggaagtacc aattagtgtt tttgttggtg gcatctccct 1920  
 ttggggaaag caatgtaagg ttatgtctgt gtatgtcatt cacacttagg caagcataca 1980  
 caggcacatg gcttttaagaa ccacactgat gcttggataa taaaaaagaa tacaagactt 2040  
 ccatgtcacac atgttcaatta gcagtttagt actgggcccac cactttccca taaaaatgg 2100  
 ccttttcaat gttgtctaat tatcattttt ccccaaattt tgcgttgtag tcaactgttt 2160  
 cgaagatttt tggagaagaa ctgagaacgg catataaaga atcagtcagat ttttttata 2220  
 aggtgaaaga aagctatagt ggcataagaa agatataaag ctcatgtagt ttttaagact 2280  
 ttattattat taaaagttaa ttcaggactg atgtgacctc ccagatttca gaactatgtt 2340  
 taatagtata tatgccactg aaaaacttagg tctgtatcca taactgtttt tttaagactt 2400  
 tttagaagaa attactttaa catgtggctt gctcagtggt taattgcaag ttttcaatct 2460  
 tggaccttga aaacaggatt aaacgttagt attcgtgta atcgtgtgaa gtcggatttc 2520  
 attttacaaa ctctgctcta cttagccttt ggatttagaa gtaaaaaata agtatctctg 2580  
 actttctggt acaaaagttg ttgtcctctg catcgaaaag ttttagtatt aatcttttct 2640  
 taataaagtt attgactctg aaaaaaaaaa aaaa

2674

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 64:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 326 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

gacaaatgag ggtttggcat gcagctcgtc atcttaagag ttactatctt cttgccctgg 60  
 tgtttcgccg ttccagtgcc cctcgctgca gaccataaag gatgggaactt tgttgagggc120  
 tatttccatc aatttttccct gaccgagaag gactcgccac tccttaccga ggagacacaal80  
 acacagctcc tgcaacaatt ccatcggaat gggacagacc tacttgacat gcagatgcat240  
 gcttctgcta cagcagccccc actgtggggg gccctgatggg tccgacaact gcattctcgcc300  
 aggaagatgc aagtggatta agcaca 326

## (2) INFORMATION ON SEQ ID NO. 65:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 888 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

004221-562296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

ctcgtgctgggt gatgttgagc agaagatata attcaaaaga gaaacagcca gtttgaact 60
gttaccgccac cagcccccga tttgtggagat gaagaaagga agcaatggct atggttttcta120
tctgaggggca ggctcagaac agaagggtca aatcatcaag gacatagatt ctgggaagtcc180
agcagaggag gctggccttga agaacaatga tctggtagtt gctgtcaacg gcgagtcctgt240
ggaaccccgt gatcatgaca gtgtggtaga aatgattaga aagggtggag atcagacttc300
actgtrtgggt gtagacaaa agacggacaa catgtacaga ctggctcatt tttctccatt360
tctctactat caaagtcag aactgcccaa tggctctgtc aaggaggctc cagctcctac420
tcccactttct ctggaagtct caagtccacc agatactaca gaggaagtag atcataagcc480
taaaactctgc aggtctggcta aaggtgaaaa tggctatggc tttcacttaa atgcgattcg540
gggtctgccca ggctcattca tcaaaagggt acagaagggtc ggtcctgctg acttggctgg600
gctagaggat gaggatgtca tcattgaagt gaatgggggt aatgtgctag atgaacctta660
tgagaagggtg gtggtatagaa tccagagcag tgggaagaat gtcacacttc tagctgtgtg720
aaagaaggcc tatgattatt tccaagccta agaaaatccc tattgttccc tgcctggctg780
atgcagttg acagccctgc aggttctaaa gaaggaatag tgggtggagtc aaaccatgac840
tcgcacatgg caaaagaacg gggtgctatt gcagacggct aatttatg 888

```

## (2) INFORMATION ON SEQ ID NO. 66:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 202 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

atcacagggg tacaaccaga acacatacag tacttgaaaa attattttcca cctttggaca 60
cgacagttag cgcataatga tcaactactat attcatggcc caaaaggaaa tgaataacga120
acatcaaaaag aagttgaacc tttcaacaat attgatattg aaattttctat gtttgaaaaa180
gggaaggtrac ctaagattgt ca
202

```

00573395.122700

## (2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1225 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

ggccggtgga ggcggcggt ggcggcacgga aggggaagcg ctgaggcggt ggggcccaca 60
gccatggcgg agctgttgca ggaggagctc tcggtctcgg ccgcgatttt ctgcaggccc 120
cacgagtggg aggtgctgag ccgctcagag acagatggga ccgtgttcag aattcacaca 180
aaagctgaag gatttatgga tcgggatata cctctggaat tgggtgtcca ttggccagtc 240
aattatcctt catgtctacc tggatctcgc attaactctg aacagttgac cagggccocag 300
tgtgtgactg tgaaagagaa gttacttgag caagcagaga gccttttctc ggagcctatg 360
gttcctgagc tgggtctctg gattcagcag aatctcagcg atatcctcag ccaaccagaa 420
actggcagtg gcagtgaaaa gtgtactttt tcaacaagca cgaccatgga tgatggattg 480
tggataactc ttttgcattt agatccatgt agagcaaaag ctaaaatagt caaaaattgtg 540
gagaagtggg cttcagattt aaggctgaca ggaagactga tgttcattgg taaaataata 600
cttgatttta ctacagggag acagaaacaa cctcaaggtg tacttgattc ttacagaaac 660
ctccaaagta gatgtggact caagtggaaa gaaatgcaaa gagaaaaatga ttagtgtact 720
gtttgaaaca aaagtacaga cagaacacaa aaggtttctg gcatttgaag tcaaaagagta 780
ttcagcgctg gatgaattac aaaaggaatt tgaactgca ggaacttaaga agcttttctc 840
cgaatttgta cttgctctcg taaaatgaaa tggaaagcac gaatctttta gtaaaatagc 900
agtgtttttt gttgtttttt cattggattt ggggagtggt taattgaaat agtcaatttt 960
aaaagtcttc tgaagcaaaa tgataggcat cattctaaat tcagggaacaa aaagccagttc 1020
tgttttatga aatattaaac atgaagaaaa cttgtatatc ctaatgtttg ccaggaaaagg 1080
ctagggtcag tagatgagac attatttaaa agataaattt aaaaagatgg taaatgaacal 1140
cttggtttta tagacaatat ttgtttgaaa ctatgtaatt ttctggtcaa ttttctgtal 1200
attaaatgat tttttaaaaa aagaa

```

## (2) INFORMATION ON SEQ ID NO. 68:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1093 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

0066225.12700

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

gagggcgggc ctgtttccgg ggagggcggt ggggcttgag gccgagaacg gcccttgctg 60  
 ccaccaacat ggagactttg taccggtgtcc cgttcttagt gctcgaaatgt cccaacctga 120  
 agctgaagaa gccgcctcgg ttgcacatgc cgtcggccat gactgtgtat gctctggtgg 180  
 tgggtgttta ctctctcacc acgggaggaa taattttatg tgttattggt gaacctocaa 240  
 gtgtcggttc tatgactgat gaacatgggc atcagagggc agtagctttc ttggcctaca 300  
 gagtaaatgg acaatatatt atggaaggac ttgcatccag ctctctattt acaatgggag 360  
 gtttaggttt cataatcctg gaccgatcga atgcaccaa tatcccaaaa ctcaatagat 420  
 tccttcttct gttcatttga ttctgtctgt tcctatttag ttttttcatg gctagagtat 480  
 tcatgagaat gaaactgccc ggctatctga tgggttagag tgcctttgag aagaaatcag 540  
 tggatactgg atttgtctct gtcaatgaag ttttaaaggc tgtaccaatc ctctaataatg 600  
 aaatgtggaa aagaatgaag agcagcagta aaagaaatat ctagtgaaaa aaacagggaagc 660  
 gtattgaagc ttggaactaga atttcttctt ggtattaaag agacaaagttt atcacagaat 720  
 tttttttctt gctggcctat tgctatacca atgatgttga gtggcatttt ctttttagtt 780  
 tttoattaaa atatatocca tatctacaac tataatatca aataaagtga ttatttttta 840  
 caacctcttt aacatttttt ggagatgaca tttctgattt tcagaaatta acataaaatc 900  
 cagaagcaag attccgtaag ctgagaactc tggacagttg atcagcttta cctatggtgc 960  
 ttgaccttta actagagtgt gtgatggtag attatttcag atatgtatgt aaaactgttt1020  
 cctgaacaat aagatgtatg aacggagcag aaataaatac tttttctaat taaaaaaaaa1080  
 aaaaaaaaaa aaa 1093

(2) INFORMATION ON SEQ ID NO. 69:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```
cacaaagtga ttgtgggtat gaacaatat ggagagaagg caccagatga gttatggaat 60
tctctagggc ccacccctat cctgtgtgat ttcaaacac agacagcaaa caggatgaga120
aatcgactcc aggtcttttc tgaactggaa accaatgcag tgttgatggt agatgatgac180
acactcatca gcaccccaga cctgtttttt gctttctcag ttgggcagca atttctgat240
caaatgttag ggatttgttt cctagaaagc acgtctttta ctttcattca aggtatctac300
agttattgg                                     309
```

(2) INFORMATION ON SEQ ID NO. 70:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 380 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```
ctcatctgat cctttttatg gccaaatcat ccttcagagt agggaaacact cagacattct 60
gtgcatgttg ttcccccaaa gcatggtcac cacaaagtcc tgagttctgg tgtgtgctcc120
cgctctctgg gtatacagag agaaggcagg aatcaggagt tcacagaagca tatacatgtg180
gctaccccag caacaagcgg catcctgtgc tcagataagc tgcattggtg ggaagtgttt240
ttctctgcac gttgaggctt agtggagatg ggcaccactg ccatttggct agaagaaggc300
tggtctggtc ctaactgcac ccacacatgc ccagatcatt ctatgatagg tattttctga360
atgtttatag attttttara                                     380
```

(2) INFORMATION ON SEQ ID NO. 71:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1253 base pairs

0067305.122700

- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```

gcggcccgac  tccagtttag  agccttgatg  cgggagggga  cagtgggtcg  ccgagagcgc  60
ccggagggaa  ccgcttgccc  ttccggggacc  accaattttg  tctggaacca  cctcccgccg  120
gtatcctact  cctctgtccg  cgaggccatc  gcttcaactg  aggggtcgat  ttgtgtgtag  180
tttggtgaca  agatttgcac  tcacctggcc  caaacctttt  ttgtctcttt  gggtgaccgg  240
aaaactccac  ctcaagtgtt  cttttgtggg  gctgcccccc  aagtgtcgtt  tgttttactg  300
taggggtccc  ccgcccggcg  ccccagctgt  tttctgaggg  cggaaatggc  caattcgggc  360
ctgcagttgc  tgggctcttc  catggccctg  ctgggctggg  tgggtctggc  ggctcgacc  420
gccatccccc  agtggcagat  gagctcctat  gcgggtgaca  acatcatcac  ggcccaggcc  480
atgtacaagg  ggctgtggat  ggactgcgtc  acgcagagca  cggggatgat  gagctgcaaa  540
atgtacagat  cgtgtctcgc  cctgtccgcg  gccttgacgg  ccaactcgag  cctaattggg  600
gtctccctgg  tctgtggctt  cctggccatg  ttgttgccca  cgatgggcat  gaagtgcacg  660
cgctgtgggg  gagaagacaa  agtgaagaag  gccgtatag  ccatgggtgg  aggcataa  720
ttcatctggg  cagggtcttc  gccttggtta  gcttgctcct  ggtagggcca  tcagattgtc  780
acagactctt  ataacccttt  gatccctacc  aacattaagt  atgagtttgg  cctctggcat  840
tttattggct  gggcagggtc  tgccctatgc  atcctggggg  gtgcactgct  ctccgtgtcc  900
tgctcctggg  atgagagcaa  ggctgggtac  cgtgcacccc  gctcttacc  taagtcacac  960
tcttccaagg  agtatgtgtg  acctggggtc  tcttggcccc  agcctgacag  gctatggggg  1020
tgtctagatg  cctgaaaggg  cctggggcgt  agctcagcct  gtgggcaggg  tgccggacaa  1080
aggcctcctg  gtcactctgt  ccttgccatc  catgtatagt  cctcttggtg  tgggggtggg  1140
gggggtccgt  tgggtggaga  gacaaaaaga  gggagagtgt  gctttttgtg  cagtaataaa  1200
aaataagtat  tgggaacaaa  aaaaaaaaaa  aaaaaaaaaa  aaaaaaaaaa  aaa  1253

```

(2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 439 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

00673355.122700

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ctaaggggag gacaggcaga aaccaggaat gccaaacttaa acctgtttgg tgctctgact 60  
gtttgttagt atcactctca agaatgaaga gaaacctcaa cctttctgtt tccggccaac120  
tttattgaat ttgttttttt aaatgcagtt tacatgcagt ttctttgaaa agtcatgttg180  
aatttagatc tgttctctga gtaagacttg gcgagtatgt gaaacttgac tcaagttaca240  
tttctttttt tctgtccccc aaacgtttcac gcttctttata ggctccactt tgaggctctg300  
atgaacattc cagtgcctgt gttggatgtc aatgatgatt ttgctgagga agtaaccaaa360  
caagaagacc tcattgagaga ggtgggaagg accttaactc ctgtttttct ggtgggtttcc420  
ctttggttgt accttttaa

439

(2) INFORMATION ON SEQ ID NO. 73:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1252 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00673395-122700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

tggacctgcc cgacgacctg ctgcccagct tgcgccgcgt ggtggggccc aagcagctga 60
tcgtgctggg aaacaaagtg gacctcctgc cccaggatgc tcctgggtac cggcagaggg 120
tgccggagcg actgtgggag gactgtgccc ggcgggggtc cctgctggcc cctggcacc 180
agggccacag cgccccgtca aggacgagcc acaggacggg gagaatcoga atccgccgaa 240
ctggtccocg acagtggcta gggacgtgcg gctgatcagc gccaaagacc gctatggagt 300
ggaagagtgt atctctgccc ttcacgcctc ctggcgctac cgtggggacg tctacttagt 360
gggcgccacc aacgcgcgca aatccactct ctttaacacg ctccctggagt ccgattactg 420
cactgccaa ggcctccgag ccattcgacag agccaccatc tcccctggc caggtactac 480
attaaacctt ctgaagtctt ctatttgcaa cccaactcct tacagaatgt ttaaaaggca 540
tcaaaagact aaaaaagatt caactcaagc tgaagaagat cttagtggag aagaacaaaa 600
tcagcttaat gtccctcaaaa agcatgggta tgcgtagga agagtggaa ggacattcct 660
gtattcagaa gaacagaaag ataacattcc ctttgagttt gatgctgatt cacttgcctt 720
tgacatggaa aatgaccctg ttatgggtac acacaaatcc accaaacaag tagaattgac 780
tgacacaagt gtgaaagatg cccactgggt ttatgacacc cctggaatta caaaagaaaa 840
ttgtatttta aatcttctaa cagaaaaaga agtaaatatt gttttgccaa cacagtccat 900
tgttccaaga acttttgtcg ttaaacaggg aatggttctg tttttgggtg ctataggccg 960
catagatttc ctgcagggaa atcag-cagc ttgggtttaca gtctggcctt ccaacatcct1020
ccctgtgcat atcacctcct tggacagggc agacgctctg tatcagaagc atgcaggtcal1080
tacgttactc cagattccaa tgggtggaaa agaacgaatg ggcaggattt cctcctcttg1140
ttgctgaaga cattaatgtt taaaagaaag gactgggggg aacctggaag cagtggggccg1200
acatcaaagt ttcctctgca ggtaatttta tgccaagcac tttttaaaaa gt 1252

```

## (2) INFORMATION ON SEQ ID NO. 74:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 695 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

tggttcattgc ctccctgagcg tagtccagtt actttcaggc tcgggggagtg aaggcctcgt 60
tgagagaagg tctcatttcgg tgttttgga agagagtcgt gtggggccag gtatcgtagc120
ggcgacacga gagagacggg cgggtgtgaca gccttccact acctgcacga gtgtattggt180
ctgctctgcta tcagcttatgc cgtctgccgt tgcgtctgcag acccgcttgg ccaagagagg240
catcctcaaa catctggagc ctgaaccaga ggaagagatc attgccgagg actatgacga300
tgatcctgtg gactacgagg ccaccagggt ggagggccta ccaccaagct ggtacaaggt360
gttcgacctt tcctgctggg tcccttacta ctggaatgca gacacagacc ttgtatcctg420
gctctcccca catgacccca actccgtggt taccaaatcg gccaaagaag tcagaagcga480
taatgcagat gctgaagaaa agttggaccg gagccatgac aagtcggaca gggggccatga540
caagtcggac cgcagccatg agaaactaga cagggggcac gacaagtcag accggggcca600
cgacaagtct gacagggatc gagagcgtgg ctatgacaag tccagggaacg ggattcggga660
ccgcggttat gaccaagcag accgggaaga gggcc 695

```

## (2) INFORMATION ON SEQ ID NO. 75:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2514 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

04673395.1.22700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

cggcgacggc gggggggcag ctgggaaatcc ggaatgctgc cggatggccc tgggtctctg 60
ctgtggggca atccgggctt gcagacgagt tttagaaaga cggtttttcg tactgtaaagc 120
acattcgata aaggatatgg aaaataacttt gcagctgggt agaaatatca tacctctctc 180
gtcttccaca aagcacaaaag ggcaagatgg aagaataaggc gtagtgggag gctgtcagga 240
gtacactgga gccccatatt ttgcagcaat ctacgctctc aaagtgtgac agccccaagt 300
gtgttcatga ggtggagaag tggctgcccc ggctgcatgc tottgtcgta ggacctggct 360
tgggttagaga tgatgctctc ctacagaaatg tccagggcat tttggaagtg tcaaaaggcca 420
gggacatccc tgttgtcatc gacgcgggtga gttgaacttc ctctctctgg ctcggaactcc 480
cggaaggcct gtgcagtgag cagcgctcct tgttctgtgc aggatggcct gtggtaggtc 540
gctcagcagc cggccctcat ccatggctac cggaaagctg tgctcaactcc caaccacgtg 600
gagttcagca gactgtatga cgtctgtctc agagggcccta tggacacgga tgacagccat 660
ggatctctgc taagactcag ccaagccctg ggcaacgtga cgggtgtcca gaaaggagag 720
cgcgacatcc tctccaaagg ccagcaggtg cttgtgtgca gccaggaaag cagcagccgc 780
aggtgtggag ggcaaggggga cctctctctg ggctccctgg gcgtccctgg acactggggc 840
ctctctgtctg gaccacagaa aacaaaatggg tccagccctc tctggtggc cgcgtttggc 900
gctctctctc tcaccagcca gtgcaaccac caagccttcc agaagcacgg tcgctccacc 960
accacctccg acatgatcgc cgaggtgggg gccgccttca gcaagctctt tgaacctgal1020
gccgcgcgca accagaagta acagggcacc ttggacgggg gagagcgtgt gtgtgtgggg1080
aaaaatccgga cccacgcgtg tgcgtgaaggc gtacgggtgt tggcagatgt tcaacttggag1140
cataaatcgg ttgccattga gaatttaaga atctggaata ttgcagcttt tgggtaaact1200
taatgcgatg ttggagatgt tatggcgaca cttaacaaaag tattcctgaa ctttctcttag1260
ctccttggta gtaactggga agacagaaat agacagaaat acatgagaat gaaagaattct1320
ttagcagctc aacagagttt ctcggcctgc tcccagatgc gcgaagtctc tacttgttacl1380
tctctctgcc ggccgccttc gttctctctc tgcttccatt ccttagtctt toctccgggcal1440
gggagctggg caggggtccc cgggtgtctc cctgagtcct gactgcaactg actgggtccal1500
tcagagggct gcttctgtct ccagctctac ttctttttaa gtggtgacta gcttgggtgg1560
atctgctctg tgggtgttgg cttattgaca tactccaggg taatcaatga tgactttgtt1620
tggaaaaact tttggaggca ccatgggaac agaaggaaac atgagtgaac ctgaccttgg1680
agtgtgtggg tggggagctc tgagacgcct cctgtcccac gctctccggg gtccgtgtct1740
acacaggggt ccccatgata cccaccggcc cagcagggc agaccggacc ggggagcggg1800
acgggtgaag gctgcagcct ggggtctgac gtggccccta gtgctgtctc agggagaagg1860
tctggaggac ttgaggcatg ctgggccttg tgcaagtatg gcgctaagga gaccggggg1920
aagacagtat cgtggtcacg tatgcttagg aagcagcaca gccgtgtcct tagggatgt1980
cgcgtccagt aaagacactg gtaactgcgg tttagcccaa cactcttcat ggcagtgct2040
accttccggt agcttctgtt gtctttgtgt atggttttcc tggagcggcc tgacgttgac2100
gtgttctctg gtccccatgc tttagcggggc atggtacggt ttctgtgctg acgctgtgat2160
taggggtctc tcttataact tcagtagcat ctttccacag caaggcccaa accctctgg2220
ttcccttcag agtcttttgg ccctgatgat gactcttgag tgataccctg tgatgcagac2280
atgccccaga tggattctac ttctttttaa actaggactt ttcaagatta aaaaaaagat2340
tgctcaacta aatttgacgc ctaacttcag aagcttcaact gtctacatgt gaaactttcc2400
agaaaaactg tgccatggac atttttctc tggggaatta acatctaaat tctggttaact2460
attaaaagac agatctgggtt aatttaaaaa aaaaaataaa aaaa 2514

```

0967395-122700

## (2) INFORMATION ON SEQ ID NO. 76:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 274 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

cagagatctg ctgtgattat tcctttttcac aaaccacaat gactctggaa aacotggctg 60  
 taaacaccag cactgccacc agctaaggat ctgtgatcag gagtgccatc tcacggtaac120  
 aggcagaaga caaaagtcaa acogggctga tgcgaatcac tgggaaactg gctttggcac180  
 ctccagagaa tgaactgttt catagcctag ctgaccatcc atgaaaatgg ctgcctggag240  
 aggcagtgat cagcccatcc cctgcaaggt gaag 274

## (2) INFORMATION ON SEQ ID NO. 77:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 449 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

cgggttttagc ggcagctctt cgggattggt tccattgcc aacctaacgt gctggcctat 60  
 gaacgggtaca ttgcgcgggt ccatgccaga gtgatcaatt ttctctgggc ctggaggggc120  
 attacctaca tctggctcta ctactggcg tgggcaggag cacctctctt gggatggaac180  
 aggtacatcc tggacgtaca cggactaggc tgcactgtgg actggaaatc caaggatgcc240  
 aacgattcct cctttgtgct tttcttattt cttggctgcc tgggtgggcc cctgggtgtc300  
 atagcccatc gctatggcca tattctatat ttccattcga atgcttcgtt ggtgtggaag360  
 atcttcagac aattcaaagt atcaagattt taaaatatga aaagaaactg gccaaaaatgt420  
 gcttttaagt atattcactt tcttggtcg 449

## (2) INFORMATION ON SEQ ID NO. 78:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 346 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

atataacatc tgaattggga gatagctcat tgtggcctgg gtgctggact ttctcatatta 60  
 agtctctgtct tagccaaggg agaagaatgt aaggataaga ccaccaatat cacaggggct120  
 gtctgagcct ttacctgtga ttttgtacca ctctgtggcc ttctggagca atggacaacc180  
 aagtCagcta tgcagttcat aaaagtggac ctggttatat gtcatccaac agcatatggt240  
 ccttgcaagc ctgtttttgga agccaatatt ctataaccta caggaatcca cttgaatctg300  
 atgtcttttg aagcaatata ttttccagg gttccaatgg actacg 346

## (2) INFORMATION ON SEQ ID NO. 79:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

09672395-122700

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

cccccatca gttcgaaatt ctgcagtgag agcatctggg gttattgtga ccaactgaaa 60  
gtctcagaga gtacccacgt gctccagccc ttctccccc gcatccttga tggcttaatt 120  
cacctagcag ccaggttcag ctccagaggtc ctcaacctgg tcatggagac cctgtgcac 180  
gtttgtacag tagaccocga attcacagca agcatggaaa gcaaaatctg ccccttcacc 240  
atcgccattt tcttaaagta cagtaatgat cccgtcgtcg cctcaactggc toaggacatc 300  
ttcaaggagc tgtccagat tgaagcctgt cagggcccaa tgcaaatgag gctgattccc 360  
actctggtca gcataatgca ggccccagca gacaagattc ctgcagggct tttgtgcaga 420  
ccattgatat cctgacaaca gtgtacgaa atacaaagcc tcccccttcc cagcttctca 480  
tctgccaaagc tttccctgct gtggcacagt gtaccttca cacagatgac aatgccatca 540  
gtgcagaatg gcggagagtg cttgcgggcc tatgtgtcag tgaccttga acaagtagcc 600  
cagtggcacg atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag 660  
ctccttgacc cccgcacctc agagtctact gcggcctttg tgggcgcctc tgtttccacc 720  
ctcatctcca aggcaggggc ggaactcggg gagaatctag accagattct tctgtccatc 780  
ctcagtaaga tgcagcaggc agagacgctc agtgcacatc agtccctgat catggtgttc 840  
gctcatctgg tgcacactca gctagaacct ctcttgaggt tctgtgtag cctcccagga 900  
cctactcgca aacctgctct agagtgtgtg atggctgagt ggacaagccg acagccactg 960  
ttctatggac agtatgaag ccaagtcacg tctgtggcac tctgtaagct gctccagcat 1020  
ggcatcaatg cagatgacaa acggctacag gatctccgtg tgaagggaga ggagatctac 1080  
agcatggatg agggcatcgc caccgcgtct aagtcagcca aaaaccaga acgctggacal 1140  
aacattctct tgcctggtcaa gatcctaaag ctgatcatca acagctctc caacgtcatg 1200  
ggaggctaat gccgctccgc caggccactc ctgcagagtg ggagtcaaa gtcacgaag 1260  
gcccttact tcccaggaag accttttagcc tgggcagatc aagttacaaa tctgcaaat 1320  
atccaggaa 1329

(2) INFORMATION ON SEQ ID NO. 80:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 805 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

gcccccatca gttcgaattt ctgcagtgag agcatctggg gttattgtga ccaactgaaa 60
gtctccagaga gtacccaagt gtccacagccc ttctcccccga gcatccttga tggcttaatt120
caccttagcag cccagtttcag ctccagagggtc ctcaacctgg tgatggagac cctgtgcatt180
gtttgtacag tagaccccca attcacagca agcatggaaa gcaaaatctg ccccttcacc240
atcgccattt tctctaaagta cagtaatgat cccgtctgtc cctcactggc tcaggacatc300
ttcaaggagc tgtcccagat tgaagcctgt cagggcccaa tgcaaatgag gctgattccc360
actctgggtca gcataatgca ggccccagca gacaagattc ctgcagggtt ttgtgcgaca420
cccatgtata tcttgacaaac agtagtacga aatacaaaagc ctcccccttc ccagcttctc480
atctgccaag ctttccctgc tgtggcacag tgtacccttc acacagatga caatgccacc540
atgcagaatg gcggagagtg cttgcccggc tatgtgtcag tgaccctgga acaagtagcc600
cagttggcatg atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag660
ctcctggacc cccgcacctc agagtctact gcggcctttg tggggccgct ttgtttccac720
cctcatctcc aaggcagggc gggaactcgg ggagaatcta gaccagattt ctcctgtgcca780
tccttcagtt aagatggcag gaggt                                     805

```

(2) INFORMATION ON SEQ ID NO. 81:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 420 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

accagggtcaa gctcacccca aactattacc ttogatgcgt gtgttgtcat accctgtgga 60
gatctccaaa gtcaaaagca actgtcagac tcagagaagt atctgtgccc cttaaagatal20
aaaggctccc cctatcaaga ccttctgttc ttaacgaatg caggaaaaca ggtctgccat180
agctggaatg aggtggtgtg gacaactgaa tatcaaggct ggacctgtc aaccggtgg240
tgtatgtcct taaaaccata cattcacttc actaaagaaa gtacccccca taattgccag300
tataaccaat gtaatccagt gcaaatcttc attctcatc caactctac tgaccctaaa360
cctactttaa gttgcggtat atggcattgg agccgaata gcaggggcac atcttattgg420

```

00673305.122700

## (2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2143 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

000221-56527960



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

cgccgcgcct tttttttttt ttttttaagt tgaacagAAC attttatttc tcagcaattc 60
tatgcgtaca aattaaacat gagatgaata gagactttat tgagaaagca agagaaaaatt 120
cctatcaaac ccaaggagga ctcaaaagtga ggctggaaga ggacttaaga gagtatgaaa 180
gtactctaaG attttatcta agttgccttt tctgggtggg aaagtttAAC cttagtgact 240
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 300
cctgcctctg tgactgtgtg cctgtagtcC cagctactcg ggagtctgtg tgaggccagg 360
ggtgccagcg caccagctag atgctctgtA actcttaggc cccattttcc cctctgaaaa 420
taagagggtt ggatcaaacg atctctgggg ccttagcatc tcaaatcctg tggatctctc 480
tacttcccc tttagagagcc ttactgggaa gtcagtcatt aatgatgtgg ccagttattt 540
gcaagtggta agagcctatt taccataaat aatactaaga accaactcaa gtcaaacctt 600
aatgccattg ttattgtgaa ttaggattaa gtagtaattt tcaaaattca cattaacttg 660
atttttaaat cagttttgtg agtcattttc cacaagctaa atgtgtacac tatgataaaa 720
acaaccattg tattcctgtt tttctaaca gtcttaattt ctaaacactg atatatcctt 780
cgacatcaat gaactttgtt ttcttttact ccagtataaa agtaggcaca gatctgtcca 840
caacaaactt gccctctcat gcccttgctc tcaccatgct ctgctccagg tcagccccct 900
tttgccctgt ttgttttctg aaaaaccctaa tctgtctctt gcttttcttg gtaatatata 960
tttagggaaG atgttgcttt gcccacacac gaagcaaaGt aaataaagac cacaattgtt 1020
caaatcttaa gccacttaat agcgttttgt acattaaaaa tgacaagggt tattatacaal 1080
tagccttttt aaaaaattct cacaacagaa agctttgtat tttagactaa agctgttgct 1140
actttgtctg tgacgtttgt gttaacagtc agtgccttag gccattgtatt gattgattgt 1200
cagaatcaga agtgactaca caagagcatt agccagactt tttagtgaga acaggttaacal 1260
ggctggcacc agcacttggt acgacgactg gacaggacga cggaaaccag agttctctgt 1320
ctctctctca cagcagatgg actcttctat aggtggctgt taattttacac aaagtatatat 1380
tcagaatca ggaagccccc tgtcgccaaC acttgaaggA gaactatgtt ccagttttgg 1440
tgttgaactt ctcaagaaat acctactacc aaaaattgtg acaccttatt agacacttcc 1500
aaaagtacccc ccaaaaagctg tttaaaagac catttccattt tttcctacac aaagtgcatal 1560
ctaaaaattc acaataatca tcttcagatg tacattttat tttagtacatt tcacagtttt 1620
cagttattcg tccctcatga acattttata gtcatctctt cggccctgtt gtgaaatatg 1680
tgattccagt tcaatttcaga gtgtatgatt ccgcttttca cgtgatcaaa gtaattttat 1740
ggtgtctctt ttctgatctt caacattaaa aacatctatg ttctgtcatg tccctgccag 1800
ggctgtcttc ttgtctgtct cagattctgc ttcattttca tccatgttgt agtcatcttc 1860
tctctcagtt tctgtcgtgt ttctcccttc cccggcagct tctgtctctt cctcctgtcc 1920
ctcggggatg acaagctgggt ctgcctcagg gccctccatc ctgggatttt cctggctcac 1980
tgacagggca cctgcacctt gtggggtctg gccagtttct cccgtccccc cgaagcctct 2040
tcacactaca ggtctgtctt caacacctgc tcccggcctg gtcctgcggg cagcctgtcc 2100
ctctgaggct ccgatcaaca ctgatctcat ggttcccttc cca

```

2143

09573395.122700

## (2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 450 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

tttttttaaa gccagctttt cttcagattt ttttggtggg caggtcgtga aagacagggtg 60
aggaagtaga tcttgggctc agcatgcctc taaaagtata atttcttttt ttttaagtgg120
aaagaaatgc ataactctgt tctgttctct gtccccctct ctgcctctgt ggtgcctgag180
atactgggga tcccacagct gggggccactc agaggctacc aggaacgctt ccagtttgca240
tctggctgtt agtgccagga ccagaaaccc acagacctct tcacagacct cctgaccgtg300
atgtccctga agcctggaag gtgtccacac aatgaagcag aattgagtga tgggggtgtt360
tgtggaaccc agtgaaactg tgtaaacaca gtggaactgt gttaattttg agtggaaagt420
caagttccgt ggagttcatt gggcccgttt                                     450

```

## (2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 408 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

00673395-122700

- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```

tgcaactgtg caccagcgtt gccagatttt tccccattac acccccagtg tggcattatcc 60
ttgggtcccc gaggcacacc ccttgatctg tggacctcca ggccctggaca agaggctgctt120
accagaaacc ccaggccccct gttactcaaa ttcacagcca gtgtggttgt gcctgactcc180
tcgcccagccc ctggaaccac atccacctgg ggagggggcct tctgaatgga gttctgacac240
cgcagagggc aggcocatgcc cttatccgca ctgcccaggtg ctgtcggccc agcctggctc300
agaggaggaa ctcgaggagc tgtgtgaaca ggtgtgtgtga gatgttcagg gctagtcca360
accaagagtg tgcctccgat gtgttggggc cctaacttgg cacagagt 408

```

- (2) INFORMATION ON SEQ ID NO. 85:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 311 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

tacagttttt atcagtgatc acattttagt gtaatacatg aaactgaggc ttgatagaaa 60
acaggagaga aggcctagtg gcatggggta catagggaga tgaggggcaag catcaccaag120
gaggggcagt gagatagacg ctctcatgga ctgctgcttt acaacctccc tggagagcaal180
tttaaaaaata tgaatcaaga tccttttgat ccactaatca tccagaaaatc tacacagaaa240
tatgcacaaa aatatgtggg catccattga ctttccaacc tcttctcttt ccagggggaaa300
tattccttaa a 311

```

- (2) INFORMATION ON SEQ ID NO. 86:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 487 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual

00573305.1.22700

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

gtcttttgaa atctgtttcc actacagcta tggtaaatgc tatcagccgg tgctaccagg 60
agtcactgcc aggggtgccc ttctcctgaa cccagtgagg cagaatcata agccctgacc120
ccatccctag aaagatgagg tcccagcaat ggccagagca tttctcacca gttctgtgag180
atagcacata aaaatagagt tctttgggca aaacttttgg gaagcaatgc atctcatatg240
ggctgatatt cagcctgagc tgttctcaag aggagagtgg tactggcagt ttatgggtga300
aatccattct gattgggtgg agtctatgct ataccagtgg ttaaacattt tgagtatcac360
tcttgcatat tgttactatt atatttcctc tatatataga cagaaaggcc atttttagga420
tattaaaggc tctgaaaatt tctgcagtag acccaactga aggttctatt aaggcagggt480
tcctaaa                                         487

```

(2) INFORMATION ON SEQ ID NO. 87:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1902 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

gaggaaaaag aacaatgaac agcaacgata ttgactgtgc aactcagaca ttcctgcaga 60
aaagacatat gttgctttac aagaaggcca aagaactatg gggccttccc agcatttgac 120
tgttcattgc atagaatgaa ttaaatatcc agtacttga atgggtataa cgcattgaatg 180

```

00673395-122700

```

tgtgatttta ttaggggcat ctgccaatc tctcactgtg gttccttctc tgaattttgcc 240
tggttcacat ctaaggaggc tagatccttc gctgaattca ccattcctca aacctgttaag 300
ttttctcact cttccaaatt ggctttggct ctttcttcaa cctttccatt caagagcaat 360
crtttgctaag gagtaagtga atgtgaagag taccacactac aacaattcta cagataatta 420
gtggattgtg ttgtttgttg agagtgaagg ttctcttgca tctgggtgctt gattaaggctt 480
tgagtattaa gtctctcagc tatctctcta ttgtcttgac ttgagtttgc tgcattttctt 540
atgtgcttgt cgtgacttgg agaacttaaa gtaatcgagc tatgccaaact tgggggtgta 600
acagagtact tcccaaccaca gtgttgaaa ggagagcaaaa gtcttatgga taaacctctc 660
tttctttttg ggaacacatg cttctcactt agaagctcac ctgtgctgaa tgtccacatg 720
gtccactaaa atgtttatct taaaccccc gtagcctga gttgaaaggg ctctctctta 780
ttaggtttttc atgggaacat gaggoagcaa atctattgct aagactttac caggctcaaa 840
tcatctgagg ctgatagata ttgactttgg taagacttaa gtaaggctctt ggtctcccag 900
ggcataagca acagtttctt gaatgtgcca tctgagaagg gagaccagg ttgtgagttt 960
tcctttgaac acatttgtct tttctcaagg ttctgtcctt gctagaactgt tagctctttg 1020
aggacaggga ctatgtctta tcaatcacta ttattttctt gttacctagc atgggacaag 1080
tacacaacac atatttgtgt agtcttctaa aagactcctc tgattggggag accatactat 1140
taattgggat gtgaatcatt tcttcagtgg aataagagca caacggcaca accctcaagg 1200
acataattac tactatgaac attttactgt gagaactctt attttgcctt ctacttgcg 1260
tgaatatgaa ccaaaacagg ccgttggggt ccacaaagta atatatgtt gatgaggatt 1320
ctgttgctctt attgggaact ctgagactta tctgggtatga gaagccagta ataaacctt 1380
gacctgtttt aaccacatgaa gattatgaat atgttaatat gatgtaaatt gctattttaag 1440
tgtaaagcag ttctaagtgt tagtatttgg gggattgttt tttattattt ttttctttt 1500
tgaataatca tgagggatct tttgataaag ttagttaatc atgttagatt ttagttttg 1560
aagcatgttg tttttcaaat atatcaagta tagaaaaagg taaaacagtt aagaaggaa 1620
gcaattatat tattctcttg tagttaagca aacacttgtt gagtgctctg tatgtgcacg 1680
gcatggggcc atatgtgtga ggagcttgtc taattatgta ggaagcaata gatctcggtat 1740
gttacgtatt gggcagatgc ttactgtatg aatgaaagaa catcacagta atcacatat 1800
cagagctgag ttatccccag ttagctcttg ttggggatcc cagtttcttg gaacgagagt 1860
tagggccatt ttatttaaaa gaaactcccg gttgagaccg gt 1902

```

## (2) INFORMATION ON SEQ ID NO. 88:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1048 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

ctcaccgtcg tctacaccgt gttctacgcg ctgctcttcg tgttcateta cgtgcagctc 60  
 tggctggtgc tgcgttacgc ccacaaagcg ctcagctacc agagcgtctt cctctttctc 120

tgcctctttt gggcctcccg gcggaccgtc ctctctctct tctacttcaa agacttcgtg 180  
 gcggccaatt cgtcagccc ctctgtcttc tggtgctct actgcttccc tgtgtgctg 240  
 cagtttttca cctcaccgt gatgaacttg tacttcaacg aggtgatttt caaagccaag 300  
 tcaaaaatatt ctccagaatt actcaaatat cggttgcccc tctactggc ctccctcttc 360  
 atcagccttg ttttctgtt ggtgaattta acctgtgctg tctgtgtaaa gacgggaaat 420  
 tgggagagga aggttatcgt ctctgtgcga gtggccatta atgacacgct ctctgtgctg 480  
 tgtgccgtct ctctctccat ctgtctctac aaaatctcta agatgtcctt agccaacatt 540  
 tacttggagt ccaaggggctc ctccgtgtgt caagtgactg ccacgtggtt caccgtgata 600  
 ctgctttaca cctctcgggc ctgctacaac ctgttcatcc tgtcattttc tcagaacaag 660  
 agcgtccatt cctttgatta tgactgggtac aatgtatcag accagggcaga tttgaagaat 720  
 cagctgggag atgctggata cgtattattt ggagtggtgt tatttgtttg ggaactctta 780  
 cctaccacct tagtctgtta tttcttccga gttagaatc ctacaaagga ccttaccaac 840  
 cctggaatgg tccccagcca tggattcagt cccagatctt tatttctttg acaaccttcg 900  
 aagatatgac agtgatgatg accttgccctg gaacattgcc cctcagggag ttcaggggag 960  
 gttttgctcc agattactat gagttgggga caacaaacta acagcttctt ggcagaagcal020  
 gggacttttg aaagcctcaa agtttggga 1048

## (2) INFORMATION ON SEQ ID NO. 89:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 804 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

gcccccatca gttcgaattt ctgcagttag agcatctggg gttatttgta ccaactgaaa 60
gtctcagaga gtacccaagt gctccagccc ttcctcccca gcctccttga tggcttaatt120
cacctagcag ccaggttccag ctccagaggtc ctcaacctgg tgatggagac cctgtgcatt180
gtttgtacag tagaccccca attcacagca agcatggaaa gcaaaatctg ccccttcacc240
atcgccattt tcctaaagta cagttaattgat ccgtctgtcg cctcactggc tcaggacatc300
ttcaaggagg tgtcccgat tgaagcctgt cagggcccaa tgcaaatgag gctgattccc360
actctgtgta gcataatgca ggcgccagca gacaagattc ctgcagggtt ttgtgcgaca420
gccattgata tcttgacaac agtagtacga aatacaaaagc ctcccccttc ccagcttctc480
atctgccaa gctttccctgc tgtggcacag tgtacccttc acacagatga caatgccacc540
atgcagaatg gcggagagtg cttgcggggc tatgtgtcag tgaccctgga acaagtgc600
cagtggtcatg atgagcaggg ccacaatgga ctgtggtatg tgatgcaagt ggtgagccag660
ctcctggacc ccgcacctc agagttcact gcggcctttg tgggcgcctt tgtttccacc720
ctcatctcca aggcaggggc ggaactcggg gagaatctag accagatttc ttcgtgccat780
ccttcagtta agatggcagg aggt                                     804

```

## (2) INFORMATION ON SEQ ID NO. 90:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 581 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

tctttgatca gatttagtgt cttaggtaat taaatcagaa agtctattta gctattctag 60
aagtgtatgt gtaggatttg ggtggttggg gttcttttag cgaacttgct agaaaactcca120
ttcttaacat cagaatcagg gcaggattga aaacatttgt gctggatctt gaaattgtcta180
taacatctat tgcagaaaat gataggtcag atggatagca ataataata tatatcagat240
cttagtaaca aaattaccaa gctttatcta gtggatatat gtaaaagaat attttttaaat300
gtccagcatt gatgtatttt ctttaagaat tattacagta tataagcatt ctttgggaat360
acagataaaa aacataaaatt ttttcgtatt ttttaatttt tttatttttt tgggtcaagga420
tgaatccccc cctgtaaaaa attgattttc gcctaaattt cgggggtttcc ctggcacata480
atagcaactg ccccaacttc ggagatggcg atgctgggta aaaaagccaa aggatggatg540
gggatccgga aatactgtgt ggaatggaag cgaatccaat a                                     581

```

0967395.122700

## (2) INFORMATION ON SEQ ID NO. 91:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

tggagatatt agtcagtttc tttagtata ttgttttcc tgaagtgcct ttttgttttt 60  
 ctttgggggtt ttttgaatcc ggaatgctgt gaagggaat agcagactcc tccagctaa 120  
 agacaggaca tgttcttgag ccactgtagc tgttgaagt ggacaccaga cgctcccat 180  
 aacccccccg ccaggccata cgtgtgatgc atgtgcactt ccacccacag aggaggggtg 240  
 gaagccttga gaacctcaag aaagggctgg attctgccat acctttgggt ctaccttggg 300  
 actgctgggt gccaaagtgt caaccagcct gtgttccctg ccacccacgc acttgcctga 360  
 gtgtggctga ggcagaatac tgtgaatggg tgcacccaag gaggtaacgg ccttgccttg 420  
 agaagaaata cttttagcac atgaaaggga aagaaacgtgc accctttttt tgtttcttta 480  
 gtgaatgcaa gatttaataa aagtgaataa tgagcttccc ctttggggagt ggagccca 540  
 gcagctcact gacaggggtg acatcagtat gatgtgttgg actgaaactg tatgtctgta 600  
 ggtaggtgtg tgcctttttg ggcagaccac ggtggccacc ccatttctcc aaggtgtgtt 660  
 accctagctg tgtatatagg acattgccac cctcaccctc ggccaaaaat tcttgattta 720  
 aaaaagaaag tctatttttg taacgacagg ctctgttcta tgtgttacta tcccaagcct 780  
 ggattatttt attttattaa aagtatttta atttccatat tggctttatt ctaatcccat 840  
 ccattccctgt ggagctgcag agcatcttca tgtgagtaga cggatggaca taaatagatt 900  
 catgctcatt taggaagctg ggagtttcgt gaagctgagg gtgagttcct gtgattcttg 960  
 ttcgcttcaa caaaaagtgg gagaccaagt ttttatagca ttttatagca ttaattgtta 1020  
 agtcttgaat gcagaaaaaa attaccctag ctttcttaag ccttaggggtt ttgtgaggt 1080  
 tcaagtgttta gcacagctgt tggcacatag taagccctag taaatgttaa atattgttat 1140  
 tagtgtttcg taaaacttga gaaatagagc tgagctcatt ccttctctgt tgattcaaaa 1200  
 ataataccta catgaataca tgaattcgaat ttgttagaat ttgttagaat ttactgtatt 1260  
 agagttagcc agttctcggc ctaccctgct ggttgggcat ttactgtatt cttgaatgca 1320  
 ctggtttgaa aatatgccag acttcaagccc ccaaggaaac aaggtgcgaa gaatttatga 1380  
 actccagctg gaaaaggtaa aggtgacctt tggctagcca catactggac cttaacccac 1440  
 tgcagctctt cagaacattc caaggggtttt cctcaaggaa catttttgag ctagaataat 1500  
 aaatgggttc tctggcagac tgcacccctt gagtcaaat taacagtatt ccttgaatg 1560  
 caataataga ggtctttctg cgttaaggga gaaggaaatg ccaattgaa ccttgcctg 1620  
 cccagggcagg tcccttttgc ggcccttaca ggtcgggggt gccctcctg tctcaggga 1680  
 tcagactccc agactgggta gttctgcagt ttccatcaa attaaaggtt attccctggc 1740  
 cgctcctctg agaaaaccga cccacacctg cgaagtgggg gcaatggggc agggattttg 1800  
 gcctctcaga acagctccta gaggctgctc atgactgaat gttttcccaa atcacctaaa 1860  
 tatcggtttt ctttttgggt tgggggagag gatttagcct cttactcccc tgatgattc 1920  
 aaagtcttat ctatctcctt atctcctgac ctgtcttggc acaactctgg atagattgca 1980  
 ggtgtggaat ttgctggagt ttggtggctc cccaaattcc ttgatctgtc cgcaagaga 2040  
 ag

2042

09673395.122700



## (2) INFORMATION ON SEQ ID NO. 92:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 430 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

gttaaaaaacc tagtattcat tttttttttt cctgtaccaa aacaatcacc ttccttttatt 60  
 ttctctggag cggaagagag agagtggaga agaagggaag aatgcgaaagt gtcactttgal20  
 acttcctcgt caccacacac gtgggagtc accatgtca gcagcctccg tgcacaggcc180  
 ccaggtgaaa gaaagaatga ggtctagtgt gaccagctaa cactgcctgc cttgtgttta240  
 cgaaaggcag ctgcctctgt ggtgtgattt caggggagcc agacagggcc ggggccacga300  
 acctgcaccc tgcaccccaa gcacctattt gccatgcggt gaggetaac ttgggaaact360  
 tcaatttgcg tggggtgcag attagcttcc caaactattg tgatgctcat gcttgacttc420  
 ccaaggactt 430

## (2) INFORMATION ON SEQ ID NO. 93:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 592 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

00673395 122700

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

aattaaaata aatagaaaca tacggagatt cttttatgtt ggatttatta taccctccac 60
catttttgct cctgaaaagg gaaaagatac acggctcgagt agtacaggta tgtgtttccc120
actacacatt atggctataa tggagttgaa ttgcaaacag taataattttg ttttggtattg180
gtttcccttg atccccccag acaggagctt cctctccac cctacotgcc tgccttaag240
ttgtgtccta ttaaaactgga cacaaatctc acogggtttt agtotaataa ttgaatcata300
gtacacacag gtgacacagg aatagctact tgttttttta tgttaccaat gagtaacttg360
tttatccctg tatgtagaaa ctaatttcac catgatcaca gatctgtgta acatctctag420
tttgatttc cacacaattt taaaatgtct actaggaaaa cttacacott tttgtccaa480
gggtgctctt catctattaa aaccgtgggg gcataactcc agtgttgott ctgaggggcca540
aattttgtgg gtctgtgggg acaattttgt attaacatac gttattttgt aa 592

```

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 674 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

aaggccgcgc aagtgcactt gcgtgtcacc gttacogtag cgactggggt tctggactgt 60
atatccctagc tgccttgcca acatcttoga gcctcggcag ctccggaggc cggggtaact120
ggcagcaggt aggaacatcat gtgaaagaat ctccgtgatg cataatttcc ggggtgcacc180
ggaacatttg atcatcattc ctttggcaat tccagccttc tgtggaaaagg ccagtagaaa240
gcattgattt attcactctc acaggaaatca gactcagcct cttttggttt tcagtgaaagt300
atgccttttc aatttggaaac ccagccaaagg aggtttccag tggaaggagg agattcttca360
attgagctgg aaacctgggct gagctccagt gctgcctgta atgggaaggga gatgtcacca420
accaggcaac tcceggaggtg cctcggaaagt cattgcctga caataactga tgttcccgct480
actgttttat gcaacaacgag aaagccacct gcacaaagca gcaaggaaat gcactcctaa540
tagcaccatt aagtcctttg tcaaggtctg actaggttcaa gggtaattga ccagtatcat600
ctggtgatct ggttaacaaa taaaagtgtt ggcaccttta gatgatgaaa aaaaaaaaaa660
aaaaaaaaaa aaaa 674

```

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 95:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

gtttttttca ttccatcact ttaggtgatg ggtaagattt ttgaaagcct tatatTTTTT 60  
 gattttgttg tctagtTTTaa tcctaccttt aatagttgtg ttgggtaaaa ttccacttTgl20  
 aatgtgacac tgataataat tatgttgatt tttagcatct cttataggaa tcaaaagtttal80  
 ttaaagttaC atagaggatt gaaaaatgta tatcactcaa tttttatcta aggaggggata240  
 ggggtataaa ggagggtacct aaatagctca aataatggat ataatccttt ttccataac300  
 catttgggat gctttaaggc aatt 324

## (2) INFORMATION ON SEQ ID NO. 96:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 709 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

09673305.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

ggatgcggca ctataacatc ccogtcagag tgtgtgagga gaccagtcta tgagagacgc 60
atgctcctga cagcctggcg acgtggcgaa gatgcacagg tggctcctgg gcttgggctg120
caggttttggg ggtctctaag aacaatctct gagaagaacc ctggggcccc tgggagccaa180
gttggacagg atgtcctgaa gactagcttt tgataagaga aattaaccaa gtctttcccc240
tcattctatga tgcaatatat ttcatgtggg gccttcagag cacacctgtt ggacggtgca300
aaccatattct tctccagaag gcaaatactt ttgtatcaga ggaaactcag ttttgggagag360
gaatatgttc tttatatctc aaatcaaaac tctctctaag ggtaaactgg cttctaattt420
ttttaagtac agtatctttt tttccccctt agtagtaacg ggtttctata gatcttctta480
tacagtctgc ttttaactcag gaccttgaga ttatgagact gacgtgtctg ccaactgcact540
gagggggctt ctaacagctc gctttaagtg gtataattct gggatagatt tggtactggc600
atagtcatga caacctctgg taatcttacc tctctctttt tatgaaggga agagcaatgg660
tttggactta catctaaatt aaggctattt taagcagatt gttttgcaa 709

```

## (2) INFORMATION ON SEQ ID NO. 97:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 562 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

gtccagatgg aatgactccc atcctctcct catctccctt ttgacgagcc tcaaaactgct 60
cagctcatca aagagccatt gccaaacttc gtatgtgggt ctgggtccca gggagccttg120
gaaccttgca cctctgggtg gtttaattcc ggacagagag catctcctgt tctcaaggga180
cacagtggcc tgcatgggcc agcatggacc ctgggctgat catgtgcatt cctgcttctc240
tggggacaca gtgggcccac atggggccagc atggaccctg ggttagagca agcacattct300
catctcttcc acctcaggca gtgtggctcc agatgtcagg agggactgac ctcaggacct360
tccagtttcc tctgtgccag gaatgagagg ccaggcccca tctaccacc tcgccttgac420
cctgaagtcca gacgaggcca gccaaagcag aagcacactg ttttaatttt tgcattggaaa480
gtaaattgtt actttgatag ggttaaaata tggctttttt taagtgtgct aaccccataa540
tttgagccat tgccttgctt aa 562

```

09673305.122700

## (2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1948 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

gataccacaa acacacaaag tagaccttgg gctcccagag aagaaaaaga agaagaaagt 60  
 ggtcaaaaga ccagagagact gatactcagt tttaaacaaat gatgattact ttgctgatgt 120  
 ttccctctta agaggtacat cccctcttaa gagtgtgtgcc catgggcagg cacctgagat 180  
 gcctctagtg aagaaaaaga agaagaaaaa gaagggtgtc agcaccccttt gcgaggagca 240  
 tgtagaacct gagaccacgc tgcctgctag acggacacag aagtcaccca gcctcaggaa 300  
 gcagggtgtt gcgaccttgg agttcctcag tggggaaaaa aaaaaataga agtcacctct 360  
 agccatgttc catgcctctg ggggtgaaac ctccccagac cctagacagg gtgaggagga 420  
 aaccagagtt ggcaagaagc tcaaaaaaca caagaaggaa aaaaaggggg cccaggaccc 480  
 cacagccttc tcggtccagg acccttgggt ctgtgaggcc agggaggcca gggatgtttg 540  
 ggacacttgc tcagtgggga agaaggatga ggaacaggca gccttggggc agaaacggaa 600  
 gcgggaagag cccagagaac acaatgggaa ggtgaagaag aaaaaaaaaa tcccaggga 660  
 gggagatgcc ctcccaggcc actccaagcc ctccaggctc atggagagca gccctaggaa 720  
 aggaagttaa aagaagccag tcaaatgtga ggctccggaa tacatcccca taagtgtatg 780  
 cctaaggccc tccgcaaaaga aaaagatgaa gtccaaaagg aaggttagagc agccagtcac 840  
 cgaggaggcca gctctgaaaa ggaagaaaaa gaaggagaga gagagtgggg tagcaggaga 900  
 ccccttggag gaggaaacac acacggactt agaggtgggt ttggaaaaaa atggccaacat 960  
 ggatgagggg cacatagacc aggtgaggcg aaaggccttg caaagaagaga tcgctcgccal1020  
 gtcaggcaaa acggaagcct ctgaaaccag gaagtggagc ggaacccagc ttggccagtg1080  
 ggatactgct ggttttgaga acgaggacca aaaaactgaa ttctccagc ttatgggtggl1140  
 cttcaaaaac cgttccctct cgttcagccg ccccgccagc acgattgcaa ggcccaacat1200  
 ggccctcgcc aagaagcgcg ctgacagcct gcagcagaat ctgcagcggg actacgacgg1260  
 ggccatgagc tggaaagtaca gccgggggagc cggcctcgcc ttctccaccg cccccaacaal320  
 gatctttttc attgacagga acgcttccaa gtcagtcaag ctggaagatt aaactctaga1380  
 gttttttccc cccaaaactg ccacaattgc ttgtgattat ccatttatgc tggagattac1440  
 aaattttttt tgtgaaaaaa tcagatcttg gtgaggacct cgagcagtaa gatataaatal500  
 actccataaa gcttagcggt ccagtaatgg aacactaggc ataaatggtt tattcagtg1560  
 tgcaaatgaa agccatctga cagttggctc acattgaaca cctgtggaga ttaaggacga1620  
 ggacaacatg attgatgggc ttggatgaac tggggcaggg cagctcatat ttccggagcc1680  
 aggaagaacga gtgagtgcata aaacctctgt tttctgtgt taaacattcc gtccctggt1740  
 gagacatcaga tatgtacagt taacttttgt tgagtgttta gcagggtacta gggacatact1800  
 agtgttttcc ttaatgtatt taactctcat ataatgaaa ttatgtgctat tattagcccc1860  
 atcttataga tgaggcaact gaggttcagg gataaagtaa taaaattgcc tgggggtccall920  
 cagccactaa aaaaaaaaaa aaaaaaaa 1948

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 483 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

aatttatggg gtctatcttt gaccacgtga taccacttac ctgattctat gtactgatta 60  
 atgtatctaa cagtttttata gtgaaagtac tttttaaaaa agtatttgaa tggtcatttc120  
 tattttttccc cctttgctgt acaagttaat ttttactcat cttttgctgt acaaatatac180  
 ttccatcaat acaataaaga ggctagtgtt aagtcattt atttgcatg agcccaggaa240  
 caattaaatt ctataaagta atgtattaaa atagtacact ttaaaaaatta ttttccctct300  
 ttttttctct ttaaatatta agaccatcat aataaattat cattacaag tcacaacatac360  
 tatatactac tatcagtcac tggggaaaaa ataagtcct atgtttttatg ggtaaaatgc420  
 tgtaatatag tgggattgtc caatttgctt tgaaaaaaat cacagcagtt tttaggtttc480  
 cct 483

## (2) INFORMATION ON SEQ ID NO. 100:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 437 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

09673395-152700

- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

cccgccttgag cgcgtaggggg tggcgctctc cgcttcggcgg cgctcccatg gcgcacatta 60
ccattaacca gtacctgcag caggtgtacg aagccatcga cagcagagat ggagcatctt120
gtgcagagtt ggtgtctttt aaacatcctc atgtttgcaa cccacgactt caaatggcct180
ctccagagga gaagtgtcaa caagtcttgg aacccctta tgatgaaatg tttgcagctc240
atttaaggtg cacttatgca gtggggaatc atgaactcat agaggcatac aagtggcaga300
ccgtgatagt ccaatcatct ttgcgagcat tccaggccca caaagaagaa aactgggctc360
tgctgtcatg tatgcagtag cgcttgacct ttcgagtgtt tgccaataat gcagttcaac420
cagttgggta aggaag

```

- (2) INFORMATION ON SEQ ID NO. 101:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 359 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

cagatctagg ggcttcagct gtgtgcagac cccatgccac ttcagggaag tgacacaggg 60
ctgtgtcatc tgcctttggc agcagggtggg tggccttctc caggggaggga ggtggcctgal20
gatgtgtttc aggtctttga cccatcacct cctacacaca cgacgtgaac accactctct180
gagcattctc agaatggaga tttgaattcc atgtggcagc ttctcacaca caaacctgcc240
atcattcccc acacaccacac tcacgacatt caacagccat gagccaaaag aagttccttg300
tttcagattt gaaggtttta tgaatccact tcttcgggat gtactctttt aatgatatt 359

```

- (2) INFORMATION ON SEQ ID NO. 102:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 501 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual

00673395-4-22700

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

tcggcgctcac atcctgagtc ggcgctctgc cgaggcggag cggacatgca ggctccccgc 60  
ggcaccctag tcttcgcccct ggtgatcgcg ctctgtcccg tcggccggga accttctagc120  
caaggatctc agagtgcctt acagacatat gagctgggaa gtgaaaaact gaaagtccct180  
atctttgagg aagatacacc ctctgttatg gaaattgaaa tggaagagct tgataaatgg240  
atgaacagca tgaatagaaa tgccgacttt gaattgttac ctaccttgaa ggaagagaag300  
gaatcaaacc acaacccaag tgacagtga tcttaaactt gaatggcgct catgttttcc360  
aagagaagca gcccctgagg gagtctgctg aggcgtgccaa cagaggatga agaggataca420  
aatttaatta atttcaaacc aacatagaca caagaacctt ttgctgtttc ttccaacgcc480  
cactcttctc aatgatggca t 501

(2) INFORMATION ON SEQ ID NO. 103:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1102 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00673355-122700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

cgggatctcc cgaaggaatt tacgggggatt cctcggacca ttatcctcag gcaagaaaca 60
aaacccaaact tggactctcg tgcagaaaaa gtagccatt accacatgta gccttggaga 120
cccagggaag gacaagtaca cgtgtactca cagagggaga gaaagatgtg tacaaaagat 180
atgtataaat attcatttta gtcattccta tatgaggagc cagtgttgca tgaatgaaa 240
atggtatgat tctacatatg tacccattgt cttgctgttt ttgtactttc ttttcaggct 300
atttacaatt gggagatttc agaacaattc ctttcaccaa catttagaaa tggtttgctt 360
taatggagac aatagcagat cctgtagtat ttccagtaga catggccttt taatctaagg 420
gcttaagact gattagtctt agcatttact gtagttggag gatggagatg ctatgatgga 480
agcataccga ggggtggcctt tagcacagta tcagtaccat tlatttgtct gcgcttttta 540
aaaaataccc attggctatg ccacttgaaa acaatttgag aagttttttt gaagtttttc 600
tcactaaaaa atgggggcaat tgttagcctt acatgttttg tagacttact ttaagttttg 660
acccctgaaa tgtgtcataa caatttctgg attcataata gcaagattag caaaggataa 720
atgccgaagt cacttcattc tggacacagt tggatcaata ctgattaagt agaaaaatcca 780
agcttttgctt gagaactttt gtaacgtgga gagtaaaaaa tatcggtttt attcctttgct 840
gatgtccttt ctgcttgaaa taacagtcac catcacagcta aaggagagga gttctcttcc 900
ttctaagtag gcagaaatgg tatcattatg ttgcgctctt ccaatctccc agagctcgct 960
ctctaagaaa tcacctctct tcgcgttttt tttttttttt gagggttaga gtctcactat1020
ttgtgccccg gactaggcctt ggggaactgtt ggggggcca ggggattgct cccgtcccgc1080
aggcctcccg agtagggcgg ga 1102

```

## (2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 306 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

gaccaacott ccttgccatt tatacggcat aaaaccctca atctcaccag tatggctacc 60
aaaattatag gttcacctga aacaaagtgg attgatgcga cttctggaa ttacaactca120
gaaaaatctt caaatctatc tgtaacaact gattttccg aaagccttca gagtctta180
attgaaatcca aagaaatcaa tggaattcat gatgaaagca atgcttttga atcaaaagca240
cttgaatccc attttttttg aaaaacctta aaaggggcga tcacaatttt ttggaacaag300
ggatcat 306

```

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2042 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

tggagatatt agtcagtttc tttagtgtata tttgtttcct tgatgtgcct ttttgttttt 60  
 ctttgggggtt tttggaatcc ggatgtgtgt gaaggccaat agcagactcc tccagctaaag 120  
 agacaggaca tgttcttgag ccaactgtagc tgttgaagct ggacaccaga cgctccctat 180  
 aacccccccg ccaggccata gctgtgtatgc atgtgcactt ccacccacag aggaggggtgt 240  
 gaagccttga gaacctcaag aaagggtctgg attctgccat accctttgggt ctaccttggg 300  
 actgtcgtgt gccaacgctgt caaccagcct gtgttccctt ccacccacgc acttgcctgag 360  
 gtgtggctga ggcagaaatca tgtgaatggg tgcattccaa gagttcaggg ccctgtcttgg 420  
 agaagaaata ctttagcatc atgaaaggga aagaacgtgc accccttttt tgtttcttta 480  
 gtgaatgcaa gatttaataa aagtgaataa tgaagctccc ctttgggagt ggagcccaagt 540  
 gcagctcact gacaggggtg acatcagtat gatgtgttgg actgaaactg tatgtctgta 600  
 ggtaggtgtg tgcctttttag ggcagaccac ggtggccacc ccatttctcc aaggtgggttt 660  
 acctagcctg tctatattag acattgccac cctcacctctt ggccaaaaat tcttggattta 720  
 aaaagaaaag tctattttgt taacgacagg cctcgttgtta tgtgttacta tcccaagcct 780  
 ggtatttttt atttattttta aagtattttta atttccatatt tggcctttatt ctaatcccat 840  
 ccactccctg ggagctgcag agcatcttca tgtgagtga cggatggaca taaatagatt 900  
 catgctcatt taggaagctg ggagtttctg gaagctgagg gtgagttcct gtgattcttg 960  
 ttcgcttcaa caaaaagtgg gagaccacagt ttttatagca aaagacccaa tttagctgtag1020  
 agtcttgaat gcagaaaaaa attaccctag ctttctttaa ttttaaggggt tttgtgagga1080  
 tcaagtgtta gcacagtgct tggcacatag taagccc . . . ttaa atattgttat1140  
 tagtgtttcg taaaaactga gaaatagagc tgaagctcatt . . . ctgt tgattcaaaa1200  
 ataataacca catgaaaaaa tgattccaag ttgattgaat gtttgcaggaa ttaactgggt1260  
 agatagacct agttctcggc ctaccctcgt ggttgggagt ttaactgtatt cttaagtgal1320  
 ctgggtttgaa aatatgccaag acttccagccc ccaaggaaaac aaggctgcga gaatttatga1380  
 acctccagctg gaaaaggttaa aggtgacctt tggctagcca catactggac ctaccacca1440  
 tgacgtcttt cagaacattc caagggtttt cctcaaggaa catttttgag ctagaataa1500  
 aaatggcttc tggcgcagac tgcacccctt gaagtcaaat taacagattt cctttgaatg1560  
 caataataga ggctttttctg cgttaaggga gaaggaaatga ccaattgaac ttacacattc1620  
 cccaggcagg tcccttttgc gccccctaca ggctgggggt gccctcctg tcccaaggga1680  
 tcagactccc agactgggtta gttctgcagt ttccatcaa attaaagggt attccctggc1740  
 cgctcctctg agaaaaacca cccaccctgc ccaactgggg gcaattgggg agggattttg1800  
 gcctctcaga acagctctcta gagggctgctc atgactgaat gttttcccaa atcacctaa1860  
 tatcggtttt ctttttgttt tgggggagag ctgttcttgc cttactccc tgatgattc1920  
 aaagtcttat ctatctcctt atctcctgcc ctgttcttgc acaactctgg atagattgca1980  
 ggtgtggaat ttgctggagt ttggtggctc cccaaattcc ttgatctgtc cgcaagaga2040  
 ag 2042

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 106:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 320 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

aatcttttta ccatgaaatt tcttcagaa ttttccccc ttgacacaaa ttccatgcat 60
gtttcaacct tcgagactca gccaaatgtc atttctgtaa aatcttccct gagtcttccal20
agcagtaatt tgccttctcc tagagtttac ctgccatttt gtgcacattt gagttacagt180
agcatgttat ttacaattg tgactctcct gggagctctg gagccatata aagtgggtcaa240
tagtgtttgc tgccttgaga gttgaatgac atttctctc tgttttggta ttactgtaga300
tttcgatcat tctttggtta                                     320

```

## (2) INFORMATION ON SEQ ID NO. 107:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 506 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

gtcgaacagc aaagccaaga cttgttaaaa aggtttgaag aggaaggacc ataacaattg 60
aaaggggggaa attataagat acagttaaatt cctcttcaaa gatttagcct gttgacttcc120
ttattctttg ttctcaaaact cgacttcctt gttgtccatg cctccttgtc cctagttaact180
gtgaacaacc ttcccaccag ttctaatcaa taactcacat ctgtccctt gggtacccac240
tctgcaccca ttcttcccac tgaactgca cttcccacca ctgtaactca catccccctt300
cccttcttta ttggaaaaag tattcacaaa tagccaatcg ggtcaactta gaatgagcgg360
tccaaccca gccctgtggg gagtgacaca gaggtaggga ctgtgttagg gataaaaacc420
ttttccttcc tttgttcagt gtgctgctgt gatcatgatt gatgcaggca gcagcctttt480
tgcagaagta aattgccttg ctgagg                               506

```

## (2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1276 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

00573395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

gcgcgggcgcg  ggcctgcggg  ggcagaggggt  cggggcggaag  gggaaagctac  gccccggagg  60
tgcggtgtgg  ggcaccgggg  ggggcccggg  gaaccggcgc  cccacggagc  tgctgtgtgc  120
agaccaaacc  cgggccccca  tcatcactgc  gccgcgcttt  caggcgccga  gaactaccgt  180
tccccggcat  cgaatcgagc  ggctcgggcg  ctgagggcg  gtcgggcccc  coaccgcgtc  240
cgccgcgcg  cgaatcgcg  tgcggagcca  tggaggagga  ggcactcgcc  cgggggctgg  300
gctgcagcaa  gccgcacctg  gagaagctga  ccttgggcat  caccgcatc  ctagaactct  360
ccccagtggt  gactgaggtg  accatcatag  aaaagcctcc  tgctgaagct  catatgattt  420
cttctgggga  acaaaagaat  aactgtgtga  tgctgaaga  tgtgaagaac  ttttacctga  480
tgaccaatgg  cttccacatg  acatggagtg  tgaagctgga  tgagcacatc  attccactgg  540
gaagcatggc  aattaacagc  atctcaaaac  tgactcagct  cccccagctc  tccatgtatt  600
cacttcctaa  tgcacccact  ctggcagacc  tggaggagca  tacacatgaa  gccagtgtg  660
atcagccaga  gaagcctcac  ttgactctc  gcagtgtgat  atttgagctg  gattcatgca  720
atggcagtg  gaaagtgttc  cttgtctaca  aaagtgggaa  accagcatta  gcagaagaca  780
ctgagatctg  gttcctggac  agagcgttat  actggcattt  tctcacagac  acccttactg  840
cctattaccg  cctgtctatc  acccacctgg  gcctgcccc  gtggcaatat  gccttcacca  900
gctatggcat  tagcccaag  gccaaagcaat  ggttcagcat  gtataaacct  atcacctaca  960
acacaaacct  gctcacagaa  gagacggact  cctttgtgaa  taagctagat  cccagcaaa  1020
tgtttaagag  caagaacaa  atcgtaatcc  caaaaaagaa  agggcctgtg  cagcctgca  1080
gtggccagaa  agggccctca  ggaccctccg  gtcctccac  ttcctccact  tctaaatcct  1140
ctctcggctc  tggggaaaac  ccaccgggga  agttgaggca  cccttccttc  caatttgcct  1200
aaccagtttc  caggagtggg  tgggggtttt  ccgtggcaca  gggtggggcc  ttaggggggg  1260
ttggcagttc  catttt  1276

```

## (2) INFORMATION ON SEQ ID NO. 109:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 373 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

aaatacattt  atgtttcttg  aaatgtgtta  agtggccttt  gtcaagggtg  ttataataga  60
agagtatata  aaaaatgaatt  tctctagaga  tgcagcatat  tctaaagatc  catcattagal  120
taattaaaaa  tatgttaagtc  atgctaacat  ttccatatat  aaatggagaa  cattaactct  180
ctactcgttt  agttataaaa  taccaaattt  tgtaattatc  ctatctggaa  ttacactata  240
cgcacaaaat  gccagttact  tcacttttaa  atttgacaat  gtatgtgatg  aattataaaa  300
tttaaatagc  tacatctttt  cctccttgta  tccaaatttc  tccggacctt  aatgcttaaa  360
ccttttggtt  acc  373

```

## (2) INFORMATION ON SEQ ID NO. 110:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 492 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

gtcttttgaa atctgttttc actacagcta tggtaagtc tatcagccgg tgctaccagg 60  
 agtcaactgcc aggggtgccg ttctcctgaa cccagtggc cagaatcata agccctgaccl20  
 ccattccctag aaagatgagg tcccagcaat ggccagagca ttctcacca gttctgtgag180  
 atagcacata aaaatagagt tctttgggca aaacttttgg gaagcaatgc atctacatg240  
 ggctgatatt cagcctgagc tgttctcaa aggagagtg tctggcagt ttatggctga300  
 aatccattct gattggttgg agtctatgct ataccagttg ttaaacattt tgagtatcac360  
 tcttgcatatc tgttactatt atatttcctc tatatataga cagaaaggcc attttaggaa420  
 tatttaaaag gctcttgaaa attttctggc attagacca actgaaggtt ctattaaggc480  
 agggttccta aa 492

## (2) INFORMATION ON SEQ ID NO. 111:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1678 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

0967395.12700

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

gcctcagcag actccttggg cggtagcagg gagatggtgc aacggcccca gcctgcacag 60  
 gaaccgagca ggctctggat tgccaacat agacacggga tatgattccc agccccagga 120  
 tgtcctgggc atcaggcagc tggaaaaggcc cctgcccctc acctccgtgt gttaccccca 180  
 ggacctcccc agacctctca ggtccaggga gttccctcag ttgaaacctc agaggtatcc 240  
 agcatgtgca cagatgctgc ctcccaatct tccccacat gctccatgga actatcatta 300  
 ccattgtcct ggaagtcccg atcaccagg gcatatggc catgactacc ctgcagcagc 360  
 ctaccagcaa gtgatccagc cggctctgccc tgggcagccc ctgcctggag ccagtgtgag 420  
 aggcctgcac cctgtgcaga aggttatcct gaattatccc agccctctgg accaagaaga 480  
 gaggcccgca cagagagact gctcctttcc ggggcttcca aggcaccagg accagccaca 540  
 tcaccagcca cctaatagag ctggtgctcc tggggagtcc ttggagtccc ctgcagagct 600  
 gagaccacag gttccccagc ctccgtcccc agctgctgtg cctagacccc ctgcaacccc 660  
 tccagccaga ggaactctaa aaacaagcaa ttgcccagaa gaattgcgga aagtctttat 720  
 cacttattcg atggacacag ctatggagggt ggtgaaattc gtgaaacttt tgttggtaaa 780  
 tggcttccaa actgcaattg acatatattga ggatagaatt cgaggcattg atatcattaa 840  
 atggatggag cgctacacctt gggataagac cgtgatgata atcgtagcaa tcagccccaa 900  
 atacaaacag gacgtggaag gcgctgagtc gcagctggac gaggatgagc atggctttaca 960  
 tactaagtac attcatcgaa tgatgcagat tgagttcata aaacaaggaa gcatgaattt1020  
 cagattcacc cctgtgctct tccccaatgc taagaaggag catgtgccca cctggcttca1080  
 gaacactcat gtctacagct ggcccaagaa taaaaaaac atcctgctgc ggctgtgag1140  
 agaggaagag tatgtggctc ctccacgggg gcctctgccc acccttcagg tggttccctt1200  
 gtgacaccgt tcatccccag atcactgagg ccaggccatg tttggggcct tgtttctgaca1260  
 gcattctcgc tgaggctggt cggtagcaat cctggctggt tttttctgt tctccccga1320  
 gaagccctct ggccccagg aaacctgttg tgacagctc ttccccggag acctccacac1380  
 accctggctt tgaagtggag tctgtgactc ctctgcattc tctgctttta aaaaaacatt1440  
 tgcaggtgac agtgtcccat atgttctccc tgacagtttg atgtgtccat tctggggctc1500  
 tcagtgtcta gcaagtagat aatgtaaggg atgtggcagc aaatggaat gactacaaac1560  
 actctcctat caatcacttc aggtactctt tatgagttag ccagatgctt gtgtatctct1620  
 agaccaaaat gattcatgta caaataataa aatgtttact cttttgtaaa aaaaaaaa 1678

00573355.1.22700

## (2) INFORMATION ON SEQ ID NO. 112:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

gtgcgcattga ctgccaaagga ctgctccatc atgattgcac tgtctccctg tctgcaggat 60  
gccagctctg atcaaaaggcc tgtggtccct tcatcgaggc ccagggttgc cttttccgtg120  
tctgtgtctg accttgcacct caagccctac gagagcattc cccatcagta taaactggac180  
ggcaagatcg tcaactatta ttcaaaagac gtacgtgcc aagacaacgc cgtgatgtcg240  
actcgggtta aggaagcgca agattgcaca ttagttctcc acaagggtcta actctttccc300  
tgcagtgtct ttgaaacttg aacataatgt gaaggctgaa tgatagagat attttctgtt360  
gtgttgggtg acctttgggt gtgaatgttt ttgcttttaa ccccttttga ggtgggattg420  
cctcttggag acatggaatt gaagagcaat agaaacaact tcctggacaa ggaatgtagg480  
aagtgaagtc tgtgtcccag gaagctgctc acactcttaa aatggaagtg tccgttaagc540  
cctgggaaga cgttctggat agttcttctt tcccaaccag ggctcattgc tgattctcta600  
atgcgaaaag ccttattcta agacccaagg tttggatctg ctaccaccag actcctaaca660  
tagaaaaact gaattgtcac atacatttta cagtttggac ttttaagaaa acatggatata720  
tactgggaac ttccccccagc tgagttacat ggggcacttt tcagtgcaag ccacatatca780  
acacagggtt ttaagggtgg tgcctggctg cacacgtgaa ccccggtggc ccccatgatg840  
cgattctgag ccaggtgtaga cccagg 866

## (2) INFORMATION ON SEQ ID NO. 113:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

09673395.122700



(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

gcgcggcgccg cgcctgcggg gcgagagggg cggggcgaa ggggaagctac gtccccggagg 60  
 tgcggtgtgg ggcacccggg ggggcggcgg gaacccggcg cccacgggagc tgctgctgtc 120  
 agaccaaccc cgggccccca tcatcactgc gccgcgcttt caggcgccga gaactaccgt 180  
 tccccgcatg ccatgaaatt gccctcgccg ctgaggcggg gtccggccct ccaccgcctc 240  
 ccgcgcggcg cgaatcgccg tcgcgagcca tggaggagga ggcctcgctc ccggggcctg 300  
 gctgcagcaa gccgcacctg gagaagctga cccctgggcat caccgcgcac ctagaattct 360  
 cccccaggtg gactgagggt accatcatag aaaagcctcc tgctgaacgt catatgattt 420  
 ctctctggga acaaaagaat aactgtgtga tgcctgaaga tgtgaagaac ttttacctga 480  
 tgaccaatgg cttccacatg acatggagtg tgaagctgga tgagcacatc attccactgt 540  
 gaagcatggc aattaacagc atctcaaaac tgactcagct caccagttct tccatgtatt 600  
 cacctctcaa tgcacccact ctggcagacc tggaggacga tacacatgaa gccagtgtat 660  
 atcagccaga gaagcctcac tttgactctc gcagtgtgat atttgagctg gattcatgca 720  
 atggcagctg gaaagtgtgc cttgtctaca aaagtgggaa accagcatta gcagaagaca 780  
 ctgagatctg gttctcggac agagcgttat actggcattt tctcacagac acctttactg 840  
 cctattaccg cctgctcacc acccacctgg gcctgcccca gtggcgaatat gccttcacca 900  
 gctatggcat tagccccacg gccaaagcaat ggttcagcat gtataaacct atcacctaca 960  
 acacaaacct gctcacagaa gagaccgact cctttgtgaa taagctagat cccagcaaa 1020  
 tgtttaagag caagaacaag atcgtaatacc caaaaaagaa agggcctgtg cagcctgcag 1080  
 gtggccagaa agggccctca ggaccctccg gtccctccac ttccctcact tctaaatcct 1140  
 cctctggctc tggaaacccc acccggaagt gagcaccctc cctcccaact cctaccagc 1200  
 tccagagtgg tggtttccat gcacagatgg ccctaggggg gacctccagt tttgcgtgtg 1260  
 gaccgtaggg ctctttctag ttgaatgacc aaaattgtaa ggcttttagt cccaccgaca 1320  
 ttagccaggg tcgtagtggg gcctccagag caggttgtgc tgtccctgc ctctggaagc 1380  
 aatgggggaa gtggaatcaa gacaatgcc aaaaaattt taatgcagct ggtc 1434

(2) INFORMATION ON SEQ ID NO. 114:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 914 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

00673395-122700

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

ttggcagcgg ggagagggaa agaggaggaa atgggggttg aggaccatgg cttacaccttc 60  
ctgcctttga cccatccacac cccatttcct cctctttccc tctccccgct gccaaaaaaa120  
aaaaaaaagg aaacgtttat catgaatcaa cagggtttca gtccctatca aagagagatg180  
tggaagagc taaagaaacc accctttgtt cccaactcca ctttaccat attttagca240  
acacaaacac tgtccttttg ggtccctttc ttacagatgg acctcttgag aagaattatc300  
gtattccacg tttttagccc tcagggttacc aagataaata tatgtatata taacctttatc360  
tattgtctata tctttgtgga taatacatcc aggtgggtgct ggggtgattta ttataatctg420  
aacctaggtta tatccttttg tcttccacag tcatgttgag gtgggctccc tggtaggta480  
aaaagccagg tataatgttaa cttcaccoca gcctttgtac taagctcttg atagtggata540  
tactctttta agtttagccc caatataggg taatggaaat ttcctgacct ctgggttccc600  
catttttact attaagaaga ccagtgtataa ttttaaatg ccaccaactc tggccttagt660  
aagtgaaggt gtgaactgtg tggcaagaga gcctcacacc tcactagggt cagagagccc720  
aggccttatg ttaaaatcat gcacttgaaa agcaaacctt aatctgcaaa gacagcagca780  
agcattatag ggtcatcttg aatgatccct ttgaaaatttt ttttttggtt gggttggttt840  
aaaatcaagc ctgaggctgg gtggaacacg gttagcctaca caccocaaat tgggggtgg900  
ccggggggaa tgtt 914

(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 685 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09673305 122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

gaaaaatccag ggggtgaagaa tagatctgtg gtggcagggg tgggaaaggc ggggaggatt 60
tgccactctga ggggcagcac aagagaattt tgccggggcga tggatctgtc tgtatcttgat120
ccatagtgat gatacatgac tgtgcatttg tcagaactca caggactgaa tgaaaaagaga180
agtgaatttt actgcattgt aattgtttaa ataaatgcta gacagtattt taaaaatcaa240
gcccagatcc tgcaagacat tatggctccc caccagaagg ggagagacgg ggaaagagaa300
gtgtcccccac agttaaccac cgtcccttgg gacccacctc cctcccccact gccacttccc360
accagcctca cgcacggggc aggccttccc ctttgagct cacagcccag cagatgttag420
gtcagaatgc gtccctcac ttgactaaag gtttacagcc agcagggtgg gaaatgaacc480

agatattaac accccctcct ccatgccctg cccaccttct gggccagtac cagtgaaggc540
aggaagccac ttctccacc cccaggctgt tcccaaagcc ctggaagaac ccaaggaaa600
gcaggagcca agttgggagt tgaccttgat gaccaggggc cagttggccc agtttccctt660
gtttagtgg ggggagggaa ccctt                                     685

```

## (2) INFORMATION ON SEQ ID NO. 116:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2646 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673305.122000

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ttaatttaaat agctttcatg tgattaaaaa tagctaacta gactcaagga ttcacaatat 60
ttaggtgtgat tttcaataacc tccagaaagg aaacctcagt taatcagagg aaatagtgttc 120
agttcttcatt tgagcatgtc tttccatctc aaaaaaatac tcttagtagg ttggagtgaa 180
gatagcaagg ttttgaagca tatttgtcct aatccacagt gacacttttt attcttccagg 240
agcactccta ggaaggttccg tgccctaata atgttgactg ctttgcagat ctcaagggaa 300
taaaattgaca aaagcaggga aagttaacaga ttcaaacagc atttttaactc atgttgatct 360
ggataattaa tcttttctaa agatgtgtag ttcttggaaa aacagtgata tcacatgat 420
aaaattacat ttttatcaac ataattgtct ggaaaagata agccctcaa ttttctacca 480
gttgactttt attcattaga tacagaaggt gcagattacc acatcaccag ctgcctttgt 540
gaatggctca ctacacagcc attgggggtac aactgtgtgc atggggaagaa acagcaagtg 600
ccctcattgt gggtcattggg tggggagtgcc cttttgtcaa ggagttctgca ggaattggct 660
tatttctcta tgccaaaagt atcaacacac caaagtctct gccataaaga atgtgggttc 720
cttgcactct ccactctgtt actctgggccc cagtaatttg atgtaactgt ctgattgtac 780
tagagcacagg agtataccca gcttatctat agactacag agagactcag attagatttg 840
atttttttagc ctctcttaga gccaaatcagg cagttaagag taataaaggaa aaaggggttg 900
gtcacaaacc ctaccattat ctggagatta ctgctgctgc cactctgtgc ttgcctatgca 960
cgtcttgcct cctcactttt gctcagccta gcagtctact tcaactttat gccctgtgaa 1020
tgtcaggcgt cctgggcgct ctggaaaaga caggggagca ggcctctcca cccctactgg 1080
taacagggtca ttgctgggtg cacaagaggg aggtgatttg catcatgtgc atgctgcagt 1140
ggcttcaact ggatgctgtt aaacacccaga ggagcccaacc tatcagaatc ccagagcaal 1200
agggaaaactc agatttttaga ggcctttttac aataaagtag cgttaactcta ggctcatgat 1260
gatttccaaat gcctggccat aatgatatttg aagtaattat gtaggatacca tcaaaagcag 1320
attgttaggct tttgaattgt cccagtggaat cccgggacccc atttcaactg ctctcttgat 1380
cgtgttaatg atgcaatcag agttcaagac agggcccatag aagtctgact gcaactgggt 1440
ggagaaatga atttcttccc actgaaggaa actctttctc attcgcagcc aagacgggag 1500
tgccactggt cctctcttca ctctcgagat actgcttctg gaagcgggtg tcaacttctc 1560
tctagtacct cttctcttct ctgaagtgtg tgactatctc ctagtgttta aatttggcag 1620
ttactcgcca tgtatgtcag catagaaaag gaaatgtttt taccttatct cctgtatgta 1680

```

```

tgatagaact taaaagaagt gtgcatttgt tttcatagcc ccagcagaga aaatcctctt 1740
catagacttaa atgtgtctgct gtggacagga gggaaaaaaa aacctctcac atattgaaag 1800
gcaccaaaatg taatatctga cactgttaag atgccccaaa gagcaaaagt gtagtggaga 1860
tgcaagggtca tttcccatcg ccatccacag tgtttgttag tgagttccagc gctgacttgc 1920
agtataaag aaaaagccatg agctgtgtct gcagacaatg gtggctgcat ctgaagtgg 1980
cttcagagggc agcacgctgt gggaaattga tgggtgtggc agtggacctg tgaagaggga 2040
gaactcagcc ttacagccctg ccagtgttaa ccactagaga aactgagctt tatatccttt 2100
tttaatgctg gtgaatttta gcattatgaa caattagagc aaataactcag gggatttttc 2160
attcaaacat cctcagataa tttagctata tatcattaga aagggaaagc tatcattttt 2220
attttaaaac taaaacaaggc catcttataa actgtcacca aagtcttccc tttttattgt 2280
ctgtgtgtgc ttgaatttca taaaacatta attcacaatg ggggtcagaa tgtactcttg 2340
ttgaaaacct tcttgtacca ttttatgttc atttatgtt tgagagggtta aaaaatgatg 2400
agcagcttaa ctgaagtaga actattctat atgcttttca cacattgtgg cataagatgt 2460
aaagtgttga attaatgtta atttctgtgc attttaatat tctttataat ttattaatgt 2520
taattttctg gcattttaat attcttttat aattatgagc attttaataa attcattttt 2580
acaaacataa aaaaaaaaaa aaaaaaggga ggaagggaaa aggaagaagg aggggggaa 2640
aggaag

```

## (2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2667 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ttatcttggga agtctgtgta tcaaaatgaa gaattcagat ggtaggaggt tctatagtc 60  
 ttttaaagct gactcttgag tgtcagttga atatccatta aattggattt ggaaaaaacc 120  
 tgaggaaagt attatgaatt cgaatctgcac agatgcctct tagctgatag gtggcaggcc 180  
 tgtgggtttg ggttctccct cttttctctg gaacatatga caattccaga ttaaaagaaa 240  
 atgtttttta ataaataacc ttggtctttc ttctagtcac ctttgaggta gatattgtga 300  
 ttttctggag tatagtatat ccgtgtctct gtgtcttagg tttactagat gcaataatac 360  
 ttctctttga catttgtact gaagtgaatt gatattaagt aaaacagtta atgtttgaat 420  
 ataggcatat ttataggttt ttccgctccc ccccacaacc acccttttta aaaaatctat 480  
 acaaagccct tgtttgagtc tcatcatgca catcaaatca tggagttagg tcttctctga 540  
 gctcaggggga acacaagtgc acagagagag atgtcttgag ggtcactacc aaagaattac 600  
 cctcattgtc cctcactcag gccatgtgta catgcgatgc tgcctgagtg gctgggggtg 660  
 gtgggtggcca cgtggtctccc ccagagcact tcttaactgg caagctggga gaccattac 720  
 tgggtgaact tgtggaatt agaactgta cttttacata atcttggcat attacatttc 780  
 ataataaaaa catacattta gttgcatgct acatcactat tgattttata attaatcttc 840

09573355.122700

```

taagcttcaa ccatgtttta taccttattt cgttacatca tatatttgta atgtgtaata 900
tgaaaccttt tgccttaaat tcttttttta aaatgtagaa tgttctaaac ttgaaaggca 960
attgaatgta gtatgatgaa aatgtgaatg ttttgctgct ttcatgacca aagatacagg1020
gctagtggac atttagaata ataattaaag ctagagtctt gtatgtcttt tctttgaagg1080
agtcttaacc ttgtaaaatt agaatactt cagagaattt tgattaagaa aacattaaaa1140
tcttaaccgg cacaacaact ccaatttttt toactgtgaa gccgcaagca attttttttc1200
tttttctttc aaaagcctgc cttctgaatt tatttcttgt ttactcattt cagagaggg1260
agtaaaagaag atctatttct ggtagtcata tcgcttgaaa ggtattggta aatgtgtttt1320
cagtcgtgac catgtggaaa gtgaacagtg ttggcaaaaca ttaccgagaa aatcatgctt1380
ttcaagatgc cctgtctttg ggatatacctt cctaggggaga aaaaaaaaaa gtagttaaac1440
aattgtgaat tccattttctt atttccagttt ctgctgcagt aatgggttcc caccocactat1500
aattcccagc atttatgttc tgttgtattc tcccttagc ccagtaaacat ttttatctaa1560
taccocattc cccaagtttt gagacagatt gacccctac tcattatgtg gctctagtgt1620
aattttaaaa tgtggaatat tgggcttgca ggcagtagga gctgcaaatc tggtagagtg1680
ggagtgtgga gttaatggtg agtatgttaa taaagggaaa ctgtctctga cagaatctca1740
gtaatgttta ccaaaaactg tctttctaca gctggtagga taaatgatgc taccctgtag1800
ctcagctaca ggctgcagtg caaacctttc ttccatccag agaaaqcaga attccctctt1860
agtaacctca ttacaaaatac tgttactaga agggcatgtg ctgtctgtca ccttcagtaa1920
tatttgtgcc atctcttgat gactgatgac ctggatcgag tatttctatg aagggcttct1980
ttaggccctt tacatacgca agaggggtgc tctagtgcga tagctgtagt tcacaggaag2040
gacaccagga gaagtataac ctagggtcac tgagcagctc atcatccctg tttctgcaca2100
gtttcctgaa actggccatc agggcctctg aggcactcaa atcagtttcc ttttagcatg2160
cccccatcag ggtgggtctc actgttagtg aggatacggg tctgtgttga tgtttttctt2220
ggcaaaatgc tcaagtgttc tggttatgoc attcattcat acgatgtgtg aaatttgctt2280
aaaaagggat ttctcatgat tgatttagat tagtatttaa atatctgctt tagatagcaa2340
ttaattttat tgtaaaaata agggaaaaata tgtgaatatg tgaatttttt aagcctgaga2400
gatgatagaa tgttcccata tttttcttgt aaagaaaaata atatttttaac ttacacatcc2460
tgtagaaaaa accacccctt ccccttgat tacagtaaaa tgtttacatt actatactgt2520
caagctgaaa gtataaaaaa tgtacatata cattttgagt tatgtatcct ttttttaaaa2580
aaaggtgcgg ggctgtggca ctggcgctgga catgactaaa gttgacagag gctatgctag2640
atttataatc actagtcttg ggactctg

```

2667

## (2) INFORMATION ON SEQ ID NO. 118:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 544 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

09672395.122700

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

catctgtgca tggatgagtg gccgactttg gagcccaggc tgttacttcc tggctctggtg 60
gtgaatcctc catagtctga gagtaagatc cttgatactg gctcagcatg gaacatctgg120
cacacagtat gcactgagga aatacttggtt ggaataatca gtgaatcata gatgaaaact180
taaccttgga attaattatg agactgtcca gaggaagaga atgggagaca aaggacctgg240
tgattagacc cccaagacac tgggctgtct gcttgtgtct cgggtggaac aggccagcg300
agagtcttta gggccagaac tcaaggaaatt tattgagcca tggcaaacag gcagtaaaaa360
gcccattctg gctgctgtat tgagaagaga atgtggtgga cagatataga agcatggaaa420
cctgataggg ctattgcaat cactcagaaa agaggcgatg gcagcttgga cctgttgaag480
cagtagagtg ctttccaggg aggagaaaag acctgaaggt taatttgatc accatggggc540
atga

```

544

(2) INFORMATION ON SEQ ID NO. 119:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1340 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

0067335-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

ttttgatact ttcttcgact taggtttgtc ctattcttca tttattcaga ctaggataga 60
aaatttttga atcagaaaaat agatccagtgt tttagctaca tacaatctag tacaaagtga 120
tttttatctt taaacatagg tgtgtttggct ctttttttta aagatgcgct ctacctgaaa 180
aggaaattgg atttttagaac tggatgtgggt gcagtgaagt attttaggcc caggctcgtg 240
tacacatttt atagaagaaa tgaagtactc tgaagtattt tggttgcctt ttcatttcaa 300
ctgtgttttg aatttgcag atcacacata tattgtgta ttggggcgctg tggatatctt 360
tataaaaact ctgtcttgtg tgcaaaaagt cctaaaaagg aacacaaagta atgcctatcc 420
attactagca tgcctatgtg catgctttac tgcattgct gtatgcttta ctgtctttgt 480
aaaaatcccc ctctccccct ttctggtaac tggaaaaagc tgctaaaaat agtcttata 540
tttcacccca taagtgcaga atcagtaatt ccttggotta aagctottat ataataaata 600
ttattgtgtg taaataccaa gtttggatct tcatagctat ctttttttaa agaaattaa 660
ttcttgaaaa tttagccaaa tcccgtttta tgggaatgct ctttagaatt cattttgttc 720
agcccccttg ttctatggtt gaaaaatctg aggccttacg aaggtttaaga gaactttccc 780
cgtgtctcac aggtaggtag aggcagagct ggaactagat atctggtctg ttgactctag 840
ctcagtgctc ttctgtaact gttgaaaaat gtcttagttt gagagatggc tgaaataatg 900
aacataaaaa gctatttata ataacaagta tatgtgaaat ttcttattgt aagactacta 960
ccggcttact gttgaatagt ttggttatag tgttttagct agaaatgcct cccacattgg 1020
taataaacat tacaaaaatac aatgtatttt taggtaggca ttttataaaa tgcattatgc 1080
catggttgct tttagatag attgtagtct gggtagcatc tttaaaatgt atgtgggctt 1140
aaactgtgtt caatacagga gatgctctga ttgtataggt gagactctgt ttctgttatt 1200
tttaattgct gtatgaaatg tgatcagatt attttactac caacagttat agtttgaag 1260

```

```

tccaaactgta ttaattgact gataatatga taatatagag attaaattgt ttgtcttcatt 1320
tccttaaaaa aaaaaaaaaa
1340

```

## (2) INFORMATION ON SEQ ID NO. 120:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2376 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673395-132700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggatgatgaat aaattgttaa tataaagtc cagacaaatt aatttatgaa atttctctaa 60
atcacacaaa acttaaaatac agatgactac tacocctgaga ctgaaaaata tgttctaat 120
tatagtcta tttttgggca gttttggtgt cagaatacct atcaacacat tcttttttta 180
ttaggaaaaa aaggatgtctt acataacaat ttgttaaagt ataaaaatcca ttagttttta 240
agtcctctga tagcattggc tattataaga aacaagtatt tgctctcggt tttaacggga 300
taataatgct agtctacat aaaatgattt ctaccacctt aaatagctca ctgtagaaat 360
tcagtataaa ttggaaccaa atagtacata catatcatc tcttaggtct gccaaatatt 420
tgaggttcat ccatttttta tattcactca tcagtattgt taaacacatt cttaaagttag 480
cattttcaga tatgaataag cagggatgaa ataagtatta gggttaaggga aatggttgag 540
gctttcctaa gtgaagtgtt aaaaccacag ctttcttttt aatgggatgt ctaatatgca 600
tttatctgtt caagcatttt aagatttcca tgaaaatgtc ctgaaaaatc aagattcttc 660
attgaggggt aggatctccc aatgggagac tgctctgaaa agagcatgtg ctttttgaat 720
tagataacct actataatca tggatgttct tgaatactta gcaaacatc cagcatccca 780
aagtcaccaa gataaacctt cctactccaa catcacatga tcttctaat ctacctgtaa 840
aaataagcat aacaattaat tagaataata ttacgttata tacattactc cacctagaaa 900
aaaaaatagt tcattatgta gaaaaatgct ttttttagta catagagaaa taaaaaatc 960
agatactcac tagtgaacaa aaaatgtcca aagccagcca caacagatcc taatgaacca 1020
tacaatattg aatgccgggc gcaggagtag ttttcaacat ctaaaaatcc tagggagctta 1080
agggactaga atgaaaaaaa agaacctaga ttgagtgaaga aagtatttca ctttgggtg 1140
ctttggcaaa aatgacaata caccatttct tttctgttag ttgaggggtt aaactagagt 1200
atgtgcccac tgacaaacct aatcagcttg cgttgtcttt gtccaccttt ggttagcagt 1260
ctgaatcttt aaatccgaaa accttcaaaa ttggaccgga aaacctttaa gcagttaggt 1320
aacttgaggc tgtatcttaa ttgctaatc aactgacttg gaatatgagt aattcatttt 1380
atgagctctt taaatgagt ttattgggaa tatgcctatc atttgaattg aaagcagcat 1440
agcttgcttc agtaactcca ataatttggg aagcagaaat ggaaaaaagta atttgagtca 1500
tgtttgctta tgtagtgcgc tttaaaattc cctagttaat tacctttcat attttatta 1560
ctaggttaac atcaactgtg gttgtaagag taaatgtttc accttaagat aaacatggg 1620
aatatattaa actctagtct gtttcttgc ctgtgaagtg aggtgcact tggatatatt 1680
tgattctttg ttcgtaatac atgggaacga cagctaagtg tggtgaaaaa cgcggggatc 1740

```

```

caaaagagctg gatttttacc tcagatctgc cgttaacctt tgtatcctat aggtcacttt 1800
tatttctatg gtctcaatct ataacatgaa tgggttgggt taaatgactg aagtctcttc 1860
aagtgtctaaa attcttttct tacagtcttc attggattta tgtatttctt attctcaata 1920
tgttttaactg ggtgtctgt cactctaggg cggcaagaca gacattttaa agtaacagct 1980
actagtctga actggcattt ctgttaaacac aaaagtttag aaaactcacg gtaactgtta 2040
cctattttaa gtgtatataa aatttttcagt aaggctgctt tttaaaggaa ccactgtcca 2100
tttaaagggt tcatagttat ctccaatggg tttagtattg ttggggcagg acattaaact 2160
agaagggtat ctataggatg aggtgatacc tagaaggtaa tatattgtaa ggcaaaagag 2220
attgaagaaa atggggggaa aggatagtaa aaggcaagtc agattaaagg gttgaaacat 2280
gaagatatcc ccattgtatt cgggccccat gtttgccctt tttggctcca gcatcgtgt 2340
tggaagaggg caatgtgcc tgggtcccta ataaag 2376

```

## (2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 225 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

cagttgtgaa gttttgtaaa atggtcacc aactaaaac taggaaatta cgaagaagag 60  
 aaaattgccc ggtatctggt aaggtctgcc tgtagatctg ctgtagggtc tgtcaccatt120  
 ggaagcaagg tcctacttca gtggcagatc ttgtggcctt tgagtggctg aagaccacca180  
 ccctgcacag ggctggggcc atgcacagc atccttccct acctt 225

## (2) INFORMATION ON SEQ ID NO. 122:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1967 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

09673051422700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

acggggcggcg cccgcgctcg caggccactc tctgtgtgtc ccggtccgcg ggcgtcctcc 60
gaccocgtcc gctccgctcc gctcggcccc ggcggcgccg tcaacatgat ccgctgcggc 120
ctggcctgcg agcgcgcgcg ctggatccgt cccctgctcc tactcagcgc catcgctctc 180
gacatcatcg cgcgtggcgg cgcggcgttg ttgcagctca gcgaccacgg ccagacgtcc 240
tcgctgtgtg ggaaatgctc ccaagagggc ggcggcagcg ggtcctacga ggagggctgt 300
cagagcctca tggagtacgc gtggggtaga gcagcggtg ccatgctctt cgtgtggctc 360
atcctctcgg tgatctgttt catcctctcc ttcttcgccc tctgtgacc ccagatgctt 420
gtcttccctg gagtgatttg aggtctcctt gccttggtcg ctgtgtcca gatcatctcc 480
ctggtaattt accccgtgaa gtacaccag accttcaccc ttcatgccc cgtgctgtgc 540
acttacatct ataactgggc ctacggcttt ggggtggcag ccacgattat cctgatcggc 600
tgtgcctctt tcttctgctg cctccccaac tacgaagatg accttctggg caatgccaa 660
cccaggtact tctacacatc tgccctaact ggggaatgat gtgggagaaa atcgctgctg 720
ctgagatgga ctccagaaga agaaactggt tctccagcgg accttgaaac cattttttgg 780
cagtgttcat attattaaac tagtcaaaaa tgctaaaaata atttgggaga aaatatTTTT 840
taagtagtgt tatagtttca tgtttatctt ttattatggt ttgtgaagtt gtgtcttttc 900
actaattacc tatactatgc caatatttcc ttatatctat ccataaacatt tatactacat 960
ttgtaagaga atatgcacgt gaaacttaac actttataag gtaaaaaatga ggtttccaag1020
atttaataat ctgatcaagt tcttgttatt tccaaataga atggactcgg tctgttaagg1080
gctaaggaga agaggaagat aaggttaaaa gtgtgtaatg accaaacatt ctaaaaa1140
tgcaaaaaaa aagtttattt tcaagccttc gaactattta aggaagacaa aatcatttcc1200
taaatgcata tcatttgtga gaatttctca ttaatatctc gaatcattoa ttttagctaa1260
ggcttcctgt tgactcgata tgtcatctag gaaagtacta ttctatggtc caaacctgtt1320
gccatagttg gtaagccttt cctttaagtg tgaatatatt agatgaatt ttctctttta1380
aagttcttta tagggttagg gtgtgggaaa atgctatatt aataaatctg tagtgttttt1440
tgtttatagt ttocagaacca gactagactg gattgaagaa tggactgggt ctaatttatc1500
atgactgata gatctggtta agttgtgtag taaagcatta ggagggtcat tctgtgcac1560
aaaagtgcac taaaaacagc tcaggagaat aaatgacttg cttttctaaa tctcaggttt1620
atctgggctc tatcatatag acaggctctc gatagtttgc aactgtaaag agaaacctac1680
atatagttaa aatcctggtc tttcttggtt aacagatttt aaatgtctga tataaaacat1740
gccacaggag aattcgggga tttgagtttc tctgaatagc atatatatga tgcactggat1800
aggtcattat gattttttac catttcgact tacataatga aaaccaattc attttaata1860
tcagattatt attttttaag tctgtgaaaa agcttaattgt agttttcatt atgaagtttt1920
cccaataaac caggtattct aaacttgaaa aaaaaaaaag tcgacgc 1967

```

00573705.122700

## (2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 612 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

cctagctgtc cccctgagat gaagaaagag ctccctgttg acagctgcct gcccgcgtca 60  
 ctgcagcttc accctcagaa gatggatccc aagagacagc acattcagct cctgagcagc120  
 ctgactgagt gcctgacggt ggacccccctc agtgccagcg tctggaggca gctgtaccct180  
 aagcacctgt cacagtcacg ccttctgtgt gagcacttgc tcagctcctg ggagcagatt240  
 cccaagaagg tacagaagtc ttgcaagaa accattcagt cctcctcagct taccacccag300  
 gagctgtga ggaagggtag cagtaacaac caggatgtcg tcacctgtga catggcctgc360  
 aagggcctgt tgcagcaggt tcagggtcct cggctgccct ggaacgcggt cctcctgttg420  
 ctgctgtgtc tcgtgtgtag cttcctgtgc catgacctcc ggtcacacag ctccttcacag480  
 gcctccctta ctggccggtt gcttcgatca tctggtctt tacctgctag ccaacaagcg540  
 tgttccaagt ttaactctac agtctgcaag gttacaggtt gggtggggga gaaatgccgt600  
 tttgggggtc ca 612

## (2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1183 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

tttcggcaca gcatgaatgg ctgcgagaag gacagctcgt ccacagattc tgctaacgaa 60
aaaccagccc ttatccctcg tgagaaaaag atctcgatag ttgaggaacc ttcaaaagca 120
cttcgtgggg tcacaggccc aaatatggag aaatcagtgaggatttgca acgctgcacc 180
gtttctctaa ctagatctcg cgctcagatt aaggaagaag tggatagttc cgtgaagaag 240
atcaaaagctg cttttgctga attacacaac tgcctcattg acaaagaagt ttcattaatg 300
gcagaaatgg ataaagttaa agaagaagcc atggaaatcc tgactgctcg tcagaagaaa 360
gcagaagaac taaagagact cactgacctt gccagtcaga tggcagagat gcagctggcc 420
gaactcaggg cagaaattaa gcactttgtc agcgagcgta aatatgacga ggagctcggg 480
aaagctgcgc ggttttctcg tgacatcgaa cagctgaagg cccaaatcat gctctgcgga 540
gaaattcacac atccaaagaa caactattcc tcaagaactc cctgcagctc cctgctgcct 600
ctgctgaatg cgcacgcagc aacctctggg aaacagagta acttttcccc aaaatcatcc 660
actcacata agcctcttga aggcgaagcg gcaaacccca aaatggtgag cagtctcccc 720
agcacgcggc accccttcca ccagaccatg ccggccaaca agcagaatgg atcttctaac 780
caaagacgga gatttaatcc acagtatcat aacaacagggc taaatggggc tgccaagtgc 840
cagggcagtg ggaatgaagc cgagccactg ggaaggggca acagccgcca cgaacacaga 900
agacagccgc acaacggctt ccggcccaaa aacaaagggc gtgccaaaaa tcaagaggct 960
tccttgggga tgaagacccc cgaggccccc gccactctgt aaaagccccc gcgaaggcag1020
gcacgtcgca ggacacctcg ggaggggcag gggcctttcc ggggttagtt ttcggttagg1080
gggttttcca ttgtcatttt ttgtccccc cggaggatta ggaagttttt ccacagatgg1140
caggcatttt ttttgagttc ccgggttttt gacgtttttg ttg 1183

```

## (2) INFORMATION ON SEQ ID NO. 125:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 891 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

cggaggcagc ggaagccga gccaggcgcc tgcgcgttg gaagagtagg ttcagagtgc 60  
 attccggaac cggggcgccg gcgcactgcg caggcgccg gactccgctc agtttccgggt120  
 cggcggaaca ccaagtcgc ggaacttaag cattttcggt ttctagggtt gttacgaagc180  
 tgcaggagcg agatggaggt ggaacgcacc ggtgttgatg gtcagagtgg tctccgggag240  
 cggcgaggct ttacgagggg agggaggcag aacttcgatg tgaggccctc gtctggggca300  
 aatggggttc ccaaacactc ctactgggtg gacctctggc ttttcacctt ttctgatgtg360  
 gtggtgtttc tctttgtgta ttttttgcca tgacttgttc gctgatactt aaatgaagaa420  
 gtggtttctt gagtgaattc tgaaaatggc tacaaacttc tgaataaag aagacaggac480  
 tctcaataga agaatttcac atctccaagg gacctctcct ttcattttac actttgttac540  
 taatttcgag aactctatta attgggttag atttcaccca ttcctagcta agttcttaaa600  
 attaaacctt ttggttcgtg tttaaaaact ttcaaacatc tgatggcttt acaggggctg660  
 aatataaaag catttgact taaagggtct gtgtattcat taagaaaatc agtaagtct720  
 tttaatgttt taagagttga tcagggggtt actatggatt gcaagtaata gggatgatta780  
 ataaggggaa ggtttttatg gaatttcaaa agtcaattta tttcaaaagc gggggaaagg840

gttttgagag gaggggggccc caaggtgttc ctgggggttg ccgagggagg c 891

## (2) INFORMATION ON SEQ ID NO. 126:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 482 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

tctctaata gtaccttttc agtcttgccc cagaagtccc ctcaatttca gcagcaccca 60  
 ggggtttata attcattcag ttttccaggc caggcgagccc gctatccctg gatggccttt120  
 ccacgcaata gcatcatgca cttgaaccac acagcaaaacc ccacctcaaa tagtaatttc180  
 ttggacttga atctcccgcc acagcacaac acaggtctcg gagggatccc tgtagcaggg240  
 gaagaagagg tgaaggtttc gaccatgcoa ctgtcaacot ctcccatc attacaacaa300  
 ggacagcagc ctacaagtct ccacactact gtggcctgac aacagaactg agagagagg360  
 attagactct ggggtgcttg catggggcaac tggatttttg catgattcct ttatgatttt420  
 gcttttaaatg tatacaccca gaagagccaa tataaacgtt cctcatgcct aaaaaaaaaa480  
 aa 482

00673395-122700

## (2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 610 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

ctcgagccgt gggcagtggc cggaatgcg cggagacact gacottcagc gcctcggctc 60  
 cagcgccatg gcgcctccca ggaagttctt cgttggggga aactggaaga tgaacgggcg120  
 gaagcagagt ctggggggagc tcctcgccac tctgaacgcg gccaaaggtg cgcccgacac180  
 cgaggtgggt tgtgtccccc ctactgcta tatcgacttc gcccggcaga agctagatcc240  
 caagattgct gtggctgcgc agaactgcta caaagtgact aatggggctt ttaactggga300  
 gatcagccct ggcattgatc aagactgcgg agccacgtgg gtggtcctgg ggcactcaga360  
 gagaaggcat gtctttgggg agtcagatga gctgattggg cagaaaagtg ccatgctct420  
 ggcagaggga ctcgagagtaa tcgcctgcat tggggagaag cttagatgaa agggaaagctg480  
 gcatcactga gaaggttggt ttcgagcaga cagaggggtc tcgcagataa cgtgaaggac540  
 tgtggcaagg tcgtcctggc ctatgagcct ttttttgggc catttggtgc ctggcgaagc600  
 cttcaaacag 610

## (2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2072 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

00673395.122700

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

gggtcatgta ggtacaacag caaccaagaa gatcgatgtc tacctgacct ctgcactcga 60
gccaggacag actgctgcc aatgacctgg tgacaatggc cagcgccagg gtgcaggacc 120
tgatcgggct catctgctgg cagtatacaa gcgaaggagc ggagccgaag ctcaatgaca 180
atgtcagtcg ctactgcctg catattgctg aggatgatgg ggagggtggac accgatttcc 240
ccccgtgga ttccaatgag ccatttcata agtttggttt cagtactttg gccctgggt 300
gaaaagtact catctcctgg ttgacatccc aaagagtcac tttttgttgc aataaatgct 360
gtccatggat tctccttat tcaggtggac aacacaaagg ttaccatgaa ggaaatctta 420
ctgaaggcag tgaagcgaag aaaaggatcc cagaagaatt caggccctca gtaccgctg 480
gagaagcaga gcgagcccaa tgtcgccgtt gacctggaca gcactttgga gagccagagc 540
gcatgggagt tctgcctggt ccgcgagaac agttcaaggg cagacggggg ttttgaggag 600
gattcgcaaa ttgacatagc cacagtacag gatattgcta gcagccacca ttacaagtca 660

```

```

ttcaaaagtc gcatgatcca cagactggga ttcaacaacg acgtacagct aggtatctct 720
ggagacaaa tagagataga cctgtttacg aatcagaaag ccagcactaa gttttggtt 780
aagcagaaa ccatctcaat cgattccgac ctgctctgtg cctgtgacct tgcgtgaagag 840
aaaagcccca gtccagcaat atttaaacct acgtatctaa gcaatcacga ctataaacac 900
ctctactttg aatcggaagc tgctaccgtc aatgaaattg tgctcaaggt taactacatc 960
ctggaatcgc gagctagcac tgcgggggct gactactttg ctcaaaaaca aagaaaactg 1020
aacagacgta cgagcttcag ctccagaag gagaaagaa cggggcagca gtgacactgg 1080
cctccagcct caatctgttc cgtagctcag agcctgcctg ccagggccaa gtgccctaga 1140
gcccccocgg tgcctgaag tctcggggg gaggcagcc cctggctcac tggcacaggg 1200
caggtgggct ctgcggggaag gtgtcggggg cccctagga gggagcgctg gggacattgc 1260
catgggacgg aagtcctgctt ggcagtggtt ttgataagcg atgcttggtg gtgcagaccac 1320
ccctagagg agccacgtgc cgcacagcca ccttcaatgc ctgccacct gcccgaggat 1380
gtacagagcc gtgcccacac atttctctgc aacttgatca aatttcttaa agcaaaaacac 1440
aaaaatgtac atttctgttt ttctttttaa taaacaggtg tactctttaa catggttggt 1500
atgatggacc attctttggg gcggaggatt gattatgtta ctctctttaa aatctgttcc 1560
catattgaac aggcagattg gaaaagctat ggttcgattt ctcaagaaga atgtttaggt 1620
cttagtcaat agttttaact atgacattty tttaaatgag tgcatttgc tgcagggtag 1680
tgtcttacta aaagtttagga acagagacct agtgggtgtt ccaaggccgt gtcactttcc 1740
ccttcagcac accccagctt ctgacctcag agcccaggag ctgcgtggac agtgtgggtg 1800
gccagaggga gggcggtgg ctggttcctca gcacgctgc actccagac catctggtc 1860
tttcgcttc ttaagttaga agttaggtt tcagctggca gttccacctg catgtctctc 1920
gcttcgctgc ctgggaagg gccacattcc ccatctctct tctcttaca gcgcctgctc 1980
ccttttttaa caggcggaag gctgctgttt ctacgctttc agggagaggg gtgaccagga 2040
gactgtgtcg tgcgtcgctc ctgggtggac ag

```

2072

00673395-122700



## (2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 980 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

tttatggagt tagagcaggg gaacttaaaa acaaaaagtgt atttaataac ttcattgagac 60
tgtgataacc agtttatatt tgaatatat acagcacttt gggagactga ggggtgaccc120
tgatagtcct ttgcacagt atcttcagat cttaaaagaa aaagaaggca tagaatatat180
tttgcttaac ttctctttta aggataaact tccatttgat cctccatttg ttcgagtggt240
gttacctgtt ctctcaggag ggtatgtatt ggttgaggga gcattatgta tggaaacttct300
cacaaaaacag ggctggagca gtgcctactc aatagaatcg gtcattcatgc aaataaatgc360
caccttagtc aaaggcaaa ccagagtgca gtttgaggca aataagaatc aatataatct420

agcaagagcc caacaatcct ataattccat tgtacagata catgagaaaa atggctggta480
caccctccca aaggaagatg gctaaaatag ttgactgttg tatgtttgga ctaatgttgc540
tttaaagaaa atctttccaa catgcagaca aaagctttga gtgccctat tacagcagta600
ccgaagatgt tagttaatag atattttagt ggataatctg tcatctgaca tccagtataa660
gttacagcct tcgcattttg ctcattttag atatcttgga ctgagcagtg gggcctttac720
tgtatttttc ctgataaata cacatactgg ccactcccta tctcttttcc ttgaaaagt780
aactttttta aggagccaa gtcaacatca gggctactga agttggagggt ctttaggggt840
aactttcccta tattgagccc atggggttac aaggggttgg caatatattg ttccctttta900
cagccaatag aggttttaat cggatgtttc aatattgggt ttaggggatt ttaaggggccc960
tcttaagtca taatagccct

```

980

00673005.122700

## (2) INFORMATION ON SEQ ID NO. 130:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 792 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

ctgtttggca gggcgggggc cctcgcgaa atgtgtggcg ggcggcggtg tggctcccg 60
cgtctggcca agtctcagcg cagcgaaccg gcccgcgctc cgttggcctg gagccacac120
ccaccgggtc cctgaccocg cgccccccgc gcccggttcc cggoatgcct cgcgcccgtal80
agggaaacac gctccggaag ggtggtcagc gccgtggagg aggtgccccg agcagtgccc240
aagctgactc gggttccagt gacgatgagg cagccagtga ggcccgcgag accgccagtg300
aatgccccag ccttctcagc accactgcag aggcacagcct tgggggggat gtcgtggatg360
agcaaggggc agcaggaaga ccttgaggaa aagctgaagg agtatgtgga ctgtctcaca420
gacaagagtg ccaagaccgc gcaggtgcct cttgagagcc tgcgcctggc cctagcgtcc480
cgccctactc ccgactctct gctggagcgc cgccctcagc tagccgatgc cctggaaaag540
tgcctcaaga aaggggaagg cgaggaacaa gccctggctg ctgctgtgct aggcctgctc600
tgcgtgcagc tgggcccctg acctaaaggg gaggagctgt ttccacagcct gcagcctctg660
ctggtctctg tgctcagtga cagcacagct agccctgctg cccggctcca cgtgagtttg720
ctgtgcccc aaaaaaccct cctgcaactt atccctcagc agagtgggtg gttccccctta780
tcttcagcct cc

```

792

## (2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1092 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

00573305-122700

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

gtgggtcccc cgggtccgg cgcggttgag gccttcggtg gtgaacgagt ctccagcacc 60  
atgtctcggt tgtctggccc accagcccgg cgcggcccctt ttccggttagc gttgctgctt 120  
ttgttcctgc tcggcccccag attggtccct gccatctcct tccatctgcc cattaactct 180  
cgcaagtgcc tccgtgagga gattccacaag gacctgctag tgaactggcg gtaacgagatc 240  
tccgaccagt ctggggggcgc tggcgccctg cgcagcacct caagatcaca gattctgctg 300  
gccatattct ctactccaaa gaggatgcaa ccaaggggaa atttgccttt accactgaag 360  
attatgacat gtttgaagtg tgttttgaga gcaaggggaa agggcggata cctgaccaac 420  
tcgtgatcct agacatgaag catggagtgg aggcgaaaaa ttacgaagag attgcaaaaag 480  
ttgagaagct caaaccatta gaggtagagc tgcgacgcct agaagacctt tcagaatcta 540  
ttgttaatga ttttgctac atgaagaaga gagaagagga gatgcgtgat accaacgagt 600  
caacaacacac tcgggtccta tacttcagca tcttttcaat gttctgtctc attggaactag 660  
ctacctggca ggtcttctac ctgcgacgct tcttcaaggc caagaaattg attgagtaat 720  
gaatgaggca tattctctct ccaccttgta cctcagccag cagaacatcg ctgggacgtg 780  
cctggctctaa ggcactctac caacagcacc atcaaggcac gttggagctt tcttgccaga 840  
actgatctct tttggtgtgg gaggacatgg ggtaccacct acaccacaaga agtcaatgag 900  
ggacttcttt ttaatttggg aggatattga ctggttttgc aacaataggt ctattattag 960  
agtcacctat gacaaaaaat agggggttac ctagataatg ccaaagtcaag catttgtccc1080  
gggtccccct gtgggagctg tgggacgatg ttttcttttc tgcccccttt cccggagcgtg1092  
ggggggcaaa ta 1092

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1523 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

0967395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

ctcatgtcta aagaaattcc tttttgtgtg aaaaagacta agagcatctt caacagtgcc 60  
 atgcaagaga tggaggttta cgtggagaac atccgcagaa gtttgggggtt ttaattact 120  
 ctccatttag gacaccctac acaccacaac gccagtatca aatgctgctc gatccacca 180  
 accccagcgc cggcactgcc aagatagaca agcaggagaa ggtcaagctc aactttgaca 240  
 tgacggcacc ccccaagatc ctgatgagca agcctgtgct gagtgggggc acagggccgcc 300  
 ggatttcctt gtccgatatg ccgcgctccc ccatgagcac aaactcttct gtgcacacgg 360  
 gctccgacgt ggagcaggat gctgagaaga aggccacgtc gagccacttc agtgcgagcg 420  
 aggagtcctt ggaattccag ggataagagc acagcttccac cagccatcca ccaagacggg 480  
 acaagcaggg agtttatccg gcagcccaaa gccctttctt cctcaactgt cagctcctat 540  
 cacgacgaaa acggacaaaa cctccaccac cggcagcacc ctgaactcta acctggatcg 600  
 aagcaaaagt gagatggatt tgaaggagct gagcgagtcg gtccagcaac agtccacccc 660  
 tgttctctct atctctccca agcgcacgat tctgtagcagg ttccagctga atcttgacaa 720  
 gaccataag agttgcaaa cacaattagg cataaatgaa atctcggaag atgtctatac 780  
 ggcgctagag cacagcgatt cggaggattc tgagaagtca gatagtgcg atagtgcgta 840  
 tatcagtgat gatgagcaga agtctaagaa cgagccagaa gacacagagg acaagaagg 900  
 ttgtcagatg gacaaaagag catctgtctg taaaaaaaag cccaagccta caaacccagt 960  
 ggagattaaa gaggagctga aaagcacgtc accagccagc gagaaggcag accctggagc1020  
 agtcaaggac aaggccagcc ctgagcctga gaaggacttt tccgaaaagg caaaaccttc1080  
 acctcacccc ataaaggata aactgaaggg aaaagatgag acggattccc caacagtccl140  
 tttgggctcg gactctgatt cagagagcga acttgtcata gatttaggag aagaccattcl200  
 tggggggggg ggtcgaaaaa ataaagagga acccaagaaa ccatctccca aacaggatgt1260  
 -tgtaggtaaa actccacat ccacgcaggt gggcagccat tctccccggg aaacaccgggt1320  
 gctacccggc tcttcggccc aaactccgc ggtggggccc acagccacca ccagcacgtcl380  
 ctccacggtc accgtcacgg ccccgggccc cgccgccaca ggaagccag tgaaaaagcal440  
 gaggccgctt ttaccgaagg aggactgccc cgcccggtgca gcgggtccgt gtggaactcal500  
 tcaagtaaa ttccaacgt cct 1523

## (2) INFORMATION ON SEQ ID NO. 133:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673305.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

cgccgccccaa  gcgcgcagaag  ccgagctgtgg  aaaaggaggag  cagaggaggcg  ggaggcagag  60
gcagaggcgag  agcccggtgc  cgagaccaag  cgacagaccg  gcggggcggtg  gcctcgcaaa  120
gcccggctctg  cgagctctcc  cgacaccgga  gccggggagg  aaaagcagcg  actcctcgct  180
cgcatccccc  ggagcccgca  tccagactgg  cccggtagtct  aggggctcag  gaggcagatcc  240
cgaggcgagcg  tttgtctcagc  ctccgacgag  ggctggccct  ttggaaggcg  ccttcaacag  300
ccggaccaga  caggccacca  tgacogagaa  ttccagctcc  gccctgtggg  ccaagcccaa  360
gcggggccaag  gcctccaaga  agtccacaga  ccaccccgaag  tattcagaca  tgatcgtggc  420
tgccatccag  gcgcagaaga  accgogctgg  ctctcgcgcg  cagtcatttc  agaagtatat  480
caagagccac  tacaaagttg  gtgagaacgc  tgactcgcag  atcaagttgt  ccatcaagcg  540
cctgtgtcacc  accggtgtcc  tcaagcagac  caaaggggtg  ggggcctcgg  ggtccttcgg  600
gctagccaag  agcgacgaac  ccaagaagtc  agtggccttc  aagaagacca  agaaggaaat  660
caagaaggta  gccacgcca  agaaggcatc  caagcccaag  aaggtcgctc  ccaagccccc  720
aaaccaagaaa  cccaaagcca  ccccggtcaa  gaaggccaa  aagaagctgg  ctgccacgcc  780
caagaaagcc  aaaaaaccca  agactgtcaa  agccaagccg  gtcaaggcat  ccaagcccaa  840
aaaggccaaa  ccagtgaaac  ccaagcaaaa  gtccagtgcc  aagagggcg  gcaagaagaa  900
gtgacaaatga  agtcttttct  tgcggacact  cctcctctgt  tctatttttc  tgtaaaaaat  960
ttctcctctt  ttctcctctt  gatgctcaac  accactttt  gcccccttct  gttctgactt  1020
tataagagac  aggatattga  ttcttcagaa  attacagaat  aattcatttt  tcttaacca  1080
gttgtgcaag  gacagcaaca  accaatctaa  tgatgagaat  gtacttatat  ttgttttgc  1140
tattaaccta  cttacggggt  tagggatttg  cgggggggct  tgtgtgtttt  gttggcctgt  1200
ttgccatgaa  ggtagatgtg  ggtggggaga  agacacaagg  cagtttgttc  tggctagatg  1260
agaggggaacc  caggaattgt  gaggttagca  ggaatatct  tagggtagt  gagttttct  1320
tgagttagggc  accggttgtg  agagtttcag  aacctttggc  cagcaggaga  gagggtgtag  1380
ggagcgagcca  gcggcgaaa  gaaggagggt  gaaaaaaaac  gccaccgggc  tgacttccac  1440
ctcccaagtgg  tgagcagtg  gggcccaaac  ccagtttctc  tctcattttt  gttagtttgc  1500
cctttcgccc  tcctattttt  cttagggaag  gggagtgagg  tccaagtgc  agctggatgg  1560
gagaagccat  agtttctccc  agtcaagctg  gatgtagcca  ttgggggatc  tttgtggctt  1620
cagcaaaatc  tcttgtaaaa  ccggaagtga  aacttcaggg  gaagggtggg  gagtcaagcca  1680
agtgcctcag  tgtgccctgt  tgaaaacttag  gtttttccac  gcaatcgatg  gattgtgtcc  1740
taggaagact  ttctttttc  tctggatttt  tgttctcctc  gtacaagagg  gctctttgtc  1800
tggtttgggt  gggctggggc  cacttaaaac  ctcccgatct  ctttttgagt  cctttattat  1860
aagtagttgt  agctcgggga  gggggagggg  gagtggggcg  tagatctgtg  gtaagactta  1920
ctgcagtcga  tttgggattt  gctaagtagt  tttacagagc  tgcatgtgtg  tgcatgtgtg  1980
tgttttgtga  tatatacata  tctagggcta  gtacttagtt  tcaacacccg  gagctggggg  2040
aaaaaacctc  tacagttgtc  ttctcttat  tttaataaaa  atagaaaaat  cgcgcaactg  2100
cgcgctcccc  cccaccccc  ttttttaaa  aagtgttact  tgtgccggga  aaattttgc  2160
gtctttgtaa  ttttaaaact  ttaaaataaa  ttggaaggag  gagaacttga  aaaaaaaaaa  2220
aaaaaaaaaa  aaaaaaaaaa  a  2241

```

067335-133700

## (2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 631 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

tgacaatggc ttctttaaaa tactcagagg acaggatcac ggtggaatcg aatcagaagt 60  
 ggtggctgga attccacgca ccatcagta ctgggaaaag atctaactcg ccgtggggcct120  
 gtcgtgccag tctctggggg gagatggggg tagaaatgca tgtgatgcgt taagttcacg180  
 taagatacaa gtttcagaca gggtcggaag gactggattg gccaaacatc agacctgtct240  
 tccaaggaga ccaagtccct gctacatccc agcctgtggt tacagtgcag acaggccatg300  
 tgagccaccg ctgccaagcac agagcgtcct tccccctccg tgatccatcc atctccaggg360  
 agcaagacag agacgcagga atggaaaagcg gagttcctaa caggatgaaa gttcccccat420  
 cagttccccc agtacctcca agcaagttagc tttccacatt tgtocacagaa atcagaggag480  
 agatgggtgt gggagccctt tggagaacgc cagtctccca ggcctccctc atctatcpg540  
 tttgcaatgt caaacctctc tgatcttgtg tcagatgatt cttaatagga gtttattttt600  
 cgggcagctg cgaatcaggg gggttaaccag g 631

## (2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 980 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

09673305.122700

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ggggccggga gggctacttag ggcGggggct ggcacaggt acggcggctg cagggctccg 60  
gcaaccgcct cggcaacgcc aaccgctccg ctgcgcgcag gctgggctgc aggcctctcg120  
ctgcagcgct gggctggatct aggatccggc ttccaacatg tggcagctct gggcctccct180  
ctgctgcctg ctgggtgttg ccaatcccg gagcaggccc tctttccatc cctgttcgga240  
tgagctggtc aactatgtca acaaacggaa taccacgtgg caggcggggc acaacttcta300  
caactgggac atgagctact tgaagaggct atgtgggtacc ttcctgggtg ggcacagcc360

acccacagaga gttatgttta cggaggacct gaagctgcct gcaagcttcg atgcacggga420  
acaatggcca cagtgtccca ccatcaaga gatcagagac cagggctcct gtggctcctg480  
ctgggccttc ggggctgtgg aagccatctc tgaccggatc tgcctccaca ccaatgcca540  
cgtcagcgct gagggtgcgg cggaggacct gctcacctgc tgtggcagca tgtgtgggga600  
cggctgtaat ggtggctatc ctgctgaagc ttggaacttc tggacaagaa aaggcctggg660  
ttctgggtgc ctctatgaat cccatgtagg gtgcagaccg tactccatcc ctccctgtga720  
gcaccacgct aacggctccc ggcctccatg caccggggag ggagataccc ccaagtgtag780  
caagatctgt gagcctgggt acagcccgcac ctacaaacag gacaagcact acggatacaa840  
ttctacagcg tctccaatag cgagaaggac atcatggcgc agatctacaa aaacggcccc900  
gtggaggagg gttctctgtg tattcggact tctgcctaga gtcagggggt acaaaagtcc960  
cgggaatttg gggggccgccc 980

## (2) INFORMATION ON SEQ ID NO. 136:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2238 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN  
(C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

cacatgtttcg gggaccgagtg ggggtcaatc ttctgggtgct gctctctccag gtctctttcca 60
ggccgggtcat agacgttactc cctctgaggc cgaccgatgg ttctaaagg tgctaaagg 120
cgctccgggct cagcagcccc aggcctcagc tgctcctctg cagccagttc tccagcctcc 180
tccaccacct gccatctccc agccagcatc acctttccaa gggaatgcac tctctaccto 240
tcagcctgtg ccagtggggtg tggctcccag cctgcaccca gcttttgtcc ctgcccagtc 300
ctatcctgtg gccaatggaa tgcctctatc agccctaat gtgcctgtgg tgggcatcac 360
tcctctccag atgggtggcca acgtatttgg cactgcaggc caccctcagg ctgccatcc 420
ccatcagcata ccagcctgtg tcaggcagca gacattccct cactacaggg caagcagtg 480
tacccacagtg cctctcttta agcctcctgc tcagcaccto aacggttctg cagctttcaa 540
tgggttagat gatggcaggt tggcctcagc agacaggcat acagagggtc ctacaggcac 600
ctgcccagtg gatccttttg aagccagtg ggctgcatta gaaaataagt ccaagcagcg 660
tactaatccc tcccctacca accctttctc cagtgaacta cagaagacgt ttgaaattga 720
acttttaagca atcattatgg ctatgtatct tgtccatacc agacaggggag cagggggtag 780
cggtccaaagg agcaaaaacag actttgtctc ctgattagta ctcttttcc taatcccaaa 840
gggtccaaagg aacaagtcca ggcccagagt actgtgagg gtgattttga aagacatggg 900
aaaaagcatt cctagagaaa agctgccttg caattagggt aaagaagtca aggaattgtt 960
gctttctgta ctcccctctc cttacccttc ttacaaact ctggcaacct agagggcaag 1020
tatctgaaca agaattctata ttccaaagcac atttactgaa atgtaaaaa caacaggaa 1080
caaagcaat tccccttgtt ttccaggcca ttacctgcc tctgtcagt agtggcctgt 1140
attagatgc aagaagagtg gtttgtgctc aggtcgggga acagagaggc acgctatgt 1200

gccagaattc ccaggagggc atatcagcaa ctgcccagca gagctatatt ttgggggaga 1260
agttgagctt ccatttttag taacagaata aatattatat atatcaaaag ccaaattc 1320
tatttttatg cattttagaat attttaaata gttctcagat attaagaagt tgtagagtt 1380
gtaagtaact ttgcccaggc taaaggggct agttgtaaaga aattgtacat aagattgatt 1440
tatcattgat gctactgaa ataaaaagag gaaaggctgg aagctgcaga caggatccct 1500
agcttgtttt ctgtcagtca ttcatgttaa gttagcacatt gcaaccaaaa tcatgcttat 1560
gaccaaatac gtcaactagtg ttagtatttt tttaaataaa ggaaaaagcag tattgtcctg 1620
gttttaaaac tatgatggaa ttctaattgc attattttta tggaaatcaat cgaatatgcl 1680
tctatagaga atatatcttt tatataattg tgcagtttcc ttatgttaat cctttaacac 1740
taaggtaaca tgacataatc ataccataga agggaacaca ggttaccata ttggtttgtal 1800
atatgggtct tgggtgggtt tgttttatcc tttaaatatt gttcccatga gttttgtggg 1860
gatggggatt ctggtttttat tagcttttgt tgtgtcctct tccccaaac ccccttttgg 1920
tgagaacatc cctttgacag ttgcagcctc ttgacctcgg ataacaataa gagagctcat 1980
ctcattttta cttttgaacg ttggccttac aatcaaatgt aagttatata tatttgtact 2040
gatgaaattc ttaatactgc tttaacaaaa ataaatgttc atggtagaaa aatttggcca 2100
tgaagggtcg ttctttcccc ttctctttat tagtaaatga atttattttt cgttcttttg 2160
gctttactct ccattctact gctgctgtaa atccctagtt tagtgactag aaaaatacco 2220
ttaagattca tatttttca
2238

```

0673305.122700



## (2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 398 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

tgcagattgg ttgggggcagc ccgggggaggc tggctccgac acacgactga gtgtgcctac 60
actgggtccca cagggttttca gctgtggagt ttgggatctg agcttgagagc ccatttgttt120
ctggcagttc cgtcatatt ttccactga agacatcgcc tccgttcctt ccaagctggg180
agaccagaag tcaacaacag gaggggtggag agggccgggtc tcacaatccg cttggctggg240
gagtcacctg aggttcttgc atccctgaagc aaaccatgga gagctgggtgg ggacttccct300
gttttgctt cctgtgtttt ctaatgcacg ccggaggtca aagagacttt gattttggca360
gatgcccttg atgaccctga aaccaccaa gaagccaa          398

```

## (2) INFORMATION ON SEQ ID NO. 138:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1084 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

0067395.122700

- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

ggcgggtggcg gaagtgggag cgggcctgga gtcttggcca taaagcctga ggcggcggca 60
cgccggagatt ggcggcgttg agagctcggg agagtccctt ggaaccagaa cttggacctt 120
ctcgcttctg tctccggtt agtctcctcc tcggcgggag cctcgcgacg gcccgggccg 180
gagcccccag cgacggcccg cgtttgaagg atgacctcta ggaagaaagt gttgctgaag 240
gttatcatcc tgggagattc tggagtcggg aagacatcac tcatgaacca gtatgtgaat 300
aagaaattca gcaatcagta caaagccaca ataggagctg actttctgac caaggagggtg 360
atggtgggatg acaggctagt cacaatgcag atatgggaca cagcaggaca ggaacgggttc 420
cagttctctg gtgtggcctt ctacagaggt gcagactgct gcgttctggt atttgatgtg 480
actgccccca acacattcaa aaccctagat agctggagag atgagtttct catccaggcc 540
agtccccgag atcctgaaaa ctctccattt gttgtgtttg gaaacaagat tgacctcgaa 600
aacagacaag tggccacaaa gcgggacag gcctgtgtgt acagcaaaaa caacattccc 660
tactttgaga ccagtgccaa ggaggccatc aacgtggagc aggcgttcca gacgattgca 720
cggaatgcac ttaagcagga aacggagggt gagctgtaca acgaatttcc tgaacctatc 780
aaactggaca agaattgacc ggccaaggcc tcggcagaaa gctgcagttg ctgaggggggc 840
agtggagatt gagcacagag tcttccacaa accaagaaca cacgtaggcc ttcaacacaa 900
ttcccccttc ctcttccaaa caaaacatac attgatctct cacatccagc tgccaaaaga 960
aaaccccatc aaacacagtt acaccccaca tattctctca cacacacaca cacacggcac1020
acacacacac acagggtttg acgttattca gattgcggcc ttgcccgtgt tgggttcgtg1080
ggggg
1084

```

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 1259 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:
- (vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

09673355-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

taaaatacac aagaagagtc cacacactgt ttcacgagaa ggagtgtatc atgattttgta 60
gtaatcgaag aacatgttta tgggaacagg gtgactcagc totcotgggg aggatgggatg 120
aggagtttag aggaagagag ggtaccaaag gaggggaaag cagcagggtg ggtctggggc 180
atggacagga agcagagagct gggaaaagct acatctttta ttcagtcgtt ttcacaggag 240
ctgaaagtggg aatcagtaga tcgagaatcc acggccgggg accagttaga cttgagggagc 300
tgcttactac taagtggctg ctgcgagggg agggaccagt ggtctcagat ttctcagagc 360
atggaaagttt aaaaatatct catgagaacc tccctattcc tcagagaaac accaactgaa 420
aagagccagg aaaaaccggg aattttccaa aaggttctca cgttaaactt gtcttatctc 480
aggagagagc ccgctcttgt ctcccagttc ctggtagggg ctgcctgttg gaaagtgtac 540
ctggatgctt ctgggctccg ttgggcaata gcaatcttgg ctgatgtgca cagtctggct 600
ccagctcac cctttttttt taaaagtaag aaaaatagtt ctaccgatag ggactcgc 660
aagtccaatt atcttctagg attgaaaggt gcattttccc cataaaaaag gcgaggaa 720
ccatggctg ctttgtgtca cctcagtgac ttacagtcoc cottggcaat tagttggtag 780
tagagccagt catccttaac aaatcttttc acattttatt tctttcacat gtagtcatct 840
tcaaaaagga aagattttgga atttttagaaa aggggcaact cttcttttta gcattctcat 900
cagaaagtcg caaaaatcga tggaaatcatt tccactggga agattgacct ttgtattta 960
tttggggggg aaatttaataa gcattccaga tgcttgagc ttcttgcatc caggagatgc 1020
tgtgttcccc gtgatgcagc tggaaaccaa gctgcagcag gagatgcaag ttccaggatg 1080
ttccccactg agctggagga atactctacg cagtgatgct tgaatttttt gtatgaattall 1140
ttttgtgctc ctaccctttt cctccaaaac aaaaatttaga ggattatttt aatactttgg 1200
attcttcccc ctttttttag aaataaaagt ttttatgaaa agccaaaaaa aaaaaaaaaa 1259

```

## (2) INFORMATION ON SEQ ID NO. 140:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1938 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

ccaagatggc ggcacgatgc ctgcccggct gttgggggtgg cgggtgacgac aggcagcaaa 60
agaccagctg gtcccaagatt cgctgctgga gtgctgggat gagcctttct ctgccctctg 120
tgacatttcc aatttttagat aatgcctcac atctctgtcc ccccgggacc cctctggagcc 180
cccatgaccc ctaagaagac agcttgaacc tagatctcac cccacaggat ttgctggagcc 240
tgctggagcg gcocttgcaag ctggccctgc ttgtgggctc ccagctggct gtcatgatg 300
acctgtcact ggggggcttc cgaagtctca gtgcccatt tggccgagat cagggaccga 360
catttgacta ttctcacctc cgtgatgtct acagtaacct cagtcacctg cctggggccc 420
cagggggtcc tccagctcct caaggtctgc cctactgtcc agaacgatct cctctcttag 480
tgggtcctgt gtcggtgtcc tttagccca gtcctactat ggcagagatg ttggagcgga 540
atccccgggt agaaccaggg ggccggtacc gccctgcagg ttgtgagccc cgctcccgaa 600
cagccatcat tgtccctcat cgtgcccggg agcaccacct gcgctgctg ctctaccacc 660
tgaccccttt cttgcagcgc cagcagcttg cttatggcat ctatgtcatc caccaggctg 720
gaaatggaac atttaacagg gcaaaactgt tgaacgttgg ggtgcgagag gccctcgctg 780
atgaagatgt ggaactgcctg ttcttgcaag atgtggacct cttgccagaa aatgaccaca 840
atctgtatgt gtgtgacccc cgggggacccc gccatgttgc cgttgctatg aacaagtttg 900
gatacagcct cccgtacccc cagtactctc gaggagtctc agcacttact cctgaccagt 960
acctgaagat gaattggcttc cccaatgaat actggggctg ggggtgtgag gatgacgacal020
ttgtaccagg ggtgcgcctg gctgggatga agatctctcg gcccccacac tctgtaggac1080
actataagat ggtgaagcac cgaggagata agggcaatga ggaataatccc cacagatttg1140
acctcctggt ccgtacccag aattcctgga cgcaagatgg gatgaactca ctgacataacc1200
agttgctggc tcgagagctg gggcctcttt ataccaatcat cacagcagac atttgggactg1260
acctctgggg tcctcgggct ccttctgggc cactttaccc acctggttcc tcccgaagcct1320
tccgtcaaga gatgctgcaa gcgcggccccc cagccaggcc tgggccccta tctactgccal380
accacacagg cctccagagt tcacactgac tccctctccc tgtctacact aatcatgaaal440
ccgaatctat ggggttgtat tctccccacc ctacagctcct cactgttctc agagggatgt1500
gagggaactg aactctgggt cgtgtctagg gggtaggggc ctctccctca ctgctggaact1560
ggagctgggc tcctgtagac ctgagggggc cctctctcta gggctctctg tagggcttat1620
gactgtgaat ccttgatgct atgattttat gtgacgattc ctaggagtcc ctgcccctag1680
agttaggagca gggctggacc ccaagccccc cctctctcca tggagagaag agtgatctgg1740
cttctcctcg gacctctgtg aatatttatt ctatttatgg ttcccgggaa gttgtttgg1800
_gaagggaagcc cctccctggg cattttctgc ctatgctgga atagctccct cttctggtcc1860
tggtctcagg ggctgggatt ttgatataat ttctaataaa ggactttgtc tcgcaaaaaal1920
aaaaaaaaa aaaaaaa 1938

```

## (2) INFORMATION ON SEQ ID NO. 141:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1874 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

0075395-12700

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

caaaaaaac tcttaattatt ctggagtcatt cattcccttc gacagcattt tccctctgctt 60  
 tgaagagccc agaaatcagtg gttggccatg atgacaaacta cagaaaaaac agaggcagct 120  
 tctttgcca gacctttcaa agccatttta ggctgttagg ggcagtgagg gtagaatgac 180  
 tctttgggta tttagatttc aaccatgaag tctotaacaa tgtattttct tcacctctgc 240  
 tactcaagta gcaattactg tgtctttggt ttgtgctagg ccccccgggtg tgaagcacag 300  
 accccttcca ggggtttaca gtctatttga gactcctcag ttcttgccac tttttttttt 360  
 aatctccacc agtcattttt cagacctttt aactcctcaa ttccaaact gatttccctt 420  
 ttgtcattct cctcctcttc cttccttgta gccttttgac ttctatttga aattaggatg 480  
 taaatctgct caggagacct ggaggagcag aggataatta gcatctcagg ttaagtgtga 540  
 gtaatctgag aaacaatgac taattctctgc atattttgta acttccatgt gaggggtttc 600  
 agcattgata tttgtgcatt ttctaacag agatgaggtg gtatcttcac gtagaacatt 660  
 ggtattcgct tgagaaaaaa agaatagttg aacctatttc tctttcttta caagatgggt 720  
 ccaggattcc tcttttctct gccataaatg attaatataa tagcttttgt gtcttacatt 780  
 ggtagccagc cagccaaaggc tctgtttatg cttttggggg gcataatgtt ggttccattc 840  
 tcacctatcc acacacata tccgtatata tcccccttac tcttacttcc cccaaattta 900  
 aagaagtatg ggaagtgaga ggcatttccc ccacccatt tctctccca cacacagact 960  
 catattactg gtaggaaact gagaacttta tttccaaagt gtccaaacat ttaaccaatc 1020  
 tattaatata atgatgctat ttgcaattcc tgcctcagg ggaggggaga taagaaaccc 1080  
 tcacctctca caggtttggg tacaaagtgg aacctgcttc catggccgtg tagagcatgt 1140  
 gtgcccctgg tctctgagg aagctggggg tcatgacaa ggcagatgta aagtattct 1200  
 tgaagtccga ttgaggctgg gagacagccg tagtagatgt tctactttgt tctgctgtct 1260  
 tctagaaaga atattttggt ttctgtgata ggaatgagat taattccttt ccaggatatt 1320  
 tataattctg ggaagcaaaa cccatgcctc cccctagcca ttttactgt tatcctatt 1380  
 agatggccat gaagaggatg ctgtgaaatt cccaacaaac attgatgctg acagtcatgt 1440  
 agtctgggag tgggggaagt atcttttgtt cccatcctct tcttttagca gtaaaatagc 1500  
 tgagggaaaa gggagggaaa aggaagttaa ggaataacct gtggtggttg tgatccctag 1560  
 gtctgggag ctcttgaggg tgtctgtatc agtggatttc ccatccctgt tgggaaatt 1620  
 gtaggctcat ttactgtttt aggtctagcc tatgtggatt ttttctaac atacctaaagc 1680  
 aaaccagctg tcaggatggt aattcttatt cttctgttca gttaagtttt tcccttcact 1740  
 tggggcactga agggatatgt gaaacaatgt taacattttt ggtagtcttc aaccagggat 1800  
 tgtttctgtt taactcttta taggaaagct tgagtaaaat aaatattgtc tttttagatg 1860  
 tcaaaaaaaa aaat

1874

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 142:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 198 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ROIWTMNLQR YWGEIPISSS QTNRSSFDLL PREFRLVEVH DPPLHQPSAN KPKPPTMLDI 60  
 PSEPCSLTIH TIQLIQHNRR LRNLIAATAQ QNQQTGEGVK TEESEPLPSC PGSPPLPDDL120  
 LPDCKNPNA PFQIRHSDPE SDFYRGKGEP VTELSWHSCR QLLYQGSBTN PGQRRAFDCA180  
 NESVLEDPNL MLAHEYWF 198

## (2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

IVWMVRLHGS EGMSSIVGGF GLLAEGWCRG GSWTSTRRNS RGSKSKELL VLWDDIGISP60  
 QYLCRFIVHM SLQQQTFFIK QQAFVGVQRL IM 92

## (2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

00573395.122700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

DPCPERSTKN RHGAQGMFKS LQGFFRSRSA GAGANHRVLR SPDVQGSRTK GRSGPEPRQG60  
 GTTLFTAAASQ SGLGGCLDLE RPEARIASDP ESWEVD 96

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

EGRVQQGSFV NVQQGPQEPF IEFIHQLTQA IKSTHGTSTI PRVSRITLKD KP 52

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

PSRTSHSGTL PIPRLKICFK KRGNMNKDPT TLLAQVLFLL NFLNLON

## (2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

LSKFKKLVRN NTCASSVVGSLFIFPLFLKH IFKRGMGNVPLWLVLGYTR YPWNGRCSMC60  
ALNCLG 66

## (2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 187 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

REGGRPEGN GDIRGGLRSG CDLSLLAPLL PPSSSESWECCYPWKIKLGL QELSVWEESSM 60  
AQHSACVFFC SGSLSPFPSSQ PQLSPSPSS SPEDSSDGRA GPPEPTGSSG CTGSWCSSLSP120  
VHFSSHWGMEC PCILCCRSPLHLRGLGSPSPQCPSLSQ TVGWNMRLEA ERGSEHHSFPC180  
TWVASC 187

006723665-122700



## (2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 147 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

REDWNRGKGE VAPCFVQPGS WQPWCWGLDP TTPAHLAEHL VPIEDCLPLL LHLQLPPLL 60  
 TFHTLQDCVC SGSPEGCS SC CHRASILILL LIVQLLSVCI RLSDQRVHQH QEGHVEQQGT120  
 HHGQVDDND LGGGLRSSY LHSRSRQ 147

## (2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 142 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

FFFFFWREIK QFNDGFELDLH TTLRQEDKIF SPCTGTTKFR DKRQPKYRGC GVQIHAQPRV 60  
 SCSNRPSGSV TVDTGERDC PDSSAGEGT GSRVCMGTPC PSARSAQGT A NTSFQCTLKT120  
 QWAQAQLSH QSCPQGSWG WG 142

## (2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 464 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

0073395-122700

- (ii) MOLECULE TYPE: ORF  
 (iii) HYPOTHETICAL: yes  
 (vi) ORIGIN  
 (A) ORGANISM: HUMAN  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

RQQTVLGSCS SSILPCQLLK HQGSSKTEMT KNWLIQTKRR YFSSPKQMSM THWPTAWLT 60  
 GCSVTFLFLFP SQYVDVASLG LVPQLTGSTL YKYNNFQMHL DRQQFLNDLR NDIEKKIGFD120  
 AIMRVRTSTG FRATDFFGGI LMNNTTDVEM AAIDCDKAVT VEFKHDDKLS EDSGALIQCA180  
 VLYTTISGQR RLRIHNLGLN CSSQLADLYK SCETDALINF FAKSAFKAVL HQPLKVIREI240  
 LVNQTAMHML CYRKNCASPS AASQLILPDS MKVLPVVMNC LLKNCVLLSR PEISTDERAY300  
 QRQLVMTMGV ADSQLFFYPQ LLPHTLDVK STMLPAAVRC SESRLSEEGI FLLANGLHMF360  
 LWLGSSSPEE LIQGIFNVPS FAHINTDML LPEVGNPYSQ QLRMIMGIIQ QKRPYSMKLT420  
 IVKQREQPEM VFRQLVEDK GLYGGSSYVD FLCCVHKEIC QLN 464

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 172 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: ORF  
 (iii) HYPOTHETICAL: yes  
 (vi) ORIGIN  
 (A) ORGANISM: HUMAN  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

TMLEKIPKEE QEETSAIRVG FITYNKVLHF FNVKSNLAQP QMMGVTDVGE VFWPLLDGLF 60  
 VNYQESQSVI HNLLDQIPDM FADSNENETV FAPVIQAGME ALKAADCPGK LFIFHSSLPT120  
 AEAPGKLKNR DDKKLNVTK EKILFQPQTN VYDSLAKDCV AHRLLCPTLP LS 172

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 141 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: ORF

00673325-122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GSTVTFTEFVI VLELHGHCILV TIDGSHFYIG GVVHQDSTKE ISGSETCAGT NPHNSIKAYF 60  
- LFNIISEVVQ KLLSIQVHLE IVVFKVGGSS ELRNQFQRGH VHILTRKEEE CHRAAGEPRSI20  
PWPMSHRHLF GAGKVSSLCI Y 141

(2) INFORMATION ON SEQ ID NO. 154:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 504 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

LDRCGLYPVS SLQVEGSLW RAAGVFQPPP GLAHANDWRF TARVHGGALG EHDKMVAAAT 60  
GSEILLMALQ AEGGGSEIGV FHLGVPVEAL FVGNQLIAT SHTGRIGVWN AVTKHWQVQEL20  
VQPITSYDAA GSFLLGCGNN GSIYYVDVQK PPLRMKNDL LVSELYRDEA EDGVTALSVY180  
LTPKTSDSGN WIEIAYGTSS GGVRVIVQHP ETVGSQFQLF QTFTVHRSPV TKIMLSEKHL240  
ISVCADNNHV RTWSVTRFRG MISTQPGSTP LASFKILALE SADGHGCCSA GNDIGPYGER300  
DDQQVFIQKV VPSASQLFVR LSSTGQRVCS VRSVDGSPPT AFTVLECEGS RRLGSRPRRY360

LLTGQANGSL AMWDLTTAMD GLGQAPAGGL TEQELMEQLE HCELAPPAPS APSWGCPLPSP420  
SPRISLTSLSH SASSNTSLSG HRGSPSPQA EARRRGGSF VERCQELVRS GPDLRRPPTP480  
APWPSSGLGT PLTPPKMKLN ETGF 504

(2) INFORMATION ON SEQ ID NO. 155:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 289 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

05673395-122700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GQPARPGAMA AAATAEGVVP SRGPPGEVIH LNVGKRFST SRQTLTWIPD SFFSSLLSGR 60  
ISTLKDEPGA IFIDROPTVF APILNFLATK ELDPKGVHGS SLLHEAQFYG LTPLVRLQL120  
REELORSSCG NVLFNGYLFP PVFPVKRRNR HSLVGPQQLG GRPAPVRRSN TMPFNLGAG180  
LLGRMLDEKT PPSPGQPEE PGMVRLVCGH HNWIAVAYTQ FLVCYRLKEA SGGQLVFSSP240  
RLDWPMRTTG ASQPGCMVGL WVNMTRWVQQ PFAARSCYGL CRRKAVAPR 289

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 161 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

VPQDQGIPIRH HGSCVVQKEV SLSFILGGVR GVPRPLEGHG AGVGGRRRSR PLRTSSWQRS 60  
TKLPPPPRRRA SACGGGLGLPR WPDKEVLLEA EWRLVREMRG EGLGRQPHEG AEGAGGASSQ120  
CSSCSISSCS VRPPAGAWPR PSMVVVRSHM AKPLAWPVS R 161

(2) INFORMATION ON SEQ ID NO. 157:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 262 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

0957305.122700

QLWGFAAGSD SRPAMGCDGG TIPKRHELVK GPKKVEKVDK DAELVAQWNY CILSQEILRR 60  
 PIVACELGRL YNKDAVIEFL LDKSAEKALG KAASHIKSIK NVTELKLSDN PAWEGDKGNT120  
 KGDKHDDLQR ARFCIPVVLG EMNGRRHRCF LRCGCVFSE RALKEIKAEV CHTCGAAFQE180  
 DDVIVLNGTK EDVDVLKTRM EERRLRANWK RKQRNPRQQS LFQNMMSVKK PQGHQKLRQG240  
 SLKKPALILE RRRKPTWLPKA QQ 262

## (2) INFORMATION ON SEQ ID NO. 158:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 138 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

CHRAQWHOGG CGRAEDKDDG EKAEESELEKK TKKPKAAESV SKPDVSEEP GPSKVKTGKP 60  
 EEASLDREK KTNLAPKSTA MNESSSGKAG KPPCGATKRS IADSESEAY KSLFTTHSSA120  
 KRSKEESAHW VHTSYCF 138

## (2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 168 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

HLVLKQTLPL WWSLFSFPPIR SQPSLLHPCL QHVHILLGAI EHDDIILLEG SPTRVANFRF 60  
 YLFQGSRLRH TAAAPKEAEP VSAVHLQAHN GADETRPLEV IVLVTFVSF IPFPGRITRK120  
 LQLCHILNAF NVRCCLPKSL FCRFVQEFEN DGIFVIKSAK FTGNYWSS 168

## (2) INFORMATION ON SEQ ID NO. 160:

00673705.122700

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 238 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

HQWHITAMGS QHSAAARPSS CRRKQEDDRD GLLAEREQEE AIAQFPYVEF TGRDSITCLT 60  
 CQGTGYIPT E QVNELVALIP HSDQRLRPQR TKQYVLLSIL LCLLASGLV FFLFPHSVLV120  
 DDDGIKVVVK TFNKQDSLVI LTIMATLKIR NSNEYTVAVT SLSSQIQYMN TVVNETGKAE180  
 MGGFFSYVYV FCTVPEILVH NIVIFMRTSV KISYIGLMTQ SSLETHHYVD CGGNSTAI 238

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 91 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

SSHEDHYVVH QDLRYRAEEV HIGKRSSH LG LPGKIRHCVH VLNLAGQAGH CHRVEVGVPD60  
 FQGGHDGENY KGVLLIKCDF HRFDAVIHK D 91

00573305.122700

## (2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

MRKQEEHQT RCQETKQDQG EDILLSSLRA QSLITVWDQS HQLIYLLCWN VACPLARETG 60  
 DAISPGEFHI WELNSGFFLL SFSQQTVPVI FLLSPAGGGA SSSGMLRPHG RDMPLVSCPA120  
 SSVGGAARTQ RAG 133

## (2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AAGAAGPHRR RHPLHPSLLR EHHSQAQAPE GVRFGQSTLS RIEAVQPQLP RPSGLPSLWG60  
 WLPWLLGTRP QRHFEIPFET QCSTAVRRS A 91

## (2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

00673305-122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

LDNPTQRNKD QLIRAAVKFL DTDTCYRVE EPETLVELQR NEWDPPIEWA EKRYGVEISS 60  
 STSIMGPSIP AKTREVLVSH LASYNWALQ GIEFVAAQLK SMVLTGLID LRLTVEQAVL120  
 LSRLEEEYQI QSWGNIWEAH DYELQELRAR TAAGTLFIHL CSESTTVKHK LLKE 174

(2) INFORMATION ON SEQ ID NO. 165:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 66 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CLGLLHPVAD GVGVQKLHGC PDQLILVSLG WVVQSRVAQC GQVHGVLVDG ILLGIPLSTL60  
 CTCQGL 66

(2) INFORMATION ON SEQ ID NO. 166:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 132 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SWRETEIKEQ LTHELCTIIQ QNELRKAKKL EELMQQLDVE ADEETLELEV EVERLLHEQE 60  
 VESRRPVVRL ERPFQPAEES VTLEFAKENR KCQEQAQVSPK VDDQCGNSS IPFLSPNCPN120  
 QEGNDISAAL AT 132

00673395-122700



## (2) INFORMATION ON SEQ ID NO. 167:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

QILMSHSPFPQ AEMASLNEPL VSLILLVVRV AISRFPQAP KSLHRLHLV VASTPPTSWP60  
FGAHFAV 67

## (2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

NGLSKRTTGL LDSTSCSCSN LTSTSSSKV SSSASTSSCC INSSNFLAFR SSFCCMIVQR60  
CSVSCSFISV SRHE 74

## (2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673395.122700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

GRGGLGCRSW RCAGSSRPYS EVFSVALLER GSSCILRIFC ISAPFSSRCH RMPQIGPVPS60  
VNQTSETASL QGQSPSTDEL ERDSEMQRP 89

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 74 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

GPLHFRIPLK LICTWTLTLK RGGFRSLIHR GDRTYLGHPM AARREGSRNA KYSQDAGGTP60  
LKERHGENFR VRAR 74

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 89 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

AVAFQNPSQA HLYLDSDEPA RRFPKSDSPR GQDLFGASDG SEKRREPCKCK IFSRCRRNPS60  
QGAPRRKLQS TGAMIQHNR TCSPAHLSP 89

00673305-122700

## (2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 100 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

PSPAVLGDPQ PSASGAVHRK LSLEVCCQCE RAQMGPVMAA TSTSCGRARL LARSAQWLTT 60  
 MLSSAAVWLW SRRLITCGEN PSYALVAFLC LSRESPSAKE 100

## (2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 495 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

SRTNTPVETW KSGKKGQSYT YIIIEENTTS FTWAFQRTTF HEASRKYTND VAKIYSINVT 60  
 NVMNGVASYC RPCALEASDV GSSCTSCPAG YYIDRDSGTC HSCPPNTILK AHOPYGVQAC120  
 VPCGPGTKNN KINSLCYNDC TFSRNTPTRT FNYNFSALAN TVTLAGGPPSF TSKGLKYFHH180  
 FTLSLCGNQG RKMSVCTDNV TDLRIPEGES GFSKSITAYV QQAVIIPPEV TGYKAGVSSQ240  
 PVSLADRLIG VTTDMTLDGI TSPAELFHE SLGIPDVIFV YRSNDVTQSC SSGRSTTIRV300  
 RCSPPQKTVPG SLLLPGTCSO GTCDGCNHFH LWESAAACPL CSVADYHATV SSCVAGIQKT360  
 TYVWREPKLC SGGISLPEQR VTICKTIDFW LKVGISAGTC TAILLTVLTC YFWKKNQKLE420  
 YKYSKLVNNA TLKDCDLPAF DSCAIMEGED VEDDLIFTSK KSLFGKIKSF TSKRTPDGF480  
 SVPLKTSSSG PDMDL 495

## (2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 118 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GHNEEISSSG CCRMLAPKSP QACKGAMQGE EAGEAGSASH RMSGPPPEV FSGTESNPSG 60  
VLEEVNDLIF PKSOFLLVKM RSSSTSSPSM MAQLSAAGRS QSLRVAFITS LEYLYSSF 118

(2) INFORMATION ON SEQ ID NO. 175:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

RNTRGHRAC QRKLKPCSVS TVYKFNRNAC QRLFEKRVF SEPVLSVQEK GVLLKRKLSL 60  
LEQDVIYNED GRNKLKKQGE TPNEVCMFSL AYGDIPPELI DVSDFECSLC MRLFFEPVTT120  
PCGHSFCKNC LERCLDHAPY CPLCKESLKE YLADRRYCVT QLLEGINSEV SA 172

(2) INFORMATION ON SEQ ID NO. 176:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 248 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00673305-102700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

QIGGTVSHSC WKELIVKYP DELSERKKIY DEETAELSHL TKNVPIFVCT MAYPTVPCPL 60  
HVFEPYRLM IRRSIQTGTK QFGMCVSDTQ NSFADYGCML QIRNVHFLPD GRSVVDTVGG120  
KRFRVLKRGK KDGYCTADIE YLEDVKVENE DEIKNLRELH DLVYSQACSW FQNLDRFRS180  
QILQHFGSMP ERRENLAAP NGPAWCWLL AVLPVDPRYQ LSVLSMKSLK ERLTKIQHIL240  
TYFSRDQF 248

- (2) INFORMATION ON SEQ ID NO. 177:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 133 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

HSTSYLLDTL LSFCKEDNM VHDLNNAQDN SYRTNVRKGL LLAQKTTSCR ENTRNLRHRL 60  
ILLEYHHKLR KTYRLHWEFL LVFSAYFFHL HLQSHPVKE TTFFSAEHLF LELTEQVLR120  
LEFFQIVLSGR HFC 133

- (2) INFORMATION ON SEQ ID NO. 178:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 152 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

SAVKGWDLN MAAVVAATAL KGRGARNARV LRGILAGATA NKASHNRTRA LQSHSSPEGK 60  
EEPEPLSPEL EYIPRKRGKN PMKAVGLAWA IGFFCGILF ILTKREVDDK RVKQMKARQN120  
MRLSNTGEYE SQRFRASSQS APSFDVGSV QT 152

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 114 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

EGRSAPQVCT PDPTSGDGAL WEEALNLWLS YSPVLNRMF CRAFTCFTRS LSTSRLVRMK 60  
 RRIPQGKPKMA QASPTAFMGF LPLFLGMYSS SGDRGSGSSL PSGLWLCRA RVLL 114

## (2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GLATAWASCA LWWTSEARTG IWAKPEDLTV NSLGGSQRSS GLHPRPNIRG RGTLLGGSPEP 60  
 LALILARVGQ PHVLPSLHLL HTVLVHFPLG EDEEEDTTRE ADGPGQSHSF HGVLAPLSGN120  
 VFQLRG 126

## (2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673005-122700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

LVKCPKGEFS FHSNKDRFAH SLKQNVAMNI QPLHTYKDVR MIPPTKHTHS HIRTHTHMHT60  
RACTHGHMHT HTHT 74

(2) INFORMATION ON SEQ ID NO. 182:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 84 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

ILISFKRQRI CAFTQAECEG EYSAPAYIQR CTHDSFQAH TQSHTHTHTH ANTRVHTRTH60  
AHTHAHVNTC THAHTCTHAN TDTL 84

(2) INFORMATION ON SEQ ID NO. 183:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 70 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

VCPCVHVCTC VHVCMCLVRV VCVHVSVCAR ACVHVCVCAC VTVCVLGGGN HAYIFVCMQG60  
LNIHGHIILE 70

002227.5662960

## (2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TVKFLRLRLKV RGTKAGEISL SPEEGEADGS QQPALFLRVI FKFANCITGG PTFCFYQEFF60  
 FCSKTLVMGI F 71

## (2) INFORMATION ON SEQ ID NO. 185:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

YLNLIQVLQE GLLSVFIKSF SFVQRHNLWE YFERVRNAGI KRCCRLILKV LTEPV 55

## (2) INFORMATION ON SEQ ID NO. 186:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673395-122700



- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

KQGRLLTSIC FSLRLTKANL PCFGSPHFQP SQEFHCS

37

(2) INFORMATION ON SEQ ID NO. 187:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

SPLLWFPALS AFGISLFII YFHDLSAKLL IFCRKKV

37

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

MPDFKIARRK QTLRIKKAGH LLNFWLHHKA LGLGFLYLYIE VFSVALGAVC LSPTPKDARK 60

TSTISHVATF TSMPHKCLSE SPNSAFPQNK PNAIRQKKKK

100

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 256 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual

00673305.1.22700

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

RSQAGPEAGQ PLPGSGKRSS CCHCSSLGACS MGFLPRTVEL FYDVLSPYSW LGFEILCRYQ 60  
 NIWNINLQLR PSLITGIMKD SGNKPPGLLP RGLYMANDL KLLRHHQLIP IHFPKDFLSV120  
 MLEKGSLSAM RFLTAVNLEH PEMLEKASRE LWMRVWSRNE DITEPQSILA AAEKAGMSAE180  
 QAQGLLEKIA TPKVKNQLKE TTEAACRYGA FGLPITVAHV DGQTHMLFGS DRMELLAHL240  
 GEKWMGPIPP AVNARL 256

(2) INFORMATION ON SEQ ID NO. 190:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 196 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

SLAFTAGGIG PIHFSPSRCA SSSIRSEPNN MWVWPSTWAT VMGSPKAPYL QAASVVSLSW 60  
 FFTFGVAIFS RSPWACSADI PAFSAAARML CGSVMSSFLD QTRIHSSRDA FSSISGCSKF120  
 TAVRRMADK LFFSSITDKK SLGKWMGIWR WCLASFKSFA MYSPLRGSRP GGLFPLSFM180  
 PVMRLGRNCR LMFQIF 196

(2) INFORMATION ON SEQ ID NO. 191:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 116 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00673305-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

EQRASAMRSS RAFRTVCSSW ATHGQLPAGL DDKTNIKTVC TYWEDFHSCT VTALDQCQEG 60  
AKDMWCKLRK ESKNLNIQGS LFEICGSGNG AAGSLLPAFP VLLVSLSAAL ATWLSF 116

## (2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 182 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

KRESGFPTIL YECFQHHRSS QRPQRTNGSS SRFFGAWSEC GWARGGSWPH AQKESQVAKA 60  
AERDTRSTGN AGSRDPAAPL PLFQSSNKLP WMLRFLDSFL SLSHISFAPS WQSVRAVTQ120  
LWKSSQYVHT VLMFVLSSRP AGSWPCVAQL EQTVRKALED RIALARCSHG LHQIRYLHRE180  
DQ 182

## (2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 105 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

HLANKTQEIK RNKKENQDFF QSYMVSFSIT ENHNVPKELM DLPLDFREHG VSVGGGRAGGA 60  
GPTLRKARS LKLPRETPGA PGTEGAGTTP PRCRCRRVRI SCLGC 105

## (2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:

00673305.122700

- (A) LENGTH: 426 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EIYSLSRFIE VKMSKKISGG SVVEMQGDEN TRIIWELIKE KLIFPYVELD LHSYDLGIEN 60  
 RDATNDQVTK DAAEAIAKKHN VGVKCATITP DEKRVEEFKL QQMWKSPNGT IRNILGGTVF120  
 REAIIICKNIP RLVSGWVKPI IIGRHAYGDQ YRATDFVVPG PGKVEITYTP SDGTQKVTYL180  
 VHNFEEGGVV AMGMYNQDKS IEDFAHSSFQ MALSKGWPLY LSTKNTILKK YDGRFKDIFQ240  
 EIYDKQYKSQ FEAQKIWYEH RLIDDMVAQA MKSEGGFIIA CKNYDGDVQS DVAQGYGSL300  
 GMMTSVLVCP DGKTVEAEAA HGTVTRHYRM YQKGQETSTN PIASIFAWTR GLAHRAKLDN360  
 NKELAFFANA LEEVSITIE AGFMTKDIAA CIKGLPNVQR SDYLTTFEEM DKLGNLKKIK420  
 LAQAKL 426

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

RLLPKHLQRR QALYCYQALL CGLTLWSRQK WKQNDWWTSP VLSGTCGSDG LQSRGQPLLL60  
 LSCHLDKPAR WSSCRESHTL GPQSPTARHH HSFYRPR 97

(2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

00673355.122700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

LILIIHPHGN TTTFFKVMYQ VCHLLGSVTW CVGYLYFSRP RNNKISCSVL IPISMTYDD60  
 RFYPSTHKPG DIFADNGFSE DRATQNISYG AIN 93

(2) INFORMATION ON SEQ ID NO. 197:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 410 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TDQPNIQSVK IHSLEPLRNPN KGCECPERRD GFGFIKCVDR DVRMFFHFSE ILDGNQLHIA 60  
 DEVFTTVPD MLSAQRNHAI RIKKLPGKT V SFHSHSDHRF LGTVEKEATF SNPKTSPNKL20  
 GKEKEAEDGI IAYDDCGVKL TIAFOAKDVE GSTSPQIGDK VEFISIDKQR PGQVATCVRL80  
 LLGRNSNSKR LLGYVATLKD NFGFIETANH DKEIFFHYSE FSGDVDSLEL GDMVEYSLSK240  
 GKGNKVSARE VNKTHSVNGI TEEADPTIYS GKVIRPLRSV DPTQTEYQGM IEIVEEGDMK300  
 GEVYFPGIVG MANKGDCQLQK GESVKFQLCV LGQNAQTMAV NITPLARATV ECVKQDFGFI360  
 NYEVGDSKKL FFHVKEVQDG IELQAGDEVE FSVIPKSSGG LAGSGACRCF 410

(2) INFORMATION ON SEQ ID NO. 198:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

LNAILNFFHM EKELLAIYSF IVNEAKLIHF TFHCGPAQGC DVVSHSLCIL AQDTQLELDA 60  
 LPFLQAIPFV GHPNDKAWID LTFHIALLN LNHSVLVSLC WINTPQGANY FARVNGGISF120  
 LSNAIH 126

09673305.123700

## (2) INFORMATION ON SEQ ID NO. 199:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

KSHTSCNLLS RPLFVTNTKF NLISYLRRSR SFHILGLKSN SQFHPTVIIS NNAILSLLLF60  
AFIWASGFRI GKSGFFFYRA QKTVI 85

## (2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

ATMRLSVCLL MVSLALCCYQ AHALVCPAVA SEITVFLFLS DAAVNQLQVAK LNFPPPEALAA60  
KLEVKHCTDQ ISFKKRLLI 79

## (2) INFORMATION ON SEQ ID NO. 201:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

09673395.122700

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

SVQCFTSNLA ARASGGGLSL ATWRFTAASL KKKTVISEA TAGQTRAWAW

50

(2) INFORMATION ON SEQ ID NO. 202:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

QVAVEKTLET QVEHFYMSHT HIFSLFPPT FSNEKPFLLR YLIGAVLHFQ LGCKSFWRWI60  
KFGNLEVYRS VT 72

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

SFSPSLTTRA MNSSASSTST CSSYTLGTRL PVGGRGPTKV TCCTSNRLTL SLD

53

00673306.122700

## (2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

ALVVRELTKR FIGDYERNAG NLYTRQVQIE GETLALQVQD TPGIQVHENS LSCSEQLNRC 60  
IRWADAVVIV FSITDYKSYE LISQLHQHVQ QLHLGHPAAC GWSWANKSDL LHIKQVDPQL120  
G 121

## (2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 205 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GPLPALAAGS TFPVLACSSA MAPKGSSKQQ SEEDLLLQDF SRNLSAKSSA LFFGNAFIVS 60  
AIPFIWLYWRI WHMDLIQSAV LYSVMTLVST YLVAFAFKNV KFVLKHKVAQ KREDAVSKEV120  
TRKLSEADNR KMSRKEKDER ILWKKNEVAD YEATTFISIFY NNTLFLVVI VASFFILKNF180  
NPTVNYILSI SASSGLIALL STGSK 205

## (2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

00673305-122700



(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

VLHQSSPSC LLAPNAPCQL HPLALCLWVA CGIWKSSRVV RVGDTACFYS LEPLKNPAEC 60  
NSVFVYWLFF DRLLKLNELK GKLRVLGRLL KGKKCLAMCC NKKRRK 106

(2) INFORMATION ON SEQ ID NO. 207:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 105 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

STYGQYVVHC GVEVLQYEEG SNNDHQEQS VVIEDGKCCS FIISNFILLP QDSFIFLLPR 60  
HLSIISFRKF SSHFFGNSIL PLLCYFVLEN KPHILVCKGY QICAY 105

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 549 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

09673355.123700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

LYPNFLVNEL ILKQKQRFEE KRFKLDHSVS STNGHRWQIF QDWLGTQDN LDLANVNLML 60  
 ELLVQKKKQL EAESHAAQLQ ILMEFLKVAR RNKREQLQEI QKELSVLEED IKRVEEMSG120  
 YSPVSEDSTV PQFEAPSPSH SSIIDSTEYS QPPGFSGSSQ TKKQPWYNST LASRRKRLTA180  
 HFEDLEQCYF STRMSRISDD SRTASQLDEF QECLSKFTRY NSVRPLATLS YASDLYNGSS240  
 IVSSIEFDRD COYFAIAGVT KRIKVVEYDT VIQDAVDIHY PENEMTCNSK ISCISWSSSYH300  
 KNLLASSDYE GTVILWDGFT GQRSKVYQEH EKRCWSVDFN LMDPKLLASG SDDAKVKLWS360  
 TNLONSVASI EAKANVCCVK FSPSSRYHLA FGCADHCVHY YDLRNTKQPI MVFKGHRKAV420  
 SYAKFVSGEE IVSASTDSQL KLNWVGKPYC LRSFKGHINE KNFVGLASNG DYIACGSENN480  
 SLYLYYKGLS KTLTLFKFDT VKSVLDKDRK EDDTNEFVSA VCWRALPDGE SNVLIAANSQ540  
 GTIKVLELV

549

## (2) INFORMATION ON SEQ ID NO. 209:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

GTVLSSLTGE YKPLISSTLL ISSSKTSSSF WICSSCSLLF LLATLRNSIR ICSWAACDSA60  
 SSCFFFTCSN SNIRLTAKS RLSWSVPNQS 90

## (2) INFORMATION ON SEQ ID NO. 210:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

FPSSLLFFFF FFFFCGSGIN FYCFVIYFYS KEFVLSQKL DNTTKSSNVH GVTLMVESWL60  
 GIPNVPKVIK EGKEKKKKIF KTNPKPMMTL GRDIT 95

0067365.1.22700

## (2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

KKMVRLGLFS CLLAIYSLW IVCIPYLLSI GLCVDILFLF VQHLLPHLLV TQPLFCIGEP60  
 IPCGLGEHVT RFGLLSPTAS 80

## (2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

LKKGKWKAKI HNRKCKWFRN MKRCSSSLIF KEKKEILPTR LAKIFKOSGL ADYRQTGILT60  
 NDGVVNW 67

## (2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

00673305.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

SPEVGQALGT AGSRASRKMT SELSSLSISA SIRVSPQTDLS LHMAQIQAYM VLGSWDLHKA60  
 FFPVVFAEVL LRAFLSLA 78

## (2) INFORMATION ON SEQ ID NO. 214:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 105 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

QAGKRALYKH TQNTSGDGC VLLEQRLIKH SVCWLSVPLL ENNELGKEQL IRKCALLTVH 60  
 ITTKSQWLLK EKGLRCRCSN LSVNSCQQPQ RLPQHTLIT CVCLA 105

## (2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 216 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LSLTSRMEEA ELVKGLQAI TDKRKIQEEI SQKRLKIEED KLKHQHLKKK ALREKWLLDG 60  
 ISSGKEQEEM KKQNNQDDHQ IQVLEQSILR LEKEIQDLEK AELQISTKEE AILKKLKSIE120  
 RTTEDIIRSV KVEREERAE SIEDIYANIP DLPKSYIPSR LRKEINEEKE DDEQNRKALY180  
 AMEIKVEKDL RTGESTVLSS IPLPSDDFKR SRSKSL 216

00673005-122700

## (2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

FCFFISSCSF PLLIPSRSHF SLKAFFFKCW CFSLSSSIFR RFCEISSCIF LLSVMAWSLP 60  
 FTSSASSILE VKDSQTGKQV QSYHKRSRL GERSGGDRRE AGRNPLFAPV EK 112

## (2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 339 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

SSQLRRRLVP APAAPRPRPN HGVLRGRLRG DRWQWSHWAK WAMLFASGGF QVKLYDIEQQ 60  
 QIRNALENIR KEMKLEQAG SLKGSLSVEE QLSLISGCPN IQEAVEGAMH IQECVPEDLE120  
 LKKKIFAQLD SIIDDRVILS SSTSCLMPK LFAGLVHVQK CIVAHFVNPP YYIPLVELVLP180  
 HPETAPTVD RTHALMKKIG QCPMRVQKEV AGFVLNRLQY AIISEAWRLV EEGIVSPSDL240  
 DLVMSEGLGM RYAFIGPLET MHLNAEGMLS YCDRYSEGK HVLQTFGPIP EFSRATAEKV300  
 NQDMCMKVDP DPEHLAARRQ WRDECLMRLA KLKSQVQPQ 339

## (2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein

00673395.122700

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

KDPQITQKGI TKIITKIFCP HINMKTITG CQILKCNQA EKEKVKISRL SAQVAGNRQP 60  
RERKCCCAAR PRAMIQSDGQ TTGLHPTQA AHKTASLGSP WAATYVTEG 109

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 98 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

LNIPISALRCM VSRGPMNAYR MPNPSDMTRS RSLGDTIPSS TSRQASLMIA YCRRFRTKPA60  
TSFWTRMGHC PIFFIRAWVL STVVGAVSGW GTSSTSGM 98

(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 129 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TMFFTCGPNF AMVVSFGFCRS PFVMVAGGRV FVLPCIQQIQ RISLNTLTIN VKSEKVIYTRH 60  
GVPISVTGIA QVKLSEFFPH SPLPHHPLSQ TLRHLLATVF STLACREVPL LVSSFPPTPR120  
HLPPPPFFP 129

00673795.122700

## (2) INFORMATION ON SEQ ID NO. 221:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

OGDPMASVNL FTLDIEGQCV ERDPLDLLDA GQDKOTPSSH HDWGASAEFG DHHGLIWATS 60  
EKHGSGWSFR DAGGSPAGVS GRAGSRRLDG AGQGFLADQL SWELAPSRVP HPAAPRCC 118

## (2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

WPSGGELTSP GQCGSQPPS SPATSDRRFP TSPCSAPGFL PVARVGVGVK VWGSHVVRGK 60  
AEREGRALSE MLLPFQGGKG GGGKCLGVPG KDETSRGTSI QARVEKTVAR RCLNVWVERG 119

## (2) INFORMATION ON SEQ ID NO. 223:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

0575306.12200

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

GRRTLFLATF GGYPGSLGCS LSGEANISLV SFFHPLNCKL RITQAHHSYR LGLASQSTLC60  
 PACHCCKELL LCQFKQRKYG FSCIIFPGW FVF 93

## (2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 94 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

NLIYPNSMY SDTFSEKARI IGAVLSIKGK SSOHLHYNFL CLFSAGEEIH IYSTPHWTLQ60  
 NACIFCPSAI CSLPFCLLKE LSNIVFPKMF STGH 94

## (2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 92 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GHRMHILDRF CTAQLEWVPV TWIGVQYTIC VQYRKPSAV ARELYSNSLS AQANQVRKTA60  
 IWLEDFQETA VVVRGRYYLR GGRGTDIKQE GF 92

## (2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 458 amino acids  
 (B) TYPE: Protein

00673395.122700



(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

RGKRRRRRLP ALPRLLLSPS AATMSASAVF ILDVKGKPLI SRNYKGDVAM SKIEHFMPLL 60  
VHGEEGALA PLLSHGQVHF LNIKHSNLYL VATTSKNANA SLVYSFLYKT IEVFCEYFKE120  
LEESIRDNF VIVYELLDL MDPGFPQTDD SKILQEYITQ QSNKLETGKS RVPPTVTNAV180  
SWRSEGIIKYK KNEVFIDVIE SVNLLVMNANG SVLLSEIVGT IKLKVFLSGM PELRLGLNDR240  
VLFELTGRSK NKSVLELDVK FHQCVRLSRF DNORTISFIP PDGDFELMSY RLSTQVKFLI300  
WIESVIEKFS HSRVEIMVKA KGQFKKQSVN NGVEIISVVP SDADSPRFKT SVGSAKYVPE360  
RNVVINSIKS FPGGKEYLMR AHFGLPSEVK EEVEGRPPIG VKFEIPYFTV SGIQVRYMKI420  
IEKSGYQGPA LGFRYIHPEW AITNFRYQLG RGEEMGGF 458

(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 120 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

LVTKVGNRPL WVNVAKPQGR ALVTTFNLNDL HVSDLDLPRDG EVGDLKLDPD GGPALHLFLF 60  
HTGEAKVGSH QVLLAPRERL NTPNHVSLR HILGAHTGL ESGGVGIAGY RHRYLHTVGH120

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 246 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

09673395-122700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

GESNLTPMGG RPSTSSSTL GRPKWARIKY SLPPGKDIL QITTFLSGTY LALPTLVNL 60  
GESASLTGTG DISTPLATDC FLNCPLALTM ISTRLENFS MTDISIQISGL TWVLRYYDMS120  
SKSPSGGME MVRSLSKRES RTHWNFTSS SSTDLFLLRP VSSKSTRSLR PSRSSGIPDR180  
NTLSLMVPTI SLRRTLPLAL TSRLTDSMTS MKTSFFLYLI PSEKQDTALV TVGGTRDLPV240  
SSLLLC 246

(2) INFORMATION ON SEQ ID NO. 229:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 275 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

MNTRLQVEHP VTEMITGIDL VEWQLRIAAG EKIPLSQEEI TLQGHAFEAR IYAEDPSNNF 60  
MPVAGPLVHL STPRADPSTR IETGVRQDGE VSVHYDPMIA KWVVWAADRO AALTKLRYSL120  
RQYNIVGLPT NIDFLNLGSG HPEFEAGNVH TDFIPQHHKQ LLSRKAALK ESQCQALGL180  
ILKEKAMTDT FTLQAHDDQS PFSSSSGRRL NISYTRNMTL KDGKNNVAIA VTYNHOGSYS240  
MQIEDKTFQV LGNLYSEGDC TYLKCSVNGV ASKAK 275

(2) INFORMATION ON SEQ ID NO. 230:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 117 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

SEVILIENTI YLFSKEGSIE IDIPVKYLS SVSSQETQGG PLAPMTGTIE KVEVKAGDKV 60  
KAGDSLMYMI AMKMEHTIKS PKDGTVKKVF YREGAQANRH TPLVEFEFESE SDKRESE 117

00673305.122700

## (2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

SLFTSNNSIN RTFQVSAVSL AVKITKDLES FIFNLHAIRP IMVIRYSVGY IVFTIFKSHV 60  
SGIRDIQSSS TARRKWRELI MCLKSESVGH GFLLDETQG CLA 103

## (2) INFORMATION ON SEQ ID NO. 232:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 234 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

ADKMFLLPLP AAGRVVVRL AVRRFGSRSL STADMTKGLV LGIYSKEKEL 100  
NFDKLLAGKL RETLNISGPP LKAGKTRTFY GLHQDFPSVV LVGLGKKAAG 100  
KENIRAAVAA GCRIQIDLEL SSVVDPCGD AQAAGAVL GLYEYDDLKQ KKKMAVS AKL180  
YGGSDQEAQW KGVLFASGQE LGHANLMGDA SQLRLTPTRF CRNYLRRFSK LVVS 234

## (2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

LPILKIFSNH FGKIWLASIS IGWRLEPSNWR AQVLAQKQTG LLSARPPDPH FHRALPTQPS 60  
SFFALGHRH RDQAPLPPQQ PERLHRDPPP QTRAPGLESA CTPLQQQL 108

(2) INFORMATION ON SEQ ID NO. 234:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 68 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CFLCLHASFP VRRFQLPFCR GQLAPRWGSP DADHKRFESS LPSEVVQICS KLSAFQLTI60  
YQNSLLHL 68

(2) INFORMATION ON SEQ ID NO. 235:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 187 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

QRVRAALLSS AMEDSEALGF EHMGLDPRL QAVTDLGWSR PTLIQEKAIP LALEGKOLLA 60  
RARTGSGKTA AYAIPMLQLL LHRKATGPFV EQAVRGLVLV PTKELARQAQ SMIQQLATYC120  
ARDVRVANVS AAEDSVSQRA VLMEKPDVVV GTPSRILSHL QQDSLKLKRS LELLVVDEAD180  
LLFSLWL 187

09675395.122700

## (2) INFORMATION ON SEQ ID NO. 236:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

DIGHS DIPST VGSQLLNHGL CLPCQLLGRN KNKASHCLFY HRTCRLPMEQ QLQHRNSISG60  
 RLPGARAGPS QEVLPF 76

## (2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

TGLCNISLS ACTSSLKQVAD MRKALLKSGG KVTRGRLEL FFKAKGKKEG QLRPPPKAPG 60  
 SHEVSGCLAA SGLICEMGSL LPHLASPSAQ LSERLSLQQL RHWPLGHPEH SR 112

## (2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

CHARLNTDSS RLAMKLLMVL MLAALLLHCY ADSGCKLLED MVEKTINSOI SIPEYKELLQ 60  
EFIDSDAAAE AMGKFKQCFL NQSHRTLKNF GLMMHTVYDS IWCNMKSN 108

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 82 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

LVEETLLEFP HSLCSGITVY ELLKKLFVFR YRYVGIDGLF NHVLQEFAAR ICIAVQEEGR60  
QHEDHQQLHG EAAAVCVQSC VA 82

(2) INFORMATION ON SEQ ID NO. 240:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

LLFILHQMLS YTVCIISPKF FRVLCDWLKRL HCLNFPIASA AASLSMNS

48

(2) INFORMATION ON SEQ ID NO. 241:

00673395-122700

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

QAVGEKLSSR DSOLMEDRCF PHFSFSPKKV LLLSPFKQPV SLNFCGHGTD KDPVFS 56

(2) INFORMATION ON SEQ ID NO. 242:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

IFVAMGQTRT PSSAELRKSP ATSLAIKLQF SHPTRASEEW PLLAGNPLQW AS 52

(2) INFORMATION ON SEQ ID NO. 243:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

WPKMSQDFSL VQLKTGSLSV PWPQKFRLTG CLKGDRSRTF LGEKEKWGKQ RSSIRSSELL60  
ESFSPTA 67

00673305-122700

## (2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 64 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

GSSWAEDFKC DISVPKTSLL FAQSCRSMYF LLQYVPIYKF ISHTYNRAHV CTCTRTHTHS60  
LSTR 64

## (2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 74 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

SGPLLPAKNR EVAGLKTLSV TFQFLKHRCY LLKVVGLCIS FSNTSPFISL FPIHTTVHMC60  
ARAHANTHTH SQLV 74

## (2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 69 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00673395.122700



- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

ARIQTPEQHS QVTLFYDNEE MKMGYKIG IPSALKVSKL LTCEQRTPL LWSSFQLRML60  
QFSKSIYYS 69

- (2) INFORMATION ON SEQ ID NO. 247:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 236 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

QLRGGVQRHD RREGEMVCVE LVASDKTNTF QGVIFQGSIR YEALKKVYDN RVSVAARMAQ 60  
KMSFGFYKYS NMEFVRMKGP QGKGHAEMAV SRVSTGDTAP CGTEEDSSPA SPMHERVTSF120  
SRPPTPERNN RPAFFSPS KKVPRNRIAE MKKSHSANDS EEFFREDDGG ADLHNATNLR180  
SRSLSGTGRS LVGSWLALWK ADGNFLLYAH LTYVTLP LHR ILTDILEVRQ KPILMT 236

- (2) INFORMATION ON SEQ ID NO. 248:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 161 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DEEVALGQRQ RGVLPGGRW SRSAQCQQA VSPVGHRTV PGRVLAAEQ SRWKLP SLCT 60  
LNLRHVAAAS DFNHRPGSSA EAHPPDLAAC GACAEPRGP ALGVLP SAYL STATGVCDGT120  
PVLEPQPGEA TRLPGPPTA RTPAQTEVPL TGPAGAASAL C 161

00673335-122700

## (2) INFORMATION ON SEQ ID NO. 249:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 218 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

VCIEKEVSIC SVQLQPGPDQ GPSCARQGPR PQVGCIVQIG STVVLPEELL AVVGRVRLH 60  
 LSDPVPGHLP LEGWGEEGRP VVPFWGGGSA EGGHPLVHGR SWAGVLFSPT GGCVTCRHS120  
 DRHLGVALAL GALHAHKLHV AVLVEAKRHL LCHAGGHARP VVIHLERLV ADGALKDDPL180  
 ERVGFTSHQ LRTDHLSFPT VMSLNTSSKL SIMKKMLG 218

## (2) INFORMATION ON SEQ ID NO. 250:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 133 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

YPQDPGGAS RRLDLDLELC PGEKTAPVWA LSAEEEEAMH FSLAFFLHGS SVFLQITCCH 60  
 EFLCMRHISS CLYAEVFFIL SIGWWTGERG PRCPTSCASA VGGDRAPRHG GGGHLPHVWG120  
 GRRHPGTEGS LQR 133

## (2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 71 amino acids  
 (B) TYPE: Protein

00673395-122700

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

RLPSVFGCLR PPQTGCRPP PPCLGARSPP TALAHVGHGL GPLSPVHQPI ERMKGTSAYR60  
HDEICLMKHN S 71

(2) INFORMATION ON SEQ ID NO. 252:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

RGLQHTDMMK YASCIKIHND MLFAKKQTNH AGKMPGKSAW QLPPQHSGPT QERFSPQDTA60  
PSRPEASVMP LLAGPEGIRA PLLLTVDAAAT HSMQH 95

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 194 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

QKKKMSFRKV NIILLVLAVA LFLVLVHHNF LSLSSLLRNE VTDGIVGFQ PIDFVFNALR 60  
HAVDGRQEEI PVVIAASEDR LGGAIAAINS IQHNTRSNVI FYIVTLNNTA DHLRSWLNSD120  
SLKSIRYKIV NFDPKLLEGK VKEDPDQGES MKPLTFARFY LPILGSQRQR KARLHGVDDV180  
ICGRWDFLPF TLQQ 194

00673395.122700

## (2) INFORMATION ON SEQ ID NO. 254:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

RFHGFPLVRI LLYFSFQKER VKIDNEVSDA FQGITVEPGP EMVCCIVESN NVENHIGASV 60  
VLNAVYSCNG PPKPVFRCSO DHRNLLSFI YCMSESIWOK VYRLRPYNS 109

## (2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

NLAKVKGFMD SPWGSSTFF PSKSLGSKLT ILYLMLFRES LLSQDRRWSA VLLRVTM 57

## (2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 230 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00673395.122700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

LPAATNRLKR GKSGSTGSSS GNHGGSGGGN GHKPGCEKPG NEARGSGKSG IQGFRGQGVV 60  
SNMREISKEG NRLLGGSGDN YRQGSSWGS GGGDAVGGVN TVNSETSPGM FNFDTFWKNF120  
KSKLGFINWD AINKNQVPPP STRALLYFSR LWEDFKQNTF FLNWKAIIEG ADASSLQKRA180  
GRAESELQLQ PACVSHCLWW EVLSQDPCKG GESHLPLRLP GCNLGLLAVG 230

(2) INFORMATION ON SEQ ID NO. 257:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 141 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

TRTRSRPPAP EPSSTSADSG RISNRTLLSS TCKQLLRVRT RHHCNRNVQAE PSQNYNYNQH 60  
AYPTAYGGKY SVKTPAKGGS LTFFLGFPGA TWACLQLGEV LVRQFLATNH RRPKKKHWR120  
QGKLLPPLGP PALWQAPGPG L 141

(2) INFORMATION ON SEQ ID NO. 258:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 165 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

RVRTLNNCFP VEERSVLFEI LPESAEEVEG SGAGGRDLVL VYGIPVDETQ LGFKILPESV 60  
KVKHPRRRRL VHSIDSTNSV TSSTAPARPL PPIIVSRASK EALALFAYFP HVAGNSLSSE120  
ALNPRFPAPA GFIPWLFTPG FMSISSAAPT VVAGGGAGAG SLPL 165

00673305 102700

## (2) INFORMATION ON SEQ ID NO. 259:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

ERSHLQPGAV GITESPILGL GSAMTTEIGW WKLTFLRKKK STPKVLYEIP DTYAQTEGDA 60  
 EPPRPDAGGF NSDFNTRLEK IVDKSTKGKH VKVNSNGRFK EKKKVRATLA ENPNLFDDHE120  
 EGRSSK 126

## (2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

YVLNTIIVGK GEEKIPHLPL RFGPCSFPLR VCDLPSAKVM AKTGTRPNY HQSSLLQHPN 60  
 RVPGSSVPFA PEGKVGPSLL PVLGGELKFS VSASGSTETS PYHVASGKCA LLRIGPGSSH120  
 R 121

## (2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

00673395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

TRVPLVYVVG RVEDPGISQA LQKWRHINTN LKNSHFLPAG INWPHSFSYG QRGQRGKVL60  
QIWLMAQSQE VLA PSSALHF DDRPSS 86

(2) INFORMATION ON SEQ ID NO. 262:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 73 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

GSGSPAPRKL HDFALCSAPL CPLFPRETSR SHIFLTDFA VCLHSDWEHW DHFHHADSGG60  
NGCIPFHDPT CVY 73

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 106 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

FVAMCSKQAS LNHGLLGLTL VFLGPLNRHR SGHGKGYIHY HHCRRHDNDP SVPNQANRQ 60  
LQNQSRKCGI WKSLLERGRG GELSRGRNRA VYAE LGTPSL RARGGR 106

00672395-122700

## (2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

VLRWYSSDPS IDTGRVMERD TSITTTVGMM KMIPVFPIRM QTDSFKISQE NVSGSLSWK60  
EGAEGS 66

## (2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

GCACFRFPSP AGGARTSAGR SPSSADVGRS TQSRSRRAA HSRCCVAFPS SFTFRSRRRP 60  
KRRRRRREND PAASSLFPAH LPCSVSQSAA GARLVLRPA CGAQAQRP 108

## (2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673305.122700



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GAPAFALLLQ REGRLPRGG VRLVLTAAE PKVDRGGGLH IPVVALRFLF LSLRAHGGGQ 60  
SGDGGGARTT RRPVLFLLRT CPARSVSRP APGLCSDLAL AAPRPSGRS 109

(2) INFORMATION ON SEQ ID NO. 267:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 157 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

IEAAGCTFPL LRCVSFLFHS ALTAATAAAA TAARERPGGQ FSSSCAPALL GQSVGGRRPA 60  
CAQTSRLRRP GPARVASVWP ENLGAPAARA PRAEPRSGSR GGRRVSESEG WPGQVVAARR120  
WSPSKGSVWP TRSTARTSPS AATSPRPREM PPKRRRL 157

(2) INFORMATION ON SEQ ID NO. 268:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 156 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

SSAQGEPEGP GRLLRAPTE SRSEGKSMFA GVPTMRESSP KQYMLGGRV LLVLMFMTLL 60  
HFDASFFSIV QNIVGTALMI LVAIGFKTKL AALTLVWNLF AINVYFNAFW TIPVYKPMHD120  
FLKYDFFQTM SVIGGLLLVV ALGPGGVSMD EKKKEW 156

00673305-122700

## (2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

LGACSWWWPW ALGVSPWMRR RSGNSHRSL PAWLRPVAVK DWFGVDSTKL PAFMYPLPFP 60  
 SLGKGTOVLR TLFAETFENR WLSLLWSHSL ASDPSVQASL AAGSLPHAEA LE 112

## (2) INFORMATION ON SEQ ID NO. 270:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 130 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

SQRVCKYSPG SLLPYPRILV RSSNGFRTWV LFSCDHSSAH CMKTGLSQCF NLTRAVSWST 60  
 PRSLLVPYDS PHQMTLAKSR FLCGQGWLAD WWKVGWTKGG HVSSQHQFCT SSASVLVGVPI20  
 VSPGPGWARA 130

## (2) INFORMATION ON SEQ ID NO. 271:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 267 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00672305.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GTSGTSHLHP RSICMIQKYN HDGEAGRLEA FSQGESVLKE PKYQEELEDR LHFYVEECDY 60  
 LQGFQILCDL HDGFSGVGAK AAE LLQDEYS GRGIITWGLL PGPYHRGEAQ RNIYRLNLTAL20  
 FGLVHLTAHS SLVCPLSLGG SLGLRPEPPV SFPYLHYDAT LPFHCSAILA TALOTVTVPY180  
 RLCSSPVSVMV HLADMLSFQK KKVVTAGATII PFFLAPGQSL PDSLMQFGGA TPWTPLCACG240  
 EFSGTRCFAQ SVVLRGIRQS MPHKKPT 267

(2) INFORMATION ON SEQ ID NO. 272:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 118 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

QVARVAGPGS HPRTRGRQES CEQSGARDQK LCLIDRCFS GPPHDGRDQV AGPRLLFPAL 60  
 NIHLVAALPP SRLPQRSHRA GHTGSGSPAS SHIPPRRNAA CPPALPGTWN PLGHFFLG 118

(2) INFORMATION ON SEQ ID NO. 273:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 133 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

LGKATCSRRL PTCTQWGPWG GSKLHQGIR KGLAWSQGER DDCSCCHLF PTEAQRVSQM 60  
 NHGNWRGTQA IRNSCCVQGC SQDGTAVEGQ SGIIMQVREA DRWLGSQAQA FTQGGQADKR120  
 AVSSQVHETK SCV 133

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 124 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

PQAWRLRCRC CSARPVAPGA RRLVPCRTPT RQPAGGTCHH PAAFGRSRH IPVPHALGFG 60  
 ASAGRSVPLQ ALSQSPGAAD LQVFSTGAAP VIHTRLLEDP ILGATLPAGP IRCRAVGLVP120  
 RHCH 124

## (2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

GSSRRHGGGY AAVALLVLLL LGPGGWCLAE PPRDSLREEL VITPLPSGDV AATFQFTRW 60  
 DSELQREGVS HYRLFPPKALG QLISKYSLRE LHLSTQGFW RTRYWGPPFL QAPSGAELWV120  
 WFQOTVTDVD KSWKELSNVL SGIFCASLNF IDSTNTVTPT ASFKPLGLAN DTDHYFLRAY180

VLPREVVCTE NLTWPWKLLP CSSKAGLSVL LKADRLFHTS YHSQAVHIRP VCRNARCTSI240  
 SWELRQTLVS VFDAFITGGG KKDWSLFRMF SRTLTEPCPL ASESRYVYDI TTYNQDNETL300  
 EVHPPPTTTY QDVILGTRKT YAIYDLLDTA MINNSRNLNI QLKWKRPPEP EAPPVPFLHA360  
 QRYVSGYGLQ KGELSTLLYN THPYRAFPVL LLDTVPWYLR LLHPLPACPG PAATPPPGDA420  
 DSAAGQ 426

## (2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 128 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

SPSILYGSCT CHSHKAFGGP DTGGHPSCRP HQVQSCGSGS KTLSLMWINL GRSSVMSSQG 60  
 SSAPLSTST PPTQSLPLPP SNPWVWPMTL TTTFCAMLCC RGRWSAPKTS PPGRSSCPVV120  
 PRQASLCC 128

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 481 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

AQDTGGPGRQ SGHGGDLQIP ISLFLRLNT QHWRPGSRKV MAVVPASLSG QDVGSFAYLT 60  
 IKDRIPQILT KVIDTLHRHK SEFFEKHGEE GVEAEKKAIS LLSKLRNELQ TDKPPFPLVE120  
 KEVDTDIWNQ VLEYQQSLLN ESDGKSRWFY SPWLLVECYM YRRIHEAIIQ SPPIDYFDVF180  
 KESKEQNFYG SQESIIALCT HLOQLIRTIE OLDENQLKDE FFKLLQISLW GNKCDLSLSG240  
 GESSQNTNV LNSLEDLKPF ILLNDMEHLW SLLSNCKKTR EKASATRVYI VLDNSGFELV300  
 TDILADFLF SSELATEVHF YGKTIWFVS DTTIHDFNWL IEQVKHSNKK WMSKCGADWE360  
 EYIKMGKVVY HNHIFWTLPH EYCAMPQVAP DLYAELQKAH LILFKGDLNY RKLTDGRKWE420  
 FSVPFHQALN GFHPAPLCTI RTLKAEIQVG LQPGQGEQLL ASEPSWWTG KYGIFQYDGP480  
 L 481

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 128 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual

00673305.122700

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

FHISVSTNFS TKGINGLSVC NSFRNLERRE IAFSTASTPS SPCFSKNSLL CRCNVSTITLV 60  
KICGILSLIV RYANDPTSCP ERDAGTTAIT FRDPGRQCWV FNRRRNREIG ICKSPPCPDC120  
RPGPPVSC 128

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 83 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

ELLNQVKGDH RTEIFHIFQW STSWAQRPGA VPLAQADQP EFQLLMFLWY RVVQDGSHE60  
PDEMEQKTPI FCHLSTSCNS NHP 83

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 168 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
(A) ORGANISM: HUMAN

00673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

FYDRRDCFVA VSFLRGLSLW LHFYLWLCY GGAEMRQKRK GDLSPAELMM LTIGDVIKQL 60  
 IEAHEQGKDI DLNKVKTKTA AKYGLSAQPR LVDIIAAPP QYRKVLMPLK KAKPIRTASG120  
 IAVVAVMCKP HRCPHISFTG NICVYCPGGP DSDFEYSTQS YTGVEQPP 168

## (2) INFORMATION ON SEQ ID NO. 281:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 70 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

GGTAAMISTR RGWAERPYLE AVLVFTLFRS MSFPCSWASI SCLITSPIVS IISSAGLRSP60  
 FRFCLISAPP 70

## (2) INFORMATION ON SEQ ID NO. 282:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

IDVFLLVGF NQLFNNISYS QHQQLSRAEI SFPLLPHFCA AVAEPPEIKM QPQTQTTEKA60  
 DSHKTIPPVV K 71

## (2) INFORMATION ON SEQ ID NO. 283:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09673395.122700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

KPRQLPNMAF LPSPAWWISL LAVPPQYRKV LMPKLKAKPI RTASGIAVVA VMCKPHRCPH 60  
 ISFTGNICVY CPGWDLILIL SIPPSLTGLY EPTSMRSYSV PDMDFPYRT RTPD 114

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 127 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

WVSPLTWASR PCDTEEGRQA MISTRGWAE RPYLA AVLVF TLFRSMSEFC SWASISCLIT 60  
 SPIVSIISA GLRSPDYGGF TTRPGSNILG SRVGHYTHQT MEDSPFDQEA TAWAPELATP120  
 PCTDEDR 127

(2) INFORMATION ON SEQ ID NO. 285:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

PHTTNPTCEK LFLIRCPCPV RKRVIHWHGI APHGGWLIAQ CKTGWNTQNG NQVPPRAVYT60  
 YISCKTDVWT SVGFHHSHD SNPTSSSDGF RL 92

09673395.122700



## (2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 76 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

DLSRPGGTRF VLTIIQTFFS KVEVQDNFKN NIKINNGDFD SLKIEKKGVG GGVNHWPPFF60  
WRGPIGIVRP WSGSL 76

## (2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 97 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

RTFVLFYHRL TLQLLINTSF GDVWCKTHKH TQKSTSPLDH PSLLSGTISA ASCTLLGPP60  
IHRGFRGTQI TAGFQFFENN TFLWSVPAL SVLLKLE 97

## (2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 77 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

09673395.122700

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ILHLEMYGVK HTNTHKKAQA RCMTRLSTLG LFLLRPAWS AHLRFTEVSG GPKSLLVNF60  
 ELTIHFEGGF QQHCEYF 77

(2) INFORMATION ON SEQ ID NO. 289:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

ILIDGVRAAF IPYREYNGAR LSROFISA

28

(2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

HQFHNYFNLL GFHLLILKF HQQWGTEK

28

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual

00673005.122700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

29

(2) INFORMATION ON SEQ ID NO. 292:

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

30

(2) INFORMATION ON SEQ ID NO. 293:

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

33

## (2) INFORMATION ON SEQ ID NO. 294:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AINKVSSGYG PLALLGFSVS VEAQRISLN FSQKWLTT

38

## (2) INFORMATION ON SEQ ID NO. 295:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

FTSFNLLIPR TILSTTNANE ILIHKRKLKT FIAYVGLSNK

40

## (2) INFORMATION ON SEQ ID NO. 296:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

00673305-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

VNLLKYGGQIH LAVKQLNIHC YLIKVFVSVL PGPNIKTTSV QKINVQRAVC SLFWYVHFKK60  
 TPLSSLANQE Y 71

## (2) INFORMATION ON SEQ ID NO. 297:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

RELYLYFILSR GTNSRHTFAR PSCRKTQSRK GKNKIAIKYM VLGAGTRNP QGDQFLARSF60  
 FRVYPVE 67

## (2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 56 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

KNLEFFSPST SYLLQNSSE GFYILSYPE GPTAGIPLPG LLAERHRAVK AKIKLQ 56

## (2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 140 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

00675305-122700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

TPNSRGAGRV VRGSARGVGR SCASWLPVGR RCRTSETGSG ASRRSRAIGS PPPSPCPWSA 60  
 NSASSARPTS SSGPKPSFIA FRFGGQSLPP FISLWVQELD FFIWSIYISY ISILRDLKQEL20  
 LLGGGQQTIIY SCSSLTGFAS 140

(2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 279 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

QSRSRPRREG VGTGSRAVLC ILATCGSKMS DIGDWFRSIP AITRYWFAAT VAVPLVGKLG 60  
 LISPAYLFLW PEAFLYRFQI WRPITATFYF PVGPGTGFLY LVNLYFLYQY STRLETGAFD120  
 GRPADYLFML LFNWICIVIT GLAMDMQLLM IPLIMSVLYV WAQLNRDMIV SFWFGTRFKA180  
 CYLPWVILGF NYIIGGSVIN ELIGNLVGHL YFFLMFRYPM DLGGRNFLST PQELYRWLPS240  
 RRGVSGPGV PPASMRRAAD QNGGGGRHNW GQGFRLGQ 279

(2) INFORMATION ON SEQ ID NO. 301:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

00673305.122700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

IDQIKKSSSW THREIKGGSD WFPNLKAIKE GFGPEEEVGR ADEAEFADQG HGDGGGGEPIA 60  
RDRRDAPEPV SDVAHLRPTG SQAQDRPTP RADPLTTRPA PRLLG 106

(2) INFORMATION ON SEQ ID NO. 302:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 207 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

LEPLEPNRLE LKKGYLTLS DSGDKVAWEVD KDHGVLHSL AEKGRGMELS DLIVFNGKLY 60  
SVDDRTGVVY QIEGSKAVPW VILSDGDDTV EKGFKAEWLA VKDERLYVGG LGKEWTTTGT120  
DVVNENFEWV KVVGYKGSVD HENWVSNYNA LRAAAGIQFP GNLIHESACW SDTLQRWFFL180  
PRRASQERY S EGRRAQGRQ PAAERLP 207

(2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 153 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RWWATRAAWT TRTGCPTTTP CGLLPASSRQ VTSSMSLPAG VTRCSAGSSC RAAPARSATA 60  
RKDDERKGAN LLLSASPOFG DIAVSHVGAV VPTHGFSSEK FIPNTDDQII VALKSEEDSG120  
RVASYIMAF T LDGRFLLPET KIGSVKYEI EFI 153

00573305.122700

## (2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```

VGTTAPTWLT AMSPKSSEAL SSRLAPLRSS SFLAVALLAG AARQEEPALQ RVTPAGRLMD 60
EVTWRLDAGS SPQGVVVGHP VLVVHAALVA HHLHPLRVLV HHITRSGRPL LAQAHVQTL120
VLHCQPFGLF AFLHGAVAVG QNHPPGHGFAA FDLVDDPRPV IGHVEFFIEN NQVG      174
  
```

## (2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

KLVCLADSK SSFSSEHLFS YHLISILKHH GCSCSKMGDV KENYLETFIS SPKWSFILCL60
S                                                    61
  
```

## (2) INFORMATION ON SEQ ID NO. 306:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

0067305.122700



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

NTMAVAARVKV VMSKRTILKH LFPVQNGALY CVCHKSTYSP LPDDYNCNVE LALTSOGRTI 60  
VCYHPSVDIP YENTKPIPRP DPVHNNEETH DQVLKTRLEE KVEHLEEGPM IEQLSKMFFT120  
TKHRWYPHGR YHRCRKNLNP PKDR 144

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 128 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

IHQTAFSQMA NEAHFSLIPP GTSASSVEWR IQILTTSVIP SMRIPTVLSS KEHFALFLYH 60  
RSFLKVENFF FQSGFQHLIM CFFIIMHRIW PRDRFCVFIW NVHRRVVAY CPAPRSQSKL120  
YVALIIVI 128

(2) INFORMATION ON SEQ ID NO. 308:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 467 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

SRSKMAALRA LCGFRGVAAQ VLRPGAGVRL PIQPSRGVRO WQPDVEWAQQ FGGAVMYPK 60  
ETAHWKPPPW NDVDPKDTI VKNITLNFSP QHPAAGVLR LVMELSGEMV RKCDPHIGLL120  
HRGTEKLIBY KTYLQALPYF DRLOYVSMCM NEQAYSLAVE KLLNIRPPPR AQWIRVLFG180  
ITRLNHNIMA VTTHALDLGA MTEFFWLFEY REKMFEFFYER VSGARMHAAY IRPGGVHQL240  
PLGLMDDIYQ FSKNFSRLRD ELEELLTNRR IWRNRITIDG VVTAEALNY GFSGVMLRGS300  
GIQWDLRAKTQ PYDVYDQVEF DVPVSGRGDC YDRYLCRVEE MRQSLRIIAQ CLNKMPPGEI360  
KVDDAKVSPF KRAEMKTSME SLIHHFKLYT EGYQVPPGAT YTAIEAPKGE FGVYLVSDGS420  
SRPYRCKIKA PGFAHLAGLD KMSKGHMLAD VVAITGTQDI VFGEVDR 467

0673395.12700

## (2) INFORMATION ON SEQ ID NO. 309:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

QPSVHEHTHT HTHTHTHTQR PISSEEQAPQ KKLIGRGDQT LLPCSPFIYS KYNILGTYDG 60  
 NDICQHVSLR HLVQTSQMGK TRSLDLASIR AAAAIRHQVH PKLSLGLSLNG SICGSRNLV120  
 ALSIQLKVMN Q 131

## (2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SQDTMRCVWL GPKVQGNVLH NCVLWRVHII PRWRLPVGCF FAWVHNSSPK LLCPFHIWLP 60  
 LPNTSAGLNR QSDSSPRFQH LGRDAPEAAQ SPQRRHLTPA 100

## (2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

0022156266

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

RRLRGGEPEST DRRRDPEST PAPPPTPRAM DPKDRKKIQF SVPAPPSQLD PRQVEMIRRR 60  
RPTPAMLFRL SEHSSPEEEA SPHQRASGEG HHLKSKRPNP CAYTPPSLKA VQRIAESHLQ120  
SISNLNENQA SEEDDELGEL RELGYPREED EEEEDDAARL KS 162

(2) INFORMATION ON SEQ ID NO. 312:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 154 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

VSLGRNLSAL PPLSLAHRHP ACISQEEVEG TSLFFRNPLY PHPVLCSSPR LLGLLALLTSR 60  
RLRLVVCVLF ARLWLIPREP GHLLPDAPHC QSLHSPSGR WDVQRPTLEN PENREQGFAL120  
HNSTPQILSP GHRRTGQDP KIWGKEVLRT LRY? 154

(2) INFORMATION ON SEQ ID NO. 313:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 101 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AQGLGLFDLR WCPSPEALWW GEASSSGEEC SESRNSMAGV GLLRRIISTW RGSSWLGGAG 60  
TENWIFLRLS GSMARGVGGG AGVRDSGSR RSVLGSPPRR R 101

00673305.122700

## (2) INFORMATION ON SEQ ID NO. 314:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 162 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

SDRWTCSPPL GARSMSRFFA VAGRAPRRQE EGRSRLDQE ERLSAVCIAD REEKGCTSQE 60  
 GGTTPTFPIQ KQRKKIIQAV RDNSFLIVTG NTGSGKTTQL PKYLVEAGFS QHGMIGVTQPI20  
 RKVAALISVAQ RVAEEMKCTL GSKVGYQVRF DDCSSKETAI KY 162

## (2) INFORMATION ON SEQ ID NO. 315:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 79 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

QIGGRARLHS GPGLCPGFPQ SRAGRQGGRR RVSGQETSRK SGSALFASPI EKRKDARPRR60  
 EELLQLFLFR NKEKRLFKL 79

## (2) INFORMATION ON SEQ ID NO. 316:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 69 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

00673395-12720

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

IGKVGVPVPPS WDVHPFSSLS AMQTAESRSS WRSLDSPSS CRLGALPATA GNRDIDLAPS60  
GGEHVHRSE 69

(2) INFORMATION ON SEQ ID NO. 317:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 173 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSSLFLP GAYKAQMYSD VWTNTKKKKK 60  
KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVLQ TSSQAIFYQK120  
GENSCLSLFK NAFLYLSIRH YTSELYKRPG GTMSLVDTFH CSVAPFLAWE ASA 173

(2) INFORMATION ON SEQ ID NO. 318:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 96 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSSLFLP GAYKAQMYSD VWTNTKKHFL60  
KRKGMSFPLF DKKQPVMKSG AQERWVSHLE AFRTQL 96

00673235.122700

## (2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLILLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFFS 105

## (2) INFORMATION ON SEQ ID NO. 320:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

IRKREQGRSS PAPWESVFAS VPFRGDDGIF DDNFIEERKQ GLEQFINKVA GHPLAQNERC60  
 LHMFLQDEII DKSYPSPKIR HA 82

## (2) INFORMATION ON SEQ ID NO. 321:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 159 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673305.122700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

RASPCPHGGQ QRRRRRLNAE GAEGARGGGS SYSEMAETVA DTRRLITKPO NLNDAYGPPS 60  
NFELEIDVSNP QTVGVGRGRF TTYEIRVKTN LPIFKLKEST VRRYSDFEW LRSELERESK120  
VVVPPLPGKA FLRQFLLEEM MEYLMITLLR KENKGWSSL 159

(2) INFORMATION ON SEQ ID NO. 322:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 114 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

FTSQPFVKTV SSSNSRFFQL ENRKICLDPD FVSGEAPAD PHRLRVAHID LEEVAGGSVG 60  
VIQVLRGLDQ PPGVSHGLRH FAVAAAAAAG SLRPLRVQPP PPLLPAVGT RARA 114

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 374 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

RRAQSEPLGR QSHLPRIYQA FLMSATFNEQ VQALKELILH NPVTLLKQES QLPGPQDLQQ 60  
FQVVCETEED KFLLLYALLK LSLIRGKSL FVNTLERSYR LRLFLEQFSI PTCVLNGELP120  
LRSRCHIIISQ FNQGFYDCVI ATDAEVLGAP VKGKRGRGRF KGDKASDPEA GVARGIDFHH180  
VSAVLNFDLP PTEAYIHRA GRTARANNFG IVLTFVLPTF QFHLGKIEEL LSGENRGFIL240  
LPYQFRMEEI EGFYRCRDA MRSVTKQAIR EARLKEIKEE LLHSEKLKTY FEDNPRDLQL300  
LRHDLPLHPA VVKPHLGHVP DYLVPPALRG LVRPHKKRKK LSSSCRKAKR AKSQNPLRSF360  
KHKGKKFRPT AKPS 374

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 324:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 224 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

QRVRAALLSS AMEDSEALGF EHMGLDPRLL QAVTDLGWSR PTLIQEKAIP LALEGGDLLA 60  
 RARTGSGKTA AYAIPLQLL LHRKATGPVV EQAVRGLVLV PTKELARQAQ SMIQQLATYCI20  
 ARDVRVANVS AAEDSVSQRA VLMKPDVVV GTPSRILSHL QQDSLKLKRS LELLVVDEAD180  
 LLFSFGFEEE LKSLWEGRV TCGFTLRLFS QQLLLTRYK HRSR 224

## (2) INFORMATION ON SEQ ID NO. 325:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 115 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

FFFFFFFFFG AAKIFILLSR GKMPAWKCG AKGRSTAGPR TVCSGCAVST RASPVHEGCK 60  
 PVLHNVLSR EAQQPQEGLA VGLNFFPLCL KLRSGFWDA LLAFLQEEDS FFRFL 115

## (2) INFORMATION ON SEQ ID NO. 326:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

00673395.122700



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

YLQCCRS LCG AKCVTWAVET RHLLSPALMT LRKEDVIQ GK FLIPKLPVHV NRTSFYSSRC60  
TGS LAP 66

(2) INFORMATION ON SEQ ID NO. 327:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 90 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

FRSCLFMLTG LLFIRQDVLV PWHLKGNPDK GKPVEFFGPI GSQDPSPVFH RYYHVFREGE60  
LEGACRTVSD VRILQSYDQ GNWCVILQKA 90

(2) INFORMATION ON SEQ ID NO. 328:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

SGLLKNHTPV SLIVVALQNS DITHSPAGTF QFSLTEHMOV TMKHRTWVLG SYGTKWLNRF60  
AFIRISLKV P GNQYILTNNK KSC 83

00672306-123700

## (2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 185 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

ERRSKSREER EKEREREREE RERKRRREEE EREKERARDR ERRKRSRSRS RHSSRTSDRR 60  
 CSRSRDHKRS RSRERRRSRS RDRRRSRSHD RSEKHSRSRS RDRRRSKSRD RKSYPKHSRS120  
 RDREQDRKSK EKEKRGSDDK KSSVKSGSRE KQSEDNTNES KESDTKNEVN GTSEDIKSEG180  
 DTQSN 185

## (2) INFORMATION ON SEQ ID NO. 330:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 178 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

YHFPSIQCLC LHSAFLDYRT SHYFFYHQIP SFLSPWIFYL VLCPDFCSCA YMTFDPGFLI 60  
 FFDPDFEICV FFLIDHGFCF FVDLYFCSAF FLYEVTFCGP ETCCIFCLMF GLSVYEVNDF120  
 SFFFLCHEPF LFLFLPLPFV FSFLFLPFLS PVLSSLCLCS CFSFLRRSSR IRLFGSSP 178

## (2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 182 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

09573395.122700

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

VSPSDLMSSL VPLTSLVLVSL SFDSEVSVSSL CFSRLPOFTL LFLSSDPLFS FSLDFLSCSL 60

SRLLLLCLYD FSRSLFDLLR SRLRLCFLS DRSWLLLLRR SLLLLRLLSL LROLLWSRDL120  
LHLLSDVRLE CLLRERLLFL LSLSRALSFS LSSSLRLFL SLSSLSLRS FLSLLLLLL180  
LS 182

(2) INFORMATION ON SEQ ID NO. 332:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 88 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GFGMQLVILR VTIFLPWCFA VPPVPAADHK GWDFVEGYFH QFFLTEKESP LLTQETQTQL60  
LQQFHRNGTD LLDQMOMHASA TAAPLWGA 88

(2) INFORMATION ON SEQ ID NO. 333:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 61 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

PRRSRSLPR RHKHSSCNNS IGMGQTYLTC RCMLLLQQPH CGVPDGSNDN ISPGRCKWIK60  
H 61

06673395.122700

## (2) INFORMATION ON SEQ ID NO. 334:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 62 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

STCIFLARCS CRTHQAPHSG AAVAEACICM SSRSVPFRWN CCRSCVCSW VRSGDSFSVR60  
KN 62

## (2) INFORMATION ON SEQ ID NO. 335:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

VCPIPMELLQ ELCLCLLGKE WRLLGQEKL MEIALNKVPS FMVCSRGHWN GETPGQEDSN60  
S 61

## (2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

09673395.122700

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

AEDTIQKRNS QFETVTPPAP NCGDEERKQW LWFLSEGRLR TERSNHQGHR FWKSSRGWL60  
EEQ 63

(2) INFORMATION ON SEQ ID NO. 337:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

KGWRSDFTVG GRQRDQHVQ TGSFFSISLL SKSRTAQWLC QGGSSSYSHF SGSLKSTRYY60  
RGSRS 65

(2) INFORMATION ON SEQ ID NO. 338:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 249 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

SCGDVEQKIQ FKRETASLKL LPHQPRIVEM KKGSSNGYGFY LAGSEQKGQ IIKDIDSGSF 60  
AEEAGLKNND LVVAVNGESV ETLDHDSVVE MIRKGGDQTS LLVVDKETDN MYRLAHFSPF120  
LYYQSQELPN GSVKEAPAPT PTSLEVSSPP DTTEEVDHKP KLCRLAKGEN GYGFLNNAIR180  
GLPGSPIKEV QKGGPADLAG LEDEDVIEV NGVNVLDPEY EKVVDRIQSS GKNVTLLVCG240  
KKAYDYFQA 249

0057395-12700

## (2) INFORMATION ON SEQ ID NO. 339:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

ITGVQPEHIQ YLKNYFHLWT RQLAHYHYH YHGPKGNEIR TSKEVEFPNN IDIEISMFEK60  
GKVPKIV 67

## (2) INFORMATION ON SEQ ID NO. 340:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

RIFITTIFMA QKEMKYEHQK KLNLSLIL KFLCLKKGRY LRLS 44

## (2) INFORMATION ON SEQ ID NO. 341:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 46 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

00673335-122700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

KVQLLLMFVF HELLGHEYSS DKYALTVVSK GGNFSSSTVC VLVVPL

46

(2) INFORMATION ON SEQ ID NO. 342:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GRWRRRLRHG RGSAAVAGPT AMAELLQEEL SVLAAIFCRP HEWEVLSRSE TDGTVFRIHT 60  
 KAEGFMDADI PLELVFHLPV NYPSCLPGIS INSEQLTRAQ CTVKKEKLE QAESLLSEPM120  
 VHELVLWQQ NLRHILSQPE TSGGSEKCTF STSTMDDDL WITLLHLDHM RAKTKYVKIV180  
 EKWASDLRLT GRMLFMGKII LDFTTGRQKQ PQGVLDSEN LQSRCGLKWK EMQREND 237

(2) INFORMATION ON SEQ ID NO. 343:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

YLILLQGDNR NLKVYLILQK TSKVDVDSGG KKCKEKMISV LFETKVQTEH KRFLAFEVKE60  
 YSALDELQKE FETAGLKKLF SEFVLALVK

89

(2) INFORMATION ON SEQ ID NO. 344:

(i) SEQUENCE CHARACTERISTIC:

0067330512700

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

PLPKSNAKTT KNTAILLKDS CLPFHFTRAS TNSEKSLSP AVSNSFCNSS NAEYSLTSNA60  
 RNLLCSVCTF VSNSTLIIFS LHFFPLESTS TLEVF 95

(2) INFORMATION ON SEQ ID NO. 345:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 72 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

RAGLFPGRRV GLEAENGPCQ HQHGDFVPCP VLSARMSQPE AEEAALVAHA VGHDCVCSGG60  
 GVLLPHHRRN NL 72

(2) INFORMATION ON SEQ ID NO. 346:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 171 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

06730512700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

GRACFRGGAW GLRFPRTALAA TMMETLYRVP FLVLECPNLK LKKFPWLHMF SAMTVYALVV 60  
 VSYFLITGGI IYDVIVEPPS VGSMTDEHGH QRPVAFLAYR VNGQYIMEGL ASSFLFTMGGL20  
 LGFIILDRSN APNIPKLNRF LLLFIGFVCV LLSFFMARVF MRMKLPGYLM G 171

## (2) INFORMATION ON SEQ ID NO. 347:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 82 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

EAGCKSFHNI LSIYSVGQES YWFLMPMFIS HRTDTWRFNH NIINYSSGDE EVRHHHQSIH60  
 SHGRRHVQPG RLLQLQVGTF EH 82

## (2) INFORMATION ON SEQ ID NO. 348:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 103 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

HKVIVVWNNI GEKAPDELWN SLGPHPIPVI FKQQTANRMR NRLQVFPELE TNAVLMVDDD 60  
 TLISTPDLVF AFSVWQQFPD QIVGICFLES TSFTFIQGIY SYW 103

## (2) INFORMATION ON SEQ ID NO. 349:

06072305.12700

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

ESKKNKVGAD ECVIIYHQHC IGFQFRKDL ESHFVCCLL FEDHRDRVGP

50

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

SGNCCQTEKA KTRSGVLMSV SSSTINTALV SSSGKTWSRF LILFAVCCCK ITGIGWGPRE60  
FHNSSGAFSP ILFHTTITL

79

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00673305-122740

## 70

## 71

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 225 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GLPARRPQCF LRAEMANSGL QLLGFSMALL GWVGLVACTA IPQWQMSSYA GDNIIITAQAM 60  
YKGLWMDCVT QSTGNMSSCKM YDSVLALSAA LQATRALMVV SLVLGFLAMF VATMGMKCTR120  
CGGDDKVKKA RIAMGGGIIF IVAGLAALVA CSWYGHQIVT DFYNPLIPTN IKYEFGPAIF180  
IGWAGSALVI LGGALLSCSC PGNESKAGYR APRSYPKSNS SKEYV 225

(2) INFORMATION ON SEQ ID NO. 355:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 111 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

QHHHGPGHVQ GAVDGLRAHE HGDELQNV R LGARPVRGLA GHSSPNGGLP GAGLPGHVC 60  
HDGHEVHALW GRRQSEEGPY SHGWRNHFH GRSCRLGSL L LVWPSDCHRL L 111

(2) INFORMATION ON SEQ ID NO. 356:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 154 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

CCHPHRSSSA TAGWRCRPPD PPSAGPWR S PATAGENWPF PPSNTGGAG RGDPTVKQTT 60  
LGGQPHKRKL EVEFSGHPRK QKGFGPGECK SCHQTHKST PPVKRWPRGT GSRIRREGGS120  
RQNWSPKAR RFPFGALGDP LSPASRLT GVGP 154

09673305.12700

## (2) INFORMATION ON SEQ ID NO. 357:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

NLTQVTFLFF CPPNVHASYS LHFEALMNIP VLVLVDVNDFF AEEVTKQEDL MREVGRTLTPE60  
 VFLVVSLLWLY LL 72

## (2) INFORMATION ON SEQ ID NO. 358:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

SPSHLSHEVF LFGYFLSKII IDIQHQHWNV HQSLKVEPIR SVNWVGTEKK KCNLSQVSHT60  
 RQVLLREQI 69

## (2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00572305-12700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

KRYNQRETR KTGKVLPTS LMRSSCLVTS SAKSSILTSNT STGMFIRASK WSL 53

(2) INFORMATION ON SEQ ID NO. 361:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 111 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

SCWETKWTSC FRMLLATGRG CGSDCGRTVP APGSCWPLAP RATAPRQGRA TGRGESAE 60  
LVPHSGQGRA ADQRQDLWS GRVLCPSAL LALPWGRLLS GRHQRRQIHS L 111

(2) INFORMATION ON SEQ ID NO. 362:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 109 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

TRNGSVFGCY RPHRFPAKGS VSLVYSRGFQ HPPCAYHLLG QGRRSVSEAC RSYVTPDSNG 60  
WKRTNGQDFL LLLKTLMMVK RKDWGQPGSS GPTSKFPLQV ILCQALFFK 109

(2) INFORMATION ON SEQ ID NO. 363:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 381 amino acids

00673305-122700

(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GPARRPAARL ARAGGPPAAD RAGKQSGPPA PGCSWLPAAE AGATVGGLCP RRAPAGPWHQ 60  
GPQRPVKDEF QDGENPNPEN WSRTVVRDVR LISAKTGYGV EELISALQRS WRYRGDVLV120  
GATNAGKSTL FNTLLESDYC TAKGSEAIR ATISPPWGT LNLKFPICN PTPYRMFKRH180  
QRLKKDSTQA EEDLSEQEON QLNVLKKHGY VVGRVGRITF YSEEQKDNIP FEFDAADSLAF240  
DMENDPVMGT HKSTKQVELT AQOVKDAHWF YDTPGITKEN CILNLLTEKE VNIVLPTQSI300  
VPRITVLKPG MVLFLGAIGR IDFLQGNQSA WETVVASNIL PVHITSLORA DALYQKRHAGH360  
TLQIPMGKK ERMGRISSC C 381

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 182 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

QPSTTCTSVL VCLLSAMFLP VALQTRLAKR GILKHLEPEP EEEIIAEDYD DDPVDYEATR 60  
LEGLPPSWYK VFDPSCLGPY YWNADTLVS WLSPHDPNSV VTKSAKKLRS SNADABEKL120  
RSHDKSDRGH DKSDRSHEKL DRGHDKSDRG HDKSDRDRER GYDKSRNGIR DRGYDQADREL80

EG

182

(2) INFORMATION ON SEQ ID NO. 365:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 149 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

00672305-132700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

RRHERDGRCD SLPLPARVYW SVCYQLCRCP LCRPFAWPRE ASSNIWSLNQ RKRSLPRTMT 60  
 MILWTTTRPPG WRAYHQAGTR CSTLPAGSLT TGMQQTLYP GSPHMTPTFW LFNRRFSSEAL20  
 VMQMLKKSWT GAMTSRTGAM TSRTAAMRN 149

(2) INFORMATION ON SEQ ID NO. 366:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

PRSRSLSDLS WPRSDLSWPL SSFSWLRSDL SWPLSDLSWL RSNFSSASAL LLSFLADLV60  
 TTELGSCGES QQTRSVSAFQ 80

(2) INFORMATION ON SEQ ID NO. 367:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 160 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

VAQQPALIHG YRKAVLTFNH VEFSLRYDAV LRGPMSDDSS HGSVLRLSQA LGNVTVVQKG 60  
 ERDILSNGQQ VLVCSQGGSS RRCGGQGDLL SGSLGVLVHW ALLAGPQKTN GSSPLLVAAF120  
 GACSLTRQCN HQAFQKHGRS TTSDMIAEV GAAFSKLFET 160

09673395-12700



## (2) INFORMATION ON SEQ ID NO. 368:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ILNGNQFMLK LKIWQAPYAF STRVGPDPFI THTLSPVQGA CLLLVCAGSG FKELAEGGPH 60  
 LGDHVGGGGG ATVLLEGLVV ALPGERAGAK RGHQERAGPI CFLWSSKERP VYQDAQGARQ120  
 EVPLPSTPAA AAFLAARKHL LAVGEDVALS FLDHRHVAQG LAES 164

## (2) INFORMATION ON SEQ ID NO. 369:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 187 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

KSGKHRTFSA HAWVRIFPSH TRSPPSKVPV YFWSARAQVS KSLKKAPTS AIMSEVVVER 60  
 PCFWKAWWLH CLVREQAPNA ATRRGLOPFV FCGPARSAQC TRTPREPDRR SPCPPHLRL120  
 PSWLHTSTCW PLERMSRSPF WTTVTLPRAW LSLSTDFWLS SLSIGPLSTA SYSLLNSTWL180  
 GVSTAFR 187

## (2) INFORMATION ON SEQ ID NO. 370:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein

01673705.123700

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

LFLFTNHNDG GKPQCKHQHC HQLRICDQEC HLTVTGRRQK

40

(2) INFORMATION ON SEQ ID NO. 371:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 34 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

QAEDKSETGL MRITGKLALA PPENELFHSI ADHP

34

(2) INFORMATION ON SEQ ID NO. 372:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 38 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

NSSFSGGAKA SFPVIRISPV SLLSSACYRE MALLITDP

38

06/23/95 12:00

## (2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

RQLFGIVSIA TLTVLAYERY IRVVHARVIN FSWANRAITY IWLYSLAWAG APLLGNRYI 60  
 LDVHGLGCTV DWKSKDANDS SFVLFLFLGC LVVPLGVIAH CYGHILYFHS NASLVWKIFR120  
 QFK 123

## (2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

TVHSRGPCQS DQFFLGLLEGH YLHLALLTGV GRSTSPGMEQ VHPGRTTRL HCGLEIQGCQ 60  
 RFLLCAFLIS WLPGGAPGCH SPLLPYSIF PFECFVGVED LQTIQVIKIL KYEKKLAKMC120  
 F 121

## (2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

00673395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

HPGAPPGSQE IRKAQRNRNW HPWISSPQCS LVRVRFPGCTC SIPGEVLLPT PVSRRRCR 58

(2) INFORMATION ON SEQ ID NO. 376:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 49 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

AFTCOFVPLC GLLEQWTTKS AMQFIKVDLV ICHPTAYGFC KPVLEANIL

49

(2) INFORMATION ON SEQ ID NO. 377:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

FCTTLWPSGA MDNQVSYAVH KSGPGYMSSN SIWSLQACFG SQYSITYRNP LESDVFSGSNI60  
FSQGSNGL 68

(2) INFORMATION ON SEQ ID NO. 378:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 64 amino acids

0057335-12270

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

HITRSTFMNC IADLVVHC SR RPQSGTKSQV KAQTAPVILV VLSLHSSPLA KTGLNMKSPA60  
PRPQ 64

## (2) INFORMATION ON SEQ ID NO. 379:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

APISSNFCSE SIWGYCDQLK VSESTHVLQP FLPSILDGLI HLAAQFSSEV LNLVMETLCI 60  
VCTVDPEFTA SMESKICPFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMRLLIP120  
TLVSIMQAPA DKIPAGLCAT PLIS 144

## (2) INFORMATION ON SEQ ID NO. 380:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 254 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

00672305 122700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

YEIQSLPFPS FSSAKLSLLW HSPVFTQMTM PSVQNGGECL RAYVSVTLEQ VAQWHDEQGH 60  
 NGLWYVMQVV SQLLDPTSE FTAAFVGRVL STLISKAGRE LGENLDQILR AILSKMQQAE120  
 TLSVMQSLIM VFAHLVHTQL EPLLEFLCSL PGPTGKPALE FVMAEWTSRQ HLFYGGYEGK180  
 VSSVALCKLL QHGINADCKR LQDIRVKGEE IYSMDGIRT RSKSAKNPER WTNIPLLVKI240  
 LKLIINELSN VMGG 254

(2) INFORMATION ON SEQ ID NO. 381:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 95 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

SLSGPNANEA DSHSGQHNAG PSRQDSCRAL CDTIDILITV VRNTKPPLSQ LLICQAFPAV60  
 AQCTLHTDDN AISAEWRRVL AGLCVSDPGT SSPVA 95

(2) INFORMATION ON SEQ ID NO. 382:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 263 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

APISSNFCSE SIWGYCDQLK VSESTHVLQF FLPSILDGLI HLAAQFSSEV LNLVMTLCI 60  
 VCTVDPEFTA SMESKICFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMRLLP120  
 TLVSIMQAPA DKIPAGLCAT PIDILTTVVR NTKPPLSLL ICQAFPAVAQ CTLHTDDNAT180  
 MQNGGECLRA YVSVTLEQVA QWHDEQGHNG LWYVMQVVSQ LLDPTSEFT AAFVGRLCF240  
 PHLQGRAGTR GESRPDFVFP SFS 263

06673395.12700

## (2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TLRCGGPGAG SPLASHTTVH CGPARHATGL LVPGLTHRP ASTLRHSAAW HCHLCEGYTV60  
PQQGKLGR 68

## (2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

HIGPQALSAI LHGGIVICVK GTLCHSRESL ADEKLGKGR L CISYYCCQDI NGCRTKPCR N60  
LVCWGLHYAD QSGNQSHLHW ALTGFNLGQL LEDVLSQ 97

## (2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 140 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673306123700

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

TRSSSPQTIT FDACVVIPCG DLQSQKQLSD SEKYLCPFKI KGSPYQDRCS LTNAGKQVCH 60  
 SWNEVVWTE YQGNTSSTGG CMSLKPVIHF TKESTPHNCQ YNQC�FVQIS ILIPTSTDPK120  
 PTLSCGIWHG SRNSRGTSYW 140

(2) INFORMATION ON SEQ ID NO. 386:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

DVPLFLRLPC HIPQLKVGLG SVEVGMRIEI CTGLHWLYWQ LWGVLSLVK 49

(2) INFORMATION ON SEQ ID NO. 387:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

SECMVLRTYN HRLTRSSLDI QLSTPPHSSY GRPVFLHSLR NKGLDRGSLI S 51

(2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids

09673395.122700



(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

SSSFLSFCWF LPSPAACSS SCPSGMTSWS RSGPSISGFS WLTDRAACTC GVWPSSPAPP60  
 KPLPPTGLSS TPAPGLAPAA ACPSEAPINT DLMVPFF 97

(2) INFORMATION ON SEQ ID NO. 389:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 148 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

GKGTMRSVLI GASEGQAAAG ARPGAGVEDR PVGGRGFGGA GELGQTPQVQ AALSVSQENP 60  
 EMEGPERDQL VIPDGGQEEQ EAAGEGRNQK KLRGEDDYNM DENEAESETD KQALAGNDR120  
 NIOFNVVEDQ KRDTINLLDQ REKRNHTL 148

(2) INFORMATION ON SEQ ID NO. 390:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 84 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

0067305 122700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GPRDRLIQPS YFQRGKWGLE VTEHLAGALA PLASHRLPSS WDYRHTVTEA GPVCNSRCHL60  
QLKHSSYYVMS LVTKVKLSPH EKAT 84

(2) INFORMATION ON SEQ ID NO. 391:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 59 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

CGKKCITLFL FLSPSLPLWC LRYWGSHSWG HSEATRNASL LHLAVSARTR NPQTSSQTS 59

(2) INFORMATION ON SEQ ID NO. 392:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 107 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

TPRNLFHSH LTQFHCNVTV SLGSTKHPIT QFCFIVWTPS RLQGHGQEV CEEVCGFLVL 60  
ALTARCKLEA FLVASEWPQL WDPQYLRHHR GREGDRNRNR VMHFFPH 107

(2) INFORMATION ON SEQ ID NO. 393:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein

00573395.12700

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

VAPAVGSPVS QAPQRQGGQ EQKQSYAFLS TLKKRNYTFR GMLSPRSTSS PVFHDLPKK60  
I 61

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 74 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

CNCAPSLPDF SPLHPQCGIS LVPRGTPLDL WTSRPGQEA TRNPRPLLLK FTASVVVPDS60  
SPAPGTTSTW GGAF 74

(2) INFORMATION ON SEQ ID NO. 395:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 112 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

ATVHPACQIF PHYTPSVAYP WSPEAHP LIC GPPGLDKRL PETPGPCYSN SQPVWLCLTP 60  
RQPLEPHPPG EGPSEWSSDT AEGRPCPYPH CQVLSAQPGS EEELEELCEQ AV 112

09673395-12700

## (2) INFORMATION ON SEQ ID NO. 396:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

DRRSHGLLLY NLPGEQFKNM NQDPFDPLII QKSTQKYAQK YVGIH

45

## (2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

ERLSHCRSLV MLALISLCTF CTHAFSPVFY QASVSCITLK CDH

43

## (2) INFORMATION ON SEQ ID NO. 398:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

0067306123700  
0067306123700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

WIKRILIHIF KLLSREVVKQ QSMRASISLP LLGDACPILP MYPMHSCLLS CFLSSLSFMY60  
YTKM 64

## (2) INFORMATION ON SEQ ID NO. 399:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 77 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

HIKIEFFGQN FWEAMHPTWA DIQPELFSRG EWYQCFMAEI HSDWLESMLY QLLNLSITL60  
AYCYVYISSI YRQKGHF 77

## (2) INFORMATION ON SEQ ID NO. 340:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 48 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

SSLGKTFGKQ CILHGLIFSL SCSQEESGTG SLWLKSILIG WSLCYTSC 48

## (2) INFORMATION ON SEQ ID NO. 401:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 48 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

09673395.122700

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

FRNPALIEPS VGSTAEIFRA FNILKMAFLS IYRGNIIVTV CKSDTQNV

48

(2) INFORMATION ON SEQ ID NO. 402:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

EQLRLNISPC RMHCFPKVLP KELYFYVLSH RTGEKCSGHC WDLIFLGMGS GLMILATGVQ60  
ENGSPGSDSW 70

(2) INFORMATION ON SEQ ID NO. 403:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

MCDFIRGICQ FSHCGSFSD F ACSSSKEARS FADFTIPQTC KFLTSSKLAL ALSSTFFPKS60  
NLC 63

(2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids

00673303 122700

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

MGITHECVIL LGASANSLTV VPSLTLPVHH LRRLDPSLTS PFLKPVSFSL LPNWLWFLQ60  
PFHSRAIFAK E 71

(2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

LGDHIYNWDV NHFFSGIRAQ RHNLQGHIIY YEHFTVRLFI LPSTCAEMKP KQAVGFHKSI60  
YVG 63

(2) INFORMATION ON SEQ ID NO. 406:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 88 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

0067395-12700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

LVEPNGLFWF HFSASRRQNK ESHSKMFIVD NMSLKVVPLC SYSTEEMIHI PIIDMVSQSE60  
 ESFRRLHKYV LCTCFMLGNR KIIVIDKT 88

## (2) INFORMATION ON SEQ ID NO. 407:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 269 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

LTVVYTVFYA LLFVFIYVQL WLVLRYRHKR LSYQSVFLFL CLFWASRRTV LFSFYKDFV 60  
 AANSLSPFVF WLLYCFPVCL QFTTLTLMNL YFTQVIFKAK SKYSPPELLKY RLPLYLASLF120  
 ISLVFLVNL TCAVLVKTN WERKVIIVSVR VAINDTLFLV CAVLSICLY KISKMSLANI180  
 YLESKGSSVC QVTAIGVTVI LLYTSRACYN LFILSFSQNK SVHSFDYDWY NVSDQADLKN240  
 QLGDAGYVLF GVVLFVWELL PTTLVVYFFR VRNPTKDLTN PGMVPSHGFS PQILFL 296

## (2) INFORMATION ON SEQ ID NO. 408:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 152 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

HRRLHRVLR AALRVHLRAAL AGAALFPQAA QLPERLPLSL PLLGLPADRP LLLLLQRLRG 60  
 GQFAQPLRLL AALLLPCVPA VFHPHADELV LHAGDFQSQV KIFSRTIQIP VAPLPLGLPLH120  
 QPCFPVGEFN LCCAGKDGKL GEEGYRLCAS GH 152

00673395.122700



## (2) INFORMATION ON SEQ ID NO. 409:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

LGFENHLREV QVHQREGEKL QAHREAVEQP EDEGAERIGR HEVFEVEGEE DGPPGGPPEA 60  
 EKEEDALVAE ELVAVTQHQP ELHVDEHEEQ RVEHGVDDGE 100

## (2) INFORMATION ON SEQ ID NO. 410:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 268 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

APISSNFCSE SIWGYCDQLK VSESTHVLQP FLPSILDGLI HLAAQFSSEV LNLVMTLCI 60  
 VCTVDPEFTA SMESKICPFT IAIFLKYSND PVVASLAQDI FKELSQIEAC QGPMQMLIP120  
 TLVSIMQAPA DKIPAGLCAT AIDILTVVR NTKPPLSQLL ICQAFFPAVAQ CTLHTDDNAT180  
 MQNGGECLEA YVSVTLEQVA QWHDEQGHNG LWYVMQVVSQ LLDPRTSEFT AAFVGAFVST240  
 LISKAGRELG ENLDQISSCH PSVKMAGG 268

## (2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein

06673305.122700

- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

HIGPQALSAI LHGGIVICVK GTLCHSRESL ADEKLGKGRLL CISYYCQQDI NGCRTKPCRN60

LVCWGLHYAD QSGNQPHLHW ALTGFNLGQL LEDVLSQ

97

(2) INFORMATION ON SEQ ID NO. 412:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

PPAILTEGWH EEIWSRFSPS SRPALEMRVE TKAPTKAQVN SEVRGSRSWL TTCITYHSPL60  
WPCSSCHWAT CSRVIDT

77

(2) INFORMATION ON SEQ ID NO. 413:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 62 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

IGFASIPPRI SGSPSILLAF YPHPPSPKLG PVLLCARETP KFRKRSIFYR GGFILDQKNK60  
KN

62

006673395 122700

## (2) INFORMATION ON SEQ ID NO. 414:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 65 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

DLIYNYYCYP SDLSFSAIDV IAISRSSHNV FNPALILMLR MEFLTSSLKE EQPNTYTYT60  
SRIAK 65

## (2) INFORMATION ON SEQ ID NO. 415:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 94 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

LDLSPFHVVF PDPHPSFWLF TRIRHLRSWG QCYYPVGKPR NLGENQYFTG EDSSLTKKIK60  
KIKNTKKFMF LYCIPKECLY TVIILKENTS MLDI 94

## (2) INFORMATION ON SEQ ID NO. 416:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 83 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00673005.127700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GRRNDQLNLH IPQAGPTAGP YRLGWPLLSS GIRLPDWLVL HVSILKLVIP WPPPGENQPH60

PASWGQWGRD FGLSEQLLEA AHD

83

(2) INFORMATION ON SEQ ID NO. 417:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 93 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

RRKASIIAFK GILLTLTQGV QSAREPILIS SSKMFLEENP WNVLKOVSGV RSSMWLAKGH60  
LYLFQLEFIN SCSLVS LGAE VWHIFKPVHS RIQ 93

(2) INFORMATION ON SEQ ID NO. 418:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 96 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

TLNPHKTLA KKA RVIFFCI QOSTANLVFC YKNLVSHFL KRTRITGTHP QLHETPSFLN60  
EHESIYVHPS THMKMLCSST GMDGIRIKPI WKLKYF 96

05673395-126700

## (2) INFORMATION ON SEQ ID NO. 419:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 68 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

YSFFFFLYQN NHLPLFFLER EEESGEEGKN AKCHFELLVH HTRGSPLMSA ASVHRPQVKE60  
RMRSSWTS 68

## (2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 60 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

KPSIHFFESC TKTIIFLYFS WSGKRRVEKX GRMQSVTLNF SFTTHVGVHS CQQPPCTGPR60

## (2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 52 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

00672305-122700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

DAGCRFVAPA LSGSFEITPQ RQLPFVNTRQ AVLAGPTRRH SFFHLGPVHG GC

52

(2) INFORMATION ON SEQ ID NO. 422:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 52 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

VLGKSSMSIT IVWKNLHPK QIEVSQVKPH RMANRCLGCR MQVRGPGPVW LP

52

(2) INFORMATION ON SEQ ID NO. 423:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 59 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

YRYVFPPTHY GYNGVELQTV KFCFGLVSPD PPRQELPLPP YLPALKLCPI KLDNTLTGF 59

(2) INFORMATION ON SEQ ID NO. 424:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 79 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

09672305 120700 002221 5662760

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

VTCLSLYVET NFTMITDLGN ISSLNFHTIL KCLLGKLTFF CSKGALHLLK FWGHTSSVAS60  
EGQILWVVG D NEVLTIVIL 79

(2) INFORMATION ON SEQ ID NO. 425:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 102 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

HKKTSSYSYGV TVCSYDSIIR LKAGEICVQF NRTQLKGRQV GWERKLLSGG IRGNQSKTKF 60  
YCLQFNSIIA IMCSGKHIPV LLDRVSFPFS GTRMVEGIN PT 102

(2) INFORMATION ON SEQ ID NO. 426:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 81 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

SMPFQFGTQP RRFVVEGGDS SIELEPGLSS SAACNGKEMS PTRQLRRCPG SHCLTITDVP60  
VTVVYATTRKP PAQSSKEMHP K 81

00221-562700

## (2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 62 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

GRASALACHR YRSDWASGLY ILAALSTSSS IGSSGGRGNW QQVGNVVKES PDVIISGCHR60  
NI 62

## (2) INFORMATION ON SEQ ID NO. 428:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

REHQLLSGND FQGTSGVAWL VTSPSHYRQH WSSAQVPAQL KNLLPLETS LAGFQIEKAY 60  
FTENQKRLSL IPVEVNKSM L STGLSTEGWN CQRNDDQMF 100

## (2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

0067205 122700



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

NSHLNVTLLI IMLIFSISYR NQSLCLKLRG LKNVYHSIFI

40

(2) INFORMATION ON SEQ ID NO. 430:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 31 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

GGIGYKGRYL NSSNNGYNPF FHNHLGCFKA I

31

(2) INFORMATION ON SEQ ID NO. 431:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 53 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

TLPIIRDASN QHNYQCHIQ VGILPNTTIK GRIKLDNLIK KYKAFKNLTH HLK

53

(2) INFORMATION ON SEQ ID NO. 432:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 31 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

0067295-122700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

IALKKPKWLW KKGLYPLFEL FRYLPLYPI P

31

## (2) INFORMATION ON SEQ ID NO. 433:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

CNIFQWGPSE HTCWTVQTIS SPEGKYFCIR GNSVLERNMF FISQIKTLSN GKLASNFFKY60  
SIFFSPLVVT GFYRSSYTVC FNSGP

85

## (2) INFORMATION ON SEQ ID NO. 434:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

LLIREINQVF PLIYDAIYFS GGLQSTPVGR CKPYLLQKAN TFWSEETQFW RGICSLYLKS60

KLSLMVNWLL IFLSTVFFFP L

81

0967395.12700

## (2) INFORMATION ON SEQ ID NO. 435:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

YKSICLLEKI WFAPSNRCAL KAPTEIYCII DEGKDLVNFS YQKLVFRTSC PTWLPGAQGF60  
 FSEIVLRDPQ TCSPPSGATC ASSPRQAVR SMRLS 95

## (2) INFORMATION ON SEQ ID NO. 436:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

SCAFLLLLWGH SGPTWASMDP GLEQAHLHLF HLRQCGRSQ EGLTSGPSRF LCARNERP60  
 ILPPRLDPEV RAGQPSRKHT V 81

## (2) INFORMATION ON SEQ ID NO. 437:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673365.122700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

94

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 91 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

91

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 456 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

ALSHAGKKKKK	KGVSTIEEHE	VEPETTLPAR	RTEKSSPLRK	QVFGHLEFLS	GEKKNKSSPL120
VMHVSGKVVV	SPDRQGESE	TRGKKLKKH	KKEKKGQADP	TAFSVDQFPWF	CSAREARDDV180
DTCSSVGKKDE	EQAAALGQKKK	RKSPVGHKK	VKKKKIHQE	GDALPGHSPK	SRSMSSPRK240
GSKKFPDVKE	APBYPIISDD	PKASAKKKKK	SKLQVQZPV	EEPALKRKKK	KRESGVGAG300
PKWKEITDKL	EVLVEKKNNM	DEAHIDQVRR	KALKEIIDE	SGKTEASETR	KWTGTQFGW360
DATFAGNEDD	KLKFLRLMGG	FKNLSPFSSR	PASTIARPNM	ALGKKAADSL	QQNLQRDY420
AMSWKYSRGA	GLGFSTFST	IFYIDRANKS	SVKLED		456

456

## (2) INFORMATION ON SEQ ID NO. 440:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

VRVCFLLP RV SCYPTLSLLL FLPPQSWLLD DWLLYLLFGL HLFLCGGLRV ITYGDVFRSL 60  
 NFDWLLFTSF PRAALHGGGG LGVAWEGISL LVDFFFLLHL PIVFSGALPL PFLPQGCLFL120  
 ILLPR 125

## (2) INFORMATION ON SEQ ID NO. 441:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 381 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

SRCRCFCCRLS AAFFLPRAMLG LAIVLAGRLN EGDRLFKPPI SLRNFSFWSS FSKPAVSHWP 60  
 NWVPVHFLVS EASVLPDSRS ISSCKAFRLT WSMCASSMLP FFSNTTSKSV SVSSFQGSAP120  
 TPLSLSPFFF LFRAGSSMTG CSTFFLDIF FFAEALGSSL MGMYSGASTL TGFFLLPFLG180  
 LLSMDLEGL WPGRASPSWW IFFFFFTFPL CSLGLFRFRF CPKAACSSSF FPTEQVSPTS240  
 LASLASQNGQ SWTEKAVGSW APFFSFLCFL SFLPTLVSSS PCLGSGEVFT PEAWDMARGD300  
 FLEFFSPLRN SKWPNTCFLR LGDFSVRLAG SVVSGSTCSS QRVLTPEFF FFFFTRGISG360

ACPWATLLEG DVALKGETSA K

381

## (2) INFORMATION ON SEQ ID NO. 442:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

09673395.122700

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

DHANKLSLQS QTYIILLSVN GEKISPYVLW VKCCNRLGLS NLP

43

(2) INFORMATION ON SEQ ID NO. 443:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 45 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

MVISIFFPLL YKLIFTHLLL YKLTFINTNK RLVLSQLICH EPRNN

45

(2) INFORMATION ON SEQ ID NO. 444:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 40 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GKPKNCCDF QGKLDNPNLL QHFTHKTYGL IFSPLTDSSI

40

(2) INFORMATION ON SEQ ID NO. 445:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 78 amino acids

002221 5532960

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

GVGGGALRSA ALPWRTILPT STCSRCKPS TAEMERLVQS WCLLNILMLQ THDFKWPLQR60  
RSVKNKSWNPL MMKCLQLI 78

(2) INFORMATION ON SEQ ID NO. 446:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

RLRRRGWRSF FGGAPMAHIT INQYLQQVYE AIDSRDGASC AELVSFKHPH VANPRLQMAS 60  
PEEKCCQVLE PPYDEMFAAH LRCTYAVGNH DFIEAYKCQT VIVQSFLRAF QAHKEENWAL120  
LSCMQ 125

(2) INFORMATION ON SEQ ID NO. 447:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00672345-12270

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

MSCKHFIIRG FQDLTLTLLW RGHLSWVCN MRMFKRHQLC TRCSISAVDG FVHLLQVLVN60  
GNVRHGSAAE RRAPPTTPQA 80

## (2) INFORMATION ON SEQ ID NO. 448:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

RSRGFSCVQT PCHFREVTA CVISLWQQVG GLPQGRRWPE MCFRSLTHHS LHTREHHSW60  
SILRMEI 67

## (2) INFORMATION ON SEQ ID NO. 449:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

PITPYTHDVN TTPGAFSEWR FEFHVAASHT QTCHSPHPTH SRHSTAMSQK KFLVSDLKVL60

## (2) INFORMATION ON SEQ ID NO. 450:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00672395.126700



- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

RATSGRSGFI KPSNLKQGTG FGSWLLNVVS GCVGNDGRFV CEKLPHGIQI SILRMLQEWCG60  
 SRRVCRE

67

(2) INFORMATION ON SEQ ID NO. 451:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

SASHPESRLC RGGADMQAPR GTLVFALVIA LVPVVGREPSS QGSQSALQTY ELGSENVKVP 60  
 IFEEDTPSVM EIEMEELDKW MNSMNRNADF ECLPTLKEEK ESNHNPSDSE S 111

(2) INFORMATION ON SEQ ID NO. 452:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

EEWALEETAK GSCVYVDLKL IKFVSSSSSV GSLSRLPQGL LLENMSAIQ V

51

(2) INFORMATION ON SEQ ID NO. 453:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids

007221-565266

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

FDSFSSFKVG KHSKSAFLFM LFIHLSSSSI SISITEGVSS SKIGTFTFSL PSSYVCKAL 59

(2) INFORMATION ON SEQ ID NO. 454:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 107 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

PITTCSLGDP GKDKYTCTHR GRERCVRIC INILFSHPDM RSQCCMMKRW YDSTYVPIVL 60  
 LFLYFLFRSF TIGRFQKHSF HHHLEMVCLN GDNRSRCSIS SRAGLLI 107

(2) INFORMATION ON SEQ ID NO. 455:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 73 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

RRGVSELLSR QKWHYHYAAL QSPRARSLEN HLLSRFFFFL RVGVSLCCPK TRPGNCWGAK60  
 GIAPVPQASR VGR 73

00673395 120700 002221 56E266

## (2) INFORMATION ON SEQ ID NO. 456:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

SWGNIIVRLLP SKKKKNAKEG DSLESELWEI GERQHNDTIS AYLEGKKLLS FSCMTVVISS60  
RKDISKE 67

## (2) INFORMATION ON SEQ ID NO. 457:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

DQPSLFPIRH KTLNLTSMAT KIIGSPETKW IDATSGIYNS EKSSNLSVTT DFSESQSSN60  
IESKEINGIH DESNAFESKA S 81

## (2) INFORMATION ON SEQ ID NO. 458:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

002215682760

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

QLISPKAFRV LILNPKKSME FMMKAMLLNQ KHLESIFFEK P

41

(2) INFORMATION ON SEQ ID NO. 459:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

IPEVASIHFV SGEPIILVAI LVRLRVLCRI NGREGW

36

(2) INFORMATION ON SEQ ID NO. 460:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

NSEGFRRNQL LQIDLKIFLS CKFQKLHQST LFQVNL

36

(2) INFORMATION ON SEQ ID NO. 461:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

09673395.122700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

GRANDQLNLH IPQAGPFAGP YRLGWPLLSS GIRLPDWLVL HVSIKLKVIP WPPPGENQPH60  
 PASWGQWGRD FGLSEQLLAE AHD 83

(2) INFORMATION ON SEQ ID NO. 462:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

RRKASIIAFK GILLTLTQGV QSAREPILIS SSKMFLEENP WNVLKDVSGV RSSMWLAKGH60  
 LYLFPQLEFIN SCSLSVLGAE VWHIFKPVHS RIQ 93

(2) INFORMATION ON SEQ ID NO. 463:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

TLNPHKTLA KKAUVIFECI QDSTANLVFC YKNLVSHFLL KRTRITGTHP QLHETPSFLN60  
 EHESIYVHPS THMKMLCSST GMDGIRIKPI WKLKYF 96

0067355-132700

## (2) INFORMATION ON SEQ ID NO. 464:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

NLFTMKFLPE FSPFDNTSMH VSTFETQPNV ISVKSSLSLP SSNLPSPRVY LPFCAHLSYS60

SMLFYNCDSP GSLGAI

76

## (2) INFORMATION ON SEQ ID NO. 465:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

NQRMIEIYSN TKTERKCHST LKAANTIDHF IWLPSQESH NCKITCYCNS NVHKMAGKL 59

## (2) INFORMATION ON SEQ ID NO. 466:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

000723001130700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

HATVTQMCTK WQVNSRRQI TAWKTQGRFY RNDIWLSELEG

40

(2) INFORMATION ON SEQ ID NO. 467:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 41 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

IPLQRFSLLT SLFFVLKLDL LVVHASLSLV TVNNLPTSSN Q

41

(2) INFORMATION ON SEQ ID NO. 468:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

LSKAIYFCKK AAACINHDHS STLNKERKRF LSLTQSLPLC HSPRGWGWT A HSKLTRLAIC60  
EYFSK

65

(2) INFORMATION ON SEQ ID NO. 469:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

0067333-132700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

PDWLFVNITFP NKEGKGDVSY SGGKCSFSGK NGCRVGNQGS RCELLIRTGG KVVHNS 56

(2) INFORMATION ON SEQ ID NO. 470:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

ARFAPAGREG RGEGEATSRG CGVGHRAQPR EPAPHGAAV RPTPGPHHC AALSGAENYR 60  
SRHAMKLASA LRAGPALHPL PPRANRGREP WRRRHRPRGW AAASRTWRS 109

(2) INFORMATION ON SEQ ID NO. 471:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 399 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

AAGACGARGS GRGGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNPGPSSLR RAFRRRLPFF 60  
PACHEIGLGA EAGSGPPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120  
PGVTEVTIE KPFAERHMIS SWEQKNCVM PEDVKNFYLM TNGFHMWTSV KLDEHIIPGL180  
SMAINSISKL TQLTQSSMYS LPNAPTLDL EDDTHEASDD QPEKPHFDSR SVIFELDSCN240  
GSGKVCVLYK SGGPALAEDT EIWFLDRLALY WHFLTDTFTA YYRLILHLG LPQWQYAFTS300  
YGISPOAKQW FMSYKPIITN TNLLEETDS FVNKLDPKV FKSKNKIVIP KKKGPVQAPAG360  
GQKGPSPGSG PSTSSTSKSS SGSGETPPGK LRHPSFQFA 399

00673395 122700



## (2) INFORMATION ON SEQ ID NO. 472:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

RSAGGFMMV TSVTPGEDSR MRVMERSVSF RCGLLQPSFG DDASSMARD RDSRAAGAGG60  
 GPDPAAPRP ISWHAGNGSS RRLKARRSDD GGPGLV 96

## (2) INFORMATION ON SEQ ID NO. 473:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

KYVSHANISI YKWRITLTL LLSYKIPNEVI ILSGITLYCK NASYFTFKFD NVCDEL 56

## (2) INFORMATION ON SEQ ID NO. 474:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN

0067305-12700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

WIFRVCCISR EIHFYILFYY KHLDKGHLTH FKKHKCI

37

(2) INFORMATION ON SEQ ID NO. 475:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 33 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

PKGLSIKVRRLDTRRKRCRLLNFIIHHIH CQI

33

(2) INFORMATION ON SEQ ID NO. 476:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

HIKIEFFGQN FWEAMHPTWA DIQPELFSRG EWYQGFMAEI HSDWLESMYQLLNILSITL60  
AYCYYYISSI YRQKGHFRNI

80

(2) INFORMATION ON SEQ ID NO. 477:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09673395-12700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

SSLGKTFGKQ CILHGLIFSL SCSQESGSGT SLWLKSILIG WSLCYTSC

48

(2) INFORMATION ON SEQ ID NO. 478:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

EQLRLNISPC RMHCFPKVLP KELYFYVLSH RTGERKCSGHC WDLIFLGMGS GLMILATGVQ60  
ENGSPGSDSW

70

(2) INFORMATION ON SEQ ID NO. 479:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 400 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

FQQTFWAVAG RWCNGFSLHR NRAGLDLPTI DTGYDSQPD VLGIQRLERP LPLTSVCYPQ 60  
DLPRPLRSRE FQFEPQRYP ACAQMLPPNL SPHAPWNYHY HCPGSPDHQV PYGHDYPRAA120  
YQQVIQPALP GQPLPGASVR GLHPVQKVIL NYSPWDQEE RPAQRDCSFP GLPRHQDQPH180  
HQPPNRAGAP GESLECPAEL RPQVPQPPSP AAVPRPSPNP PARGLTKTSN LPEELRAKVF1240  
TYSMDTAMEV VKFVNFLLVN GFQTAIDIFE DRIRGIDIIK WMERYLRDKT VMIIVAI5PK300  
YKQDVEGAES QLDEDEHGLH TKYIHRMMQI EPIKQGSMMNF RFIPVLPFNA KKEHVPTWLQ360  
NTHVYSWFKN KKNILLRLLR EEEYVAPPRG PLPTLQVVL

400

0667395.12700

## (2) INFORMATION ON SEQ ID NO. 480:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 225 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

SSSGWRVARG SRHSSWGRRL GNLWSQLCRA LQGLPRSTSS IRWLVMWLVL VPWKPRKGAV 60  
 SLCGPLFLVP GAGIIQDNLL HRVQASHTGS RQGLPRQSRL DHLLVGCSRV VMALVHLVIG120  
 TSRTVMVIVP WSMWKGICRQ HLCCTCWIPLR FKLRELPGPE RSGEVLGVTH GGEQGQPFQL180  
 PDAQDILGLG IISRVYGWQI QACSVPVQAG AVAPSPCYRP RSLLR 225

## (2) INFORMATION ON SEQ ID NO. 481:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

KQRMQSSSHL HFKA RVCGGL RGRALHNRFP GGORASRGGT EKNQPGVLPT SLSQNAVTRR 60  
 PQTWFGLSDL GMNGVTREPP EGWAEAEVEE PHTLPLSAAA AGCFFYSWAS CRHECSEARN120  
 AHAPS 125

## (2) INFORMATION ON SEQ ID NO. 482:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein

09673395-122700

- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

VAMTAKDCSI MIALSPCLQD ASSDQRPVVP SSRSRFAFSV SVLDLDLKPYP ESIPHQYKLD60  
GKIVNYYSKT VRAKDNVMS TRFKESEDCT LVLHKV 96

(2) INFORMATION ON SEQ ID NO. 483:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 66 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

LHCLPVCRMP ALIKGLWSLH RGPGLRFPCL CWTLTSSPTR AFPISINWTA RSTIIQRLY60  
VPKTTT 66

(2) INFORMATION ON SEQ ID NO. 484:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 109 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

NKAFRIRES D MSPGWERTI QNVFPGLNGH FHFKSVSSFL GHSTHFLHSL SRKLFVLVFN 60  
SMSPRGNPTS KGKVKSKNIH QRSPTNTENI SIIQPSHYVQ VSKTLQGKS 109

00673295-12700

## (2) INFORMATION ON SEQ ID NO. 485:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

CSSIPLCLQEA IPPQKGLKAK TTTTKGHPTQ QKISLSFSLH IMFKFQRHCR ERVRPCGELM60  
CNLRFP 66

## (2) INFORMATION ON SEQ ID NO. 486:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

ARPAPAGREG RGEGEATSRG CGVGHRAGPR EPAPHGAAAV RPTPGPHHHC AALSGAENYR 60  
SRHAMKLASA LRRGPALHPL PPRANRGREF WRRRRHPRGW AAASRTWRS 109

## (2) INFORMATION ON SEQ ID NO. 487:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 389 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00673395.122700

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNPGPSSLR RAFRRRELFF 60  
 PACHEIGLGA EAGSGPPFAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120  
 PGVTEVTIE KPFAERHMIS SWEQKNVCYM PEDVKNFYLM TNGFRMTWSV KLDEHIIFLG180  
 SMAINSISKL TQLTQSSMYS LPNAPTLADL EDDTHEASDD QPEKPHFDSR SVIFELDSN240  
 GSGKVCLVYK SGKPALAEDT EIWFLDRLAL WHFLTDFTTA YYRLTLHLG LPQWQYAFST300  
 YGISPQAKQW FSMYKPIITN TNLLEETDS FVNKLDPSTV FKSNNKIVIP KKKGPVQPA360  
 GQKPGSPGSG PSTSSTSKSS SSGSNPTRK 389

(2) INFORMATION ON SEQ ID NO. 488:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 96 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

RSAGGFMMV TSVTPGEDSR MRVMPRVSFS RCGLLQSPSG DDASSMARD RDSRAAGAGG60  
 GPDPAAPRP ISWHAGNGSS RRLKARRSDD GGPGLV 96

(2) INFORMATION ON SEQ ID NO. 489:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 152 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

LAAGRGKEE MGFEDHGLPF LPLTHHTPPF PLGLSPLPKK KKKETFMNQ QGFSPYQREM 60  
 WKELKKPPFV PNSTLPIFYA TQTLSEFWVF LQMDLLRRII VFHVTFSPQVT KINICIYNYL120  
 YCYIFVDNTE RWCWVIYYNL NLGISFGLPQ SC 152

00673395-12700

## (2) INFORMATION ON SEQ ID NO. 490:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

GPWLTFPAFD FSHPISSSFP LPAAKKKKKG NVYHESTGFQ SLKRDVERA KETTLCSQLH60  
 FTHILCNTNT VLLGPFLTDG PLEKNYRIPR F 91

## (2) INFORMATION ON SEQ ID NO. 491:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

KWGTQRAGNF HYPILGLNLK EYIHYQELST KAGVKLHYTW LFTIPGSPFQ HDCGRPKDIP60  
 RFRL 64

## (2) INFORMATION ON SEQ ID NO. 492:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673395.122700



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

RFTASRVGNE PDINTPSSMP CPPSGVPVVK AGSHFSPQA VPKALEEPKE RQEPSWELTL60  
MTRGQLAQFP LFSWGEGTL 79

(2) INFORMATION ON SEQ ID NO. 493:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 100 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

KSSPDPARHY GSPPEGERRG KRSVPKVNPR SLGPTSLPTA TSHQPHARAR PFPLQLTAQQ 60  
MLGQNASPHL TKGLQPAGWE MNQILTPPPP CPAHLGQYQ 100

(2) INFORMATION ON SEQ ID NO. 494:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 82 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

KGSLPPTKQG KLGQLAPGHQ GQLPTWLLFF LGFFQFGNS LGVGEVASCL HWYWPRRWAG60  
HGGGGVNIWF ISHPAGCKPL VK 82

0067305 42200

## (2) INFORMATION ON SEQ ID NO. 495:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 79 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

RVFSPQLNKG NWANWPLVIK VNSQLGSCLS LGSSRALGTA WGWEKWLPAP TGTGPEGGQG60  
MEEGVLSIGS FPTLLAVNL 79

## (2) INFORMATION ON SEQ ID NO. 496:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 88 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

IQKVQYYTSP AAFVNGSLHS HWGTTVCMGR NSKCPHCGHW VGS AFCQGV C RNWLISVCQS60  
DQHTKVSAIK NVASLHPPSC YSGPSNLM 88

## (2) INFORMATION ON SEQ ID NO. 497:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 98 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00667395.122700

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

SHTSEKRRTG REEVTPASRS SISGVKRGTV ALPSWLRMRK SFLQWEEIHF SIPVQSDFMG60  
PVLNSDCIIN TIKRDSEMGs RIHWONSKAY NTALMDPT 98

(2) INFORMATION ON SEQ ID NO. 498:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

AGYTPVSSSTI RQLHQITGPR VTGWRMQGSH ILYGRDFGVL ITLAYRNKPI PADSLTKGTP60  
HPMTTMRALA VSAHAHSCTP MAV 83

(2) INFORMATION ON SEQ ID NO. 499:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

GKICEYVNFL SLRDDRMFPY FSCKENNILT YTSCRKYHLF PLYYSTMTFL LYCQAESIKN60  
VHIHFELCIL FLKKGAGLWH WAGHD 85

06673305-122700

## (2) INFORMATION ON SEQ ID NO. 500:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

SYRLKGIGKC VFSRDHVESE QCWQTLPRKS CFSRCPCFGI SFLGRKKKSS LTIIVNSISYF60  
SFCCSNGFPP TIIPSIYVLL YSPLSEVTFL SNTFPFKF 98

## (2) INFORMATION ON SEQ ID NO. 501:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

VSSCTSNRQV RSSLSSGEHK CTERDVLVLT TKELPSLSLT QAMCTCDAE CAGVGGGHA60  
PPEHFLTGKL GDPFLVNEVE IRTVSFT 87

## (2) INFORMATION ON SEQ ID NO. 502:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

00673355.122730

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

TPKTLGCLLV SRVEQAQRES LGPELKEFIE FWQTGSKQPI LAAVLRRECG GQI

53

- (2) INFORMATION ON SEQ ID NO. 503:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

PSGPFSSLES TLLQVQAA IASFLSDCNS PIRFPFCFYIC PPHSLNTAA RMGCLLPVCH60  
GSINSLSSGP KDSRWACSTR DTSRQPSVLG V 91

- (2) INFORMATION ON SEQ ID NO. 504:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

VFIYDSLIIIP TSISSVHTVC QMFHAEPVSR ILLSDYGGFT TRPGSNSLGS KVGHSSMHR 59

- (2) INFORMATION ON SEQ ID NO. 505:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual

09673395 12700

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

DRKFWNQKID PVFSYIQSST SEFLFLNIGV LALFLKDALY LKRKLOFRITG CGAVKYFRFR60  
SVYTFYRRNE VL 72

(2) INFORMATION ON SEQ ID NO. 506:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 102 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

SILGPGLCTH FIEEMKYSEV FWLPFHENCV LNLSHDITYIV LLGAVVSFIK PLACVQKFLK 60  
GNTSNAYPLL ACYAACTAI AVCFTVFVKI PLSPLVTGK AC 102

(2) INFORMATION ON SEQ ID NO. 507:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 68 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

NNEHKMLFII TSICEISYCK TTTGLLLNSL VIVFRLEMPF TLVINITYKYN VFLGRHFIFKC60  
IMPWLLLR 68

09673395.12700

## (2) INFORMATION ON SEQ ID NO. 508:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

LKFLQVLKFF FYSLHWIYVF LIPNMFNWDV CHSRAARQTF KNSHTAELA FLTTQKFRKL60  
TVTVT 65

## (2) INFORMATION ON SEQ ID NO. 509:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

GPRAHWPLPN TMLEPKRANM GPEYNGDIFM FQPFNLICLL LSFPPISNL ECULTYYLQGL  
ITSSYRIPSS LMSCPQY 78

## (2) INFORMATION ON SEQ ID NO. 510:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

00673305.12700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

SLKLLGFLDV ENTPCARHSI LYGSLGSVVA GFGHFLETSE YLYFLFLYVL KKAFLYIMNY60  
FFF 63

(2) INFORMATION ON SEQ ID NO. 511:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 53 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

SFVKWSPNLK LGNYEEKIA RYLLRSACRS AVGLVTIGSK VLLQWQILWP LSG 53

(2) INFORMATION ON SEQ ID NO. 512:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 43 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

ICCRACHHWK QGTSVADLV AFEWLKTTTL HRAGAMHRHP SLP 43

(2) INFORMATION ON SEQ ID NO. 513:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 37 amino acids

0067395 122700



(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

QALQQIYRQT LTDTGQFSL RNFLVLSWVT ILQNFTT

37

(2) INFORMATION ON SEQ ID NO. 514:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 228 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

TGGARARRPL SAVARPARSS DPLRSAPLGP APPVNMIRCG LACERCRWIL PLLLLSAIAF 60  
DITALAGRGW LQSSDHGQTS SLWWKCSQEG GSGSYEEGC QSLMEYAWGR AAAAMLFCGFI20  
IILVICFILS FFALCGPQML VFLRVIGGSL ALAAVFQIIS LVITYPVKYTQ TFTLHANRAV180  
TYIYNWAYGF GWAATILILG CAFFFCCLPN YEDDLLGNAG PRYFYTSA 228

(2) INFORMATION ON SEQ ID NO. 515:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 94 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

0067395-12700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

DPLPPPSWEH FHHSEDEVWFW SLDCNQPRPA SAMMSKAMAL SRSRGRIQRQ RSQARPQRIM60  
 LTGGAGPSGA ERSGSEERAG RATAESGLRA RAPP 94

## (2) INFORMATION ON SEQ ID NO. 516:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 208 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

TLPKNGFKVA WRNSFFWFSP SQQRFSPTF IPKLGRCVEV PGLGIAQKVI FVVGAEAE 60  
 GTADQNRGC PPKAVGPVID VSDSTVGMKG EGLGV LHGVN YQGDDLEHSS QGKETS NHSQL20  
 EDKHLGSTEG EGEDETDHQ DDEATEEHGS RCSTPRVLHE ALTALLVGPA AAALLGAFPP180  
 QRGRLAVVAR LQPAAGQRD DVEGDGAE 208

## (2) INFORMATION ON SEQ ID NO. 517:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 204 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

PSCPPEMKKE LPVDSCLPRS LELHPQKMDP KRQHIQLLSS LTECLTVDPPL SASVNRQLYP 60  
 KHLQS SLL L EHLSSWEQI PKKVQKSLQE TIQSLKLTNQ ELLRKSSNN QDVVTCMAC120  
 KGLLQQVQGP RLPWTRILL LLLVFAVGFLC HDLRSHSSFQ ASLTGRLLRS SGFLPASQQA180  
 CSKPTFTVCK VTGWLGEKCR FGVP 204

09673395-122700

## (2) INFORMATION ON SEQ ID NO. 518:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 90 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

PEVMAQEAYS EDQQQQEPR PGQPRTLNL QQALAGHVTG DDILVVTATL PQQLLVGKLE60  
GLNGFLQRL YLLGNLLPGA EQVLQKAGL 90

## (2) INFORMATION ON SEQ ID NO. 519:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 76 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

GTKRHFSPN QPVTLQTVGV NLEHACWLAG KKPDDRSNRP VREAWKELCD RRSWHRKPTA60  
KTSSNNRRSRV QGSRGF 76

## (2) INFORMATION ON SEQ ID NO. 520:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 355 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

0673395.12700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

FRHSMNGCEK DSSSTDSANE KPALIPREKK ISILEEPSKA LRGVTPGNIE KSVKDLQRCT 60  
VSLTRYRVMI KEEVOSSVKK IKAFAELHN CIIDKEVSLM AEMDKVKEEA MEILTARQKK120  
AELKRLTDL ASQMAEMQLA ELRAEIKHFV SERKYDEELG KAARFSCDIE QLKAQIMLCG180  
EITHPKNNYS SRTFCSSLLP LLNAHAATSG KQSNFSRKSS THNKPSEGKA ANPKMVSSLP240  
STADPSHQTM PANKQNGSSN QRRRFNPQYH NNRLNGPAKS QGSGNEAEPL GKGNRSRHEHR300  
RQPHNGFRFK NKGGAKNQEA SLGKMTPEAP AHSEKPRRRQ ARCRTPREGQ GPFGR 355

(2) INFORMATION ON SEQ ID NO. 521:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 120 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

NONVKNRGTO KKCLPSVEKL PNPPWGQKNA TVKTPNRKLT PERPLALPRC PAACLPSPL 60  
FRMGRGLGGL HPQGSLLIFG TAFVFGPEAV VRLSSVFVAA VALSQWLGF I PTALRLGRPI120

(2) INFORMATION ON SEQ ID NO. 522:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 116 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

RAVRISMAS LTLISISAIN TSLSMMLCN SAKAALIFFT ELSTSSLIMIT RYLVRTVQR 60  
CKSFTEFSIF GPVTPRSFAE GSSSIEIFFS RGIRAGFSLA ESDVLSFSQ PFMLCR 116

09673395 \*122700

## (2) INFORMATION ON SEQ ID NO. 523:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 130 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```

RRQRKAEPGA CALGRVGSEC IPEPGARRTA QAAGLRVSG AANTKVRELK HFRFLGLLRS 60
CRSEMEVDAP GVDGRDGLRE RRGFSEGGRQ NFDVRPQSGA NGLPKHSYWL DLWLFI LFDV120
VVFLEVYFLP                                     130

```

## (2) INFORMATION ON SEQ ID NO. 524:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```

ISANKSWQKI HKEKHHHIEK DEKPEVQPVG VFGKPICPRL RPHIEVLPPS LAKASPLPET60
ISTINTRCVH LHLAPAAS                                     78

```

## (2) INFORMATION ON SEQ ID NO. 525:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

09673395.122700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

(2) INFORMATION ON SEQ ID NO. 526:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

(2) INFORMATION ON SEQ ID NO. 527:

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

RRPCHCQPL PIHYNKDSSL QVSTLLWPDN RTERRGLOSG VLAWATGFLH DSFMILLMLY60  
TPRRANINVP HA 72

(2) INFORMATION ON SEQ ID NO. 528:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 102 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

RNHAKIQLPM QAPQSLILSS QFCCQATVVM RLVGCCPCCN EWEEVDSGMV ETFTSSSPAT 60  
GIPPRPVLCC GGRFKSKLL FEVGFAVWFK CMMLLRGKAI QG 102

(2) INFORMATION ON SEQ ID NO. 531:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1708 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00672305 122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

```

CCTGGAAACA AGATCCAAAC CCAAGTGACC CGCCGGGAAA GTGACCCAGT CAGGTTTAAA 60
AATTCACACA AACCGAGCTG AACAAATAGA CCGACCAACC AAATATACAA TCCGTCAAAA 120
TACATTCACT TCCACTACGA AACCCCAACA AAGGGTGTGA ATGCCCGCCC AGGAGAGACG 180
GTTTTGGTTT CATCAAGTGT GTGGATCGTG ATGTTCTGTAT GTTCTTCCAC TTCAGTGAAA 240
TTCTGGATGG GAACCGAGCTC CATATTGCAG ATGAAGTAGA GTTTACTGTG GTTCCTGATA 300
TGCTCTCTGC TCAAGAAAT CATGCTATTA GGATTAAGAA ACTTCCCAAG GGCACGGTTT 360
CATTTTCATT CCATTTCAGT CACCGTTTTT TGGGCACGGT AGAAAAAGAA GCCACTTTTT 420
CCAATCCTAA AACCACTAGC CCAAAATAAG GCAAAGAGAA GGAGGCTGAG GATGGCATT 480
TTGCTTATGA TGA CTGTGGG GTGAAACTGA CTATTGCTTT TCAAGCCAAG GATGTGGAAG 540
GATCTACTTC TCCTCAAATA GGAGATAAGG TTGAATTTAG TATTAGTGAC AAACAGAGGC 600
CTGGACAGCA GGTTCGCACT TGTGTGCGAC TTTTAGGTCG TAATTCTAAC TCCAAGAGGC 660
TCTTGGGTTA TGTGGCACT CTGAAGGATA ATTTTGGATT TATTGAAACA GCCAATCATG 720
ATAAGGAAAT CTTTTTCCAT TACAGTGAGT TCTCTGGTGA TGTTGATAGC CTGGAAGTGG 780
GGGACATGCT CGAGTATAGC TTGTCCAAAG GCAAAGGCAA CAAAGTCAGT GCAGAAAAAG 840
TGAACAAAAC ACACTCAGTG AATGGCATT  CTGAGGAAGC TGATCCCACC ATTTACTCTG 900
GCAAAGTAAT TCGCCCCCTG AGGAGTGTG ATCCAACACA GACTGAGTAC CAAGGAATGA 960
TTGAGATTGT GGAGGAGGGC GATATGAAAG GTGAGGTCTA TCCATTTGGC ATCGTTGGGA1020
TGGCCACAAA AGGGGATTGC CTGCAGAAAG GGGAGAGCGT CAAAGTCCAA TTGTGTGTC1080
TGGGCCAAAA TGCACAACT ATGGCTTACA ACATCACACC CCTGCGCAGG GCCACAGTG1140
AATGTGTGAA AGATCAGTTT GGCCTCATT  ACTATGAAGT AGGAGATAGC AAGAAGCTCT1200
TTTTCCATGT GAAAGAAGTT CAGGATGGCA TTGAGCTACA GGCAGAGAT GAGGTGGAGT1260
TCTCAGTGAT TCTTAATCAG CGCACTGGCA AGTGCAGCGC CTGTAATGTT TGGCGAGTCT1320
GTGAGGGGCC CAAGGCTGTT GCAGCTCCTC GACCTGATCG GTTGGTCAAT CGCTTGAAG1380
ATATCACTCT GGATGATGCC AGTGCTCCTC GCCTAATGGT TCTTCGTCAG CCAAGGGGAC1440
CAGATAACTC AATGGGGTTT GGTGCAGAAA GAAAGATCCG TCAAGCTGGT GTCATTGACT1500
AACCACATCC ACAAAGCACA CCATTAATCC ACTATGATCA AGTTGGGGGG AATCTGGTGA1560
AGGGTTCTGA ATATCTCCCT CTTCAATCCCT CCCGAAATCT GGAATACCTA TTCTATTGAG1620
CTATTACACC AGTTTTTAACA CCTTCTCTGT GTTATGTTTA AAAAAATAAA TAAATTTAAG1680
AAAACCATTT TAAATAATGA AAGTTTG

```

1708

09673395.12700



## (2) INFORMATION ON SEQ ID NO. 532:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2128 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

00673395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

CTGTATCCTA ATTTCTTGGT GAATGAATC ATTCCTTAAAC AGAAGCAAAG ATTTGAGGAA 60  
 AAGAGGTTCA AATTGGACCA CTCAGTGAGT AGCACCRAATG GCCACAGGTG CGAGATATTT 120  
 CAAGATTGGT TGGGAACCTGA CCAAGATAAC CTTGATTTTGG CCAATGTCAA TCTTATGTTG 180  
 GAGTTACTAG TGCAGAGAA GAAACAATG GAAGCAGAAT CACATGCAGC CCAACTACAG 240  
 ATTCCTTATGG AATTCTCTCA GGTTCGAAGA AGAATAAGA GAGAGCAACT GGAACAGATC 300  
 CAGAAGGAGC TAAGTGTITT GGAAGAGGAT ATTAAGAGAG TGAAGAAAT GAGTGCCTTA 360  
  
 TACTCTCCTG TCAGTGAGGA TAGCACAGTG CCTCAATTTG AAGCTCCTTC TCCATCACAC 420  
 AGTAGTATTA TTGATTCCAC AGAATACAGC CAACCTCCAG GTTTCAGTGG CAGTTCTCAG 480  
 ACAAAGAAAC AGCCTTGCTA TAATAGCAGC TTAGCATCAA GACGAAAACG ACTTACTGCT 540  
 CATTTTGAAG ACTTGGAGCA GTGTTACTTT TCTACAAGGA TGTCTCGTAT CTCAGATGAC 600  
 AGTCGAAGTG CAAGCCAGTT GGATGAATTT CAGGAATGCT TGTCCAGTT TACTCGATAT 660  
 AATTCACTAC GACCTTTAGC CACATTGTCA TATGCTAGTG ATCTCTATAA TGGTTCCAGT 720  
 ATAGTCTCTA GTATTGAATT TGACCGGGAT TGTGACTATT TTGCGATTGC TGGAGTTACA 780  
 AAGAAGATTA AAGTCTATGA ATATGACACT GTCATCCAGG ATGCGAGTGA TATTCATTAC 840  
 CCTGAGAATG AAATGACCTG CAATTGCAAA ATCAGCTGTA TCAGTTGGAG TAGTTACCAT 900  
 AAGAACCTGT TAGCTAGCAG TGATTATGAA GGCACCTGTT TTTTATGGGA TGGATTACA 960  
 GGACAGAGGT CAAAGGTCTA TCAGGAGCAT GAGAAGAGGT GTTGGAGTGT GACTTTAAT1020  
 TTGATGGATC CTAACCTCTT GGCTTCAGGT TCTGATGATG CAAAAGTGAA GCTGTGGTCT1080  
 ACCAATCTAG ACAACTCAGT GGCAAGCATT GAGGCAAGG CTAATGTGTG CTGTGTTAAA1140  
 TTCAGCCCCT CTTCCAGATA CCATTGGGCT TTGCGGTGTG CAGATCACTG TGTCCACTAC1200  
 TATGATCTTC GTAACCTAA ACAGCCAAATC ATGGTATTCA AAGGACACCG TAAAGCAGTC1260  
 TCTTATGCAA AGTTTGTGAG TGGTGAGGAA ATTGCTCTCG CCTCAACAGA CAGTCAGCTA1320  
 AAACGTGGA ATGTAGGGAA ACCATACTGC CTACGTTTCT TCAAGGGTCA TATCAATGAA1380  
 AAAAATTTT TAGGCCTGGC TTCCAATGGA GATTATATAG CTTGTGGAAG TGAATAAAT1440  
 TCTCTCTACC TGTACTATAA AGGACTTTCT AAGACTTTGC TAACTTTTAA GTTTGATACA1500  
 GTCAAAAGTG TTCTCGACAA AGACCGAAAA GAAGATGATA CAAATGAATT TGTAGTGT1560  
 GTGTGCTGGA GGGCACTACC AGATGGGGAG TCCAATGTGC TGATTGCTGC TAAACAGTCAG1620  
 GGTACAAATTA AGGTGCTAGA ATTGGTATGA AGGGTTAACT CAAGTCAAAAT TGACTTTGAT1680  
 CCTGCTGAAA TACATCTGCA GCTGACAATG AGAGAAGAAA CAGAAAATGT CATGTGATGT1740  
 CTCCTCCCAA AGTCATCATG GGTTTTGGAT TTGTTTTGAA TATTTTTTTC TTTTTTCTT1800  
 TTCCTCCTTT TATGACCTTT GGGACATTGG GAATACCCAG CCAACTGTCCT ACCATCAAT1860  
 TAACCTCATG GACATTGCTG CTCTTGGTGG TGTATCTAAA TTTTGTGAT AGGGAACAA1920  
 ATTCCTTTGA ATAAAAATAA ATAAACAAAC AATAAAAGTT TATTGAGCCA CAAAAAAA1980  
 AAAAAAATAA AAAAAAATAA ACAAAGAGA AAACRAAGGT TACGAAGTAG CATATGTGA2040  
 CTATAATGTA ACAGTGAATA ATTTGTAAAG TTCGTATTTC CCAACCTCTT TGGGAATTAC2100  
 ACATATCAAT ATAAACAAA TATAAAGT 2128

0673395.122700

## (2) INFORMATION ON SEQ ID NO. 533:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2640 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

00673305.12000

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

CTAGCAAGCA GGTAACCGAG CTTGTACAA ACACACACAG ACCAACACAT CCGGGGATGG 60  
 CTGTGTGTG CTAGACGAGA GGCTGATTAA ACACCTAGTG TGTGGCTCT CTGTGCCATC 120  
 CCTGGAAAT AATGAATTGG GTAAGGAACA GTTAATAAGA AATGTGCGCT TGCTAACTGT 180  
 GCACATTACA ACAAAGAGCT GGCAGCTCCT GAAGGAAAAG GCGTTGTGCC GCTGCCGTTG 240  
 AAACCTTGTA GTCAACTCAT GCCAGCAGCC TCAGGGCTCG COTCCCCAGC ACACCCCTCAT 300  
 TACATGTGTC TGCTGTGGCT GATCTGTGCA TGTGCTCGGA GACGCTCCTG ACAAGTCCGGG 360  
 AATTTCTCTA TTTCTCCACT GGTGCAAGA GCGGATTTCT CCCTGCTTCT CTTCGTGAC 420  
 CCCCCTCCT CTCCCCCAGG AGGCTCCTTG ATTTATGTA GCTTTGGACT TGCTTCCCCG 480  
 CTCGACTGTC CTGACTTCT AGAATGGAAG AAGCTGAGCT GGTGAAGGGA AGACTCCAGG 540  
 CCATCACAGA TAAAGAAAA ATACAGGAAG AAATCTCACA GAAGCGTCTG AAAATAGAGG 600  
 AAGACAAAT AAAGCACCAG CATTTGAAGA AAAAGGCCTT GAGGGAGAAA TGGCTTCTAG 660  
 ATGGAATCAG CAGCGAAAA GAACAGGAAG AGATGAAGAA GCAAAATCAA CAAGACCAGC 720  
 ACCAGATCCA GGTTCATGAA CAAAGTATCC TCAGGCTTGA GAAAGATC CAAGATCTTG 780  
 AAAAGCTGA ACTGCAAAAT TCAACGAAG AGAGGCCAT TTTAAGAAA CTAAAGTCAA 840  
 TTGAGCGGAG AACAGAAGAC ATTATAAGAT CTGTGAAGT GGAAGAGAAA GAAAGAGCAG 900  
 AAGAGTCAAT TGAGGACATC TATGCTAATA TCCCTGACCT TCCAAAGTCC TACATACCTT 960  
 CTAGTTTAAG GAAGGAGATA AATGAAGAAA AAGAAGATGA TGAACAAAAT AGGAAAGCTT 1020  
 TATATGCCAT GGAAATTAAG GTTGAAAAAG ACTTGAAGAC TGGAGAAAGT ACAGTTCTGT 1080  
 TCTCCAATAC CTCTGGCCAT CAGATGACTT TAAAAGGTAC AGGAGTAAAA GTTTAAGTG 1140  
 ATGGGCAAAA GTCCAGTGTA TTCAGTAAAG TGCTAATCAC AAGTTGGAGG TCAATGGCAG 1200  
 CGATGGCCTG GCACCACTTG AAGTAGAGGA ACTTCTAAGA CAAGCCTCAG AGAGAAATCT 1260  
 TAAATCCCCA ACAGAGATCT ATGAGCCTGT ATATGCCAAT CCCTTTTACA GGCCTACAAC 1320  
 CCGACAGAGA GAACCGTGTA CCCCTGGACC AAACTTTCAA GAAGTAAAAA AGATTTAAAC 1380  
 TAATGGACTG GGTATTGGTG TAAATGAATC CATACACAAT ATGGGCAATG GTCTTTCAAG 1440  
 GGAAGGGGGA AACAACTTCA ATCACATCAG TCCCATTCGG CCAGTGCCTC ATCCCCGATC 1500  
 AGTGATTCAA CRAAGCAGAAG AGAAGCTTCA CACCCCGCAA AAAAGGCTAA TGACTCCTTG 1560  
 GGAAGAATCG AATGTCAATC AGGACAAAAG TGCACCCCTCT CCAAGGCCAA GGCTGAGCCC 1620  
 CAGAGAGACA ATATTTGGGA AATCTGAACA CCAGAATTCT TCACCCACTT TCGAGGAGG 1680  
 CAGGGAAGAT GTCAGATATA ATATCGTTCA TTCCCTGCCT CCAGACATAA ATGATACAGA 1740  
 ACCGGTGACA ATGATTTTCA TGGGGTATCA GCAGGCAGAA GACAGTGAAG AAGATAAGAA 1800  
 GTTTCGTACA GGATATGATG GGATCATCCA TGCTGAGCTG GTTGTGATTG ATGATAGGAA 1860  
 GGAGGAGGAT GAAGGAGAAG CAGAGAAACC GTCTACCAC CCATAGCTCT CCCATAGTCA 1920  
 GGTGTACCAG CCAGCCAAAC CAACACCAC TCTAGAAAA AGATCAGAAG CTAGTCTCTA 1980  
 TGAACAACA AATCATAAAT CCCCCACAA AATTTCCATA TCTCTGAAG AGCAAGAAGA 2040  
 AAGCTTAGGC AGCCCTGTCC ACCATTCCC ATTTGATGCT CAGACAACCT GAGATGGGAC 2100  
 TGAGGATCCA TCTTAAACAG CTTTAAAGAT GAGAATGGCA AAAAGGTGAT 2160  
 CTAAAGATTC TACCACCTAT ATAAACATCC TTTGAAGAG AAACATAAGAA GCATTTGCA 2220  
 ATTTCTCTTC TGGATATTTT GTTTATTTTT TCTGAAGTCC AAAAAATAT CATTACAGTG 2280  
 TACCATATTA AGCCATGTGA ATAAGTAGTA GTCATTATTT TGAAAAAAT CCCCCAAAGC 2340  
 TGGGGAACAC AAATGTGTAA CTTTCCAGT TACTTGACAC GATTCACTGG GGGAAAAACA 2400  
 GCATTTTTTA TTCTATTGAT ACCAAAGCAT TTCTAATAAG AGCTTGTTAA ATTTAAGAAT 2460  
 AAAGTTATTT AAAATATICT GAGTATAGTA TATTAACATG CATGTGAATT TTGATGATAC 2520  
 AAGATTGAA AGATCATAGG AAAGCATTCG CCTTCATCAC AACTCATATC AACTCTGACA 2580  
 AATAAATATG TCATCTCGAA TTAATAATGC CTTAATAAAA GTACATCCTC CTGCTAAAAA 2640

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 534:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1245 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

TGCAGCGCGT GCGTGCTGCG CTA CTGAGCA GCGCCATGGA GGACTCTGAA GCACTGGGCT 60  
 TCGAACACAT GGGCCTCGAT CCCCGGCTCC TTCAGGCTGT CACCGATCTG GGCTGGTGGC 120  
 GACCTACGCT GATCCAGGAG AAGGCCATCC CACTGGCCCT AGAAGGGAAG GACCTCCTGG 180  
 CTCGGGCGCG CACGGGCTCC GGAAGACGG CGCTTATGC TATTCGGATG CTGCAGCTGT 240  
 TGCTCCATAG GAAGGCGACA GGTCCGGTGG TAGAACAGGC AGTGAGAGGC CTGTGTTCTG 300  
 TTCCTACCAA GGAGCTGGCA CGGCAAGCAC AGTCCATGAT TCAGCAGCTG GCTACCTACT 360  
 GTGCTCGGGA TGTCCGAGTG GCCAATGTCT CAGCTGCTGA AGACTCAGTC TCTCAGAGAG 420  
 CTGTGCTGAT GGAGAAGCCA GATGTGGTAG TAGGGACCCC ATCTCGCATA TTAAGCCACT 480  
 TGCAGCAAGA CAGCCTGAAA CTTGCTGACT CCCTGGAGCT TTTGGTGGTG GACGAAGCTG 540  
 ACCTTCTTTT TTCCTTTGGC TTTGAAGAAG AGCTCAAGAG TCTCCTCTAG TCACTTGCCC 600  
 CGGATTTACC AGGCTTTTCT CATGTGAGCT ACTTTTAACG AGGACGTACA AGCACTCAAG 660  
 GAGCTGATAT TACATAACCC GGTACCCCTT AAGTTACAGG AGTCCCAGCT GCCTGGGGCA 720  
 GACCAAGTTAC AGCAGTTTCA GGTGGTCTGT GAGACTGAGG AAGACAAATT CCTCTGCTG 780  
 TATGCCCTGC TCAAGCTGTC ATTGATTGCG GGCAAGTCTC TGCTCTTTGT CAACACTCTA 840  
 GAACGGAGTT ACCGGCTACG CTTGTTCTTG GAACAGTTCA GCATCCCCAC CTGTGTGCTC 900  
 AATGGAGAGC TTCCACTGCG CTCACGGTGC CACATCATCT CACAGTTCAA CCAAGGCTTC 960  
 TACGACTGTG TCATAGCAAC TGATGCTGAA GTCTGGGGG CCCCACGTCA ACGGGCAATG 1020  
 CGACCCCGCG GACGAGCCAA AACGGGGACA ATGGCCCTCT GATTCCTGGA ACGCACGGTCT 1080  
 GTGGCCCTGG GGCCTAGAC CTTCCACCAT CGTGCTGCA TGTGCTCAAC TTTTGATCTT 1140  
 CCCCCCAAC CCCTGAGGCC TAACATCCAT CGAGCTTGGC AGGACAGCAA CGCGCTAAC 1200  
 ACCCAGGGCA TAGGTCTTAA CCTTTGGTGC TTTCCACAGG AGGCG 1245

0673395-122700

## (2) INFORMATION ON SEQ ID NO. 535:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 822 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

AAGATCGGTC TTTGTCCTTA TCCTTATCCT TATTCTAATG GCAGTTAGAT GCNNTTCTTT 60  
 AGAGGGGGCA ATGAGACAGC CAGGTGGGAA GGGGTCCCCA GAGAACTCC AGCCTGCACAL20  
 CTGGGAGGAG TGTGCACTGG GGTGAAGCCA CCGGAAGTTT GCGCCATCTC CAGTGGGGAA180  
 GAGCCCGACC CCTCCTCTTC CTGGGTGGGA AACTGCGATT CAAACTGCCA GGTGGGAAGT240  
 CCATGGGCAG GAAACAGGCT CTCGNTTTGC TAAGAGTCTC TGTTCCTCCC TTTTTCCTT300  
 TATGCCTAAT TAATAAATTC CATTTTTCTC ACCCTTCAAA CAGCCTGTGA GCCTAAATTT360  
 TTGTGCCCAT GGGACAGACA AGGACCCCGT CTTCAAGTGA ACTAAGGAGA AAGTCCCCAA420  
 ACAATGGGAA GAAAGGCAGG GAGTAGACAT CCAATTTTCT GCGGTGGATT GTGGAGGGGT480  
 ACCATGGTTC TGACCAGATG TGTATCAGGA GCTGTGTTGC AGGAAGTCTC AGGAATGAAG540  
 TTGATAGCTT TCTTTCATC ACATGATGAC TGAAAAGACG AAGGCATCTA ATGAGTTAGA600  
 GTCACACCAT CTCATGCTTG TATACTATCA AACAACTTTT GGGAAAGCTAG CCTTGGTTGG660  
 GAAAACATCA TTTCTTAACT GAATGCCTGG ATGCAAGCAA AGTCTCATT TTGATCATGA720  
 TGAGGTTTAC CATGTCTTCT TGACAGGATC CTGCAAAACA ACCCACAAAT GCTACTATGA780  
 CATGCAACTC CATGGTTAAT TCCTTGGATA GCAATAGTCT CG 822

## (2) INFORMATION ON SEQ ID NO. 536:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2703 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

09673395-12700

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

AGTTGCGCAC AGGGGGAGGA ACCTGGCCCT GGGAGGAGGC TGTTCGCTGC TCCTAGAGAA 60  
 TCCGCTTCTG AAGGGAAGAG CATGTTTGGG GGGCTCCCCA CCATGCGTGA GAGCTCCCCC 120  
 AAACAGTACA TGCAGCTCGG AGGCAGGGTC TTGCTGGTTC TGATGTTTCA GACCCTCCTT 180  
 CACTTTGACG CCAGCTTCTT TTCTATTGTC CAGAACATCG TGGNGCAGAN GCTCTGATGA 240  
 TTTTNACTGG CCATTGGTGT TAAACCAAG CTGGCTGCTT TGACTCTTGT TGTGTGGCTC 300  
 TTTGCCATCA ACGTATATTT CAACGCCTTC TGGACCATTC CAGTCTACAA NGCCCATGCA 360  
 TGACTTCNNT GAAATACGAC NTTCTCCAG ACCATGTCGG TGATTGGGGG CTTCCTCTG 420  
 GNTGGNTGGC CTGGGCCCT NGGGGGTGTC TCCATGGATG AGAAGAAGAA GGAGTGGTAA 480  
 CAGTCACAGA TCCCTACCTG CCTGGCNTNA AGACCCNGTN GSCCGTCAAG GNACTGGNTT 540  
 CNGGGGTGGG TTCAACNAAA ANCTGNCCAG CTTTNNATGT ATCCTCTTCC CTTCGCCCTCC 600  
 CTGTTAAAG GCACAGATGT TTTGAGAANC TTTATTTGCA GAGACACCTG AGAATNCGAT 660  
 GGNCTCAGT TGCTCTGGAG CCACAGTCTG CGCTCTGACC CTTCASTNGC AGGCCNAGCC 720  
 TGGCANGCTG GNAAGCCNCT CCCCACGCC GAGGCTTTNG GNAGTGAANC AGNCCCGCTT 780  
 NGGNCTGTGG CATNCTCAGT CANTATTTT GAGTTTTTT GTGGGGGTAN NCAGGAGGGG 840  
 GCCTCTCAAG TGACTCTGA NGCAGACGCA NTGTTTATTA TCATTCAAAG CAGTCTCCCT 900  
 CTNNATTTGT AAGTTTNACA TTTTNNAGC GGAACTACT AAATTATTTT GGGNTGGTTC 960  
 AGCCAAACCT CAAAACAGT AATCTCCCT GGNTTTNAAT ATCACACAGC TGGNCTTTNG1020  
 ATGTTGTTTC TGCCCGCAT TNGTATTTA TAGGNNAATA GTGAAAACAT TTAGGGNACA1080  
 CCAANAGAA TGATNCGAGT ATTAAGGGG TGSTAGAAGC TGCTGTTTAT GATAAAGTC1140  
 ATCGCTCAGA AAATACACTT GGATTNGGTG CCAAGTGNNN TTTTATGGG TACACCCCTG1200  
 GGAGTTTATG TAGCTTGAGG CAAGGTGGAG GGGCAAGAAG TCCTTGGGGA AGCTGCTGTT1260  
 TGGGTNGCT NGCTGGGCTC CAAGCTGGCA GTGGGAAGGG CTAGTNAGA CCACACANGG1320

GGTAGCCCCN AAGACGAGCA CCCTGCAANG CCAGCCNTGG CCNAGCTNNG CTCNAGACCA1380  
 GCNTTNGCAG ANGCCCGAGN CCGCTGTNNG GGCANGGGGG GTNGGGCAGG AGCTCCCNAG1440  
 CACTNNGNAG ACCCAGCGAG NTCACCCAG TNAACCTCAC ATGGGGCAGT TTTCTGAGC1500  
 AAGGTCTNCG AAGCGCGAG CCGCCCTGGM CTGACGAGCA CCGCCCTTTC CCAGCTGCAC1560  
 TCGCCCTGTG GACAGCCCCG ACACACCANC TTCTCTNAG GCTGTGCGTC ACTCAGATTG1620  
 TCCGTTTGCT ATGCCGAATG CAGCCAAAAN TTCTTTTGA CAATTTGTGA TGCCCTACCG1680  
 ATTTGATCTT AATCCTGTAT TTAAGGTTT CTAACTCTGN NCCTTAAACT GTGTTTCTCT1740  
 TTTTGGGGGA GCTTAACCTG TTGTTGCTCC CTGTGCTCTN GACCATAGT AAATGCCACA1800  
 AGGGTATGCG AACACTCTCT TGGCCCTAG ACCTATCTGG GGACAGGCTG GCTCAGNCTG1860  
 TCTNCTANG GCTGCTGCGG CCGAGCCCG AGCCTGCCCT CCTCTTGGNC CTCTCATCCA1920  
 TTGGMCTCTG CAGGGCANGG GGTGAGGCG GTTCTCNGCN CTAATAAGTC TTTTNGGAAG1980  
 TCACCTACCT TTTTAACACA GCGCAACTAN GTCCCAACGC NTNTTGCAAA TATCTCCCTN2040  
 GTAGGCTGCT TTNCTTANM CCGCGAANTA TTGGTAAGAT CGAGCAATGG NNCTCAGGA2100  
 NCATNGGGTT CTCTTCTCT GTGATCATTN CAAGTGTCTA CTGCNATNNG ANGACTNNGC2160  
 TTGNTCNTCA GTGTTTCNAA CCTNACCAG GGCNTGTCTC TTGGTCCACN ACCTCGCTCC2220  
 CTGTTAGTGC CGTATGACAG CCCCNCATCN AAATGACCTT GGGCNAAGTN CACNGGTTT2280  
 TCTGTGGTNC AAGGTTGGTT GGCTGATTGG TGAANGTN AGGGTGNAG CNAAANGGAG2340  
 GNCCACGTGA NGCAGNTCNA GCACCANNGT TNCCTGCANCC AGCAGCGNCC TCCGTCNCT2400  
 GTGGGCTGTN CCTNGTTTCN TNCTTGGCCC NTGGGTNGGG CTNAGGNGCC TGATTCCGGN2460  
 AANGATGCC TTGNCANGGG AGGGGAGGAN TAAGTGGGAT CTACCNCAAT TNGATTCTGG2520  
 CAAAACAAAT TCTTAAGANT TTTTGTGCTT TATGTGGGNA AACAGATCTA AATCTCATTT2580  
 TATGCTGTAT TTTATATCNT TNAGTTGTGT TTGAAAACNG TTTNTGATTT TTGGAACAC2640  
 ATCAAAATAA ATAATGGCGT TTGTGTGAAA AAAAAAAAAA AAAAAAAAAA2700  
 AAAA

2703

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 537:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2664 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

09673395.12700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

CTCGCCAGGGA GTGCTGAGTA GTGATGGTGT CTGGAGGGTC AAATCCATTC CCAATGGCAA 60  
 AGGTTCTCTCA CCACTCCCCA CCGCTACAAC TCCAAAACCA CTTATCCCTA CAGAGGCCAG 120  
 CATCAGGGTC TGGGGCAAGA GCGGCACGAG CCATCTCCAT CCCCGGAGCA TGTGTATGAT 180  
 TCAGAAGTAC AACCACGATG GGAAGACGAG TCGGCTGGAG GCTTTTAGCC AAGGGGAAAG 240  
 TGTCTCTAAG GAACCCAAGT ACCAGGAAGA GCTGGAGGAC AGGCTGCATT TCTACGTGGA 300  
 GGAATGTGAC TACTTGCAGG GCTTCCAGAT CCTGTGTGAC CTGCACGATG GCTTCTCTGG 360  
 GGTAGGCGCG AAGCGGCGAG AGCTGCTACA AGATGAATAT TCAGGGCGGG GAATAATAAC 420  
 CTGGGGCGCTG CTACCTGGTC CCTACCATCG TGGGGAGGCC CAGAGAAACA TCTATCGTCT 480  
 ATTAACACA GCTTTTGGTC TCGTGCACCT GACTGCTCAC AGCTCTCTTG TCTGCCCTTT 540  
 GTCCTTGGGT GGGAGCGTGG GCCTGCGACC CGAGCCACCT GTCAGCTTCC CTTACCTGCA 600  
 TTATGATGCC ACTCTGCCCT TCCACTGCAG TGCCATCCTG GCTACAGCCC TGGACACAGT 660  
 CACTGTTCCCT TATCGCCTGT GTTCCCTCTCC AGTTTCCATG GTTCATCTGG CTGACATGCT 720  
 GAGCTTCTGT GGGAAAAAGG TGGTGACAGC AGGAGCAATC ATCCCTTTTC CCTTGGCTTC 780  
 AGGCCAGTCC CTTCCTGATT CCCTGATGCA GTTTGGAGGA GCCACCCCAT GGACCCCACT 840  
 GTCTGCATGT GGGGAGGCGTT CTGGAACACG TTGCTTTGCC CAGTCAGTGG TGTCTAGGGG 900  
 GTATAGACAG AGCATGCCAC ACAAGCCACA GAACCAAAGG GACACCTCCA CCCTCTGCCC 960  
 TTCACTGATG TACCAGTGGG GAAGAATCT TGGCTCAGTA TTTACAACAG CAGCAGCCTG1020  
 GAGTCATGAG TTCTTCCCAT CTGCTGCTGA CTCCTCTGAC GGTGGCTCCT CCTTACCCCC1080  
 ACCTCTTCTC AAGCTGCAGT CCACCGGGTA TGGTTCTGGA TGGTTCCCC AAGGGAGCAG1140  
 GTCTCTGTGT TCCCTCTCCC TTCCACAGCA GTGGAGAGCA TCCCACTGTT TGGGGCACTG1200  
 TGTTCCTCTT CGTCCCTGCA CCAGACCCCTG GAAGCCTTGG CCAGAGACCT CACCAAACTC1260  
 GACTTGGCGG GCTGGGCCAG CTTTCATGGT GCTGGAGTGG AGCAGATGA CGTAGCAGAG1320  
 CTGCTGCAGG ACCTGCAAAG CCTGGCCAG TGTACCAGG GTGGTGACAG CCTCTGGAC1380  
 TAAAGTTCCT AGTGTGGGAG AAAGGAGCTA GTTTGCATA AAAACAGCTG GATGCGAGAG1440  
 CCCAGTGTCT TCATGCGAGG GAGCTCAATG TCGCGGAGCT AGCTACACCA ACATATGCAC1500  
 TTTTACATT TAGAACAACCT GTGATTAGAC CACAGAACAA TAAATATGTG CCATCAGACC1560  
 AAAAAAAGT AGAGAAAGGA GCTGAACCTC ACTCTCGATG CTATTTACAG AGGACATCTG1620  
 TAAAGTCTTC ATAAAGACCT TTGAATGATG CCTAGGATGG CAGAGCCCCC GGGTCTCTACT1680  
 CATCTCTCCA GCCTTTGTCC TTGTCTTGGC CTCCTGCTCT CCAGATCTGT AAACCTGGGT1740  
 CAAGAGCTGT ACAAGCAGAG TACAACCTACC CCTCCCGGG TGCCAGGGCG CCTGTTGGGT1800  
 TTGGTCTGTG TAGATGATT CCCAGAGTCT CATTATCCA GCTCCTCTTC AGACAGAAAG1860  
 TCCCCATGGT CAGACAGCTG GTCTGCATTG TTGGTACTGG TTGCATATC CTCATCTCTCA1920  
 GAGCTGGCTG CACAGGCGAT GTGGAAGAGC TGCATGAGTT CTCGAAAACG GTGGGAAACC1980  
 TCAGCAGGGG TCTTATTTCC CAGCTGCTGG GAGATGATGT TGAAGTGTGT TGGCTGTGCC2040  
 CCTTGTCTCT GGCACATGGT GAGGATCACA CGGTGAGCTT CCCTTGTCCA CAGGACAACC2100  
 TTTTCCCCAG TGGAGCTGAC CTTGCTGTGG TTGGCACACA CGGTAGCTTC TGGGGCTTT2160  
 GGCCTGCTGCT CCCCCTCTGG ACCCTTGGCC TGTGTTCCAC TGTCTTTAGC CAAACCCCT2220  
 CTAGGGGCTT TGGGAGAAGT CTCTGAGGTG TCAATTTCTG ATGGAGATTC ATGGACAGGG2280  
 CAGCTGCTGT CTCTTGTCTT CACCCTAGCT CTGCTTGAGG GAGGCCATCT CTTTGTAGT2340  
 TCTGTTTTCG CGGACACATG TCTTCTCCCT GCATCTCTGG TCTTTGAGGA AACGAGACT2400  
 AGGAAGGAAG CAGGGGGTTC CAGGCTACCA GGCAATTTCT CAGTTTCTGA TGCATCCCAG2460  
 ACCAGCATCA AAGCTCTGTA CTCACCTACT GCCTTTTGGC CTTCCCTCTC TTTCTGAAGT2520  
 TCTGGGGATG CCTTGGGGCA GGAGCGAACC TCAAGGCCAA CCTGGTTTCT CTTAAACAGT2580  
 TACAGTACAG CTCAGTTGTG GGGGGGAAAT TGAGAGTCT CTGGTGAATG AGGTGTTGGG2640  
 CCATCCAGGA GGAGCCGTTT TGTA

2664

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 538:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3888 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

00221-56E7960

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

GAATTCGCCG CCGGACTGAC GGAGCCCACT CGGGTGC GGTGGCGCG GGCACGGAGG 60  
 ACCGGGGCAG GCAGCGCAAG CGACCCCGAG CGSAGCCCGG GAGCCATGGC CCGTAGGCGAG 120  
 CTGGCGCTGG TCCGCTGGGT GCAGGAGAGC CGCCGCTCGC GGAAAGCTCAT CCGTGTTCAT 180  
 GTGTTCTCTG CGCTGCTGCT GGACAACATG CTGCTCACTG TCGTGGTCCC CATCATCCCCA 240  
 AGTTATCTGT ACAGCATTTA GCATGAGAAG AATGCTACAG AAATCCGAGC GGCCAGGCCA 300  
 GTGCACACTG CCTCCATCTC AGACAGCTTC CAGAGCATCT TCTCTATTA TGATAACTCG 360  
 ACTATGGTCA CCGGGAATGC TACCAGAGAC CTGACACTC ATCAGACCGC CACAGCAGCA 420  
 ATGGTGACCA ACGCGTCCGC TGTTCCTTCC GACTGTCCCA GTGAAGACAA AGACCTCCTG 480  
 AATGAAAACG TGCAGTGTGG TCTGTGTGTT GCCTCGAAAG CCACCGTCCA GCTCATCACC 540  
 AACCCCTTTC TAGGACTACT GACCAACAGA ATTGGCTATC CAATTCCCAT ATTTGCGGGA 600  
 TTCTGCATCA TGTTTGTCTC AACAATTATG TTTGCCCTCT CCAGCAGCTA TGCCTTCTCG 660  
 CTGATTGCCA GGTCGCTGCA GGGCATCGGC TCGTCTCTGT CCTGTGTGGC TGGGATGGGC 720  
 ATGCTTGCCA GTGTCTACAC AGATGATGAA GAGAGAGGCA ACGTCATGGG AATCGCCTTG 780  
 GGAGGCGTGG CCATGGGGGT CTTAGTGGGC CCCCCCTCG GAGTGTGCTC CTATGAGTTT 840  
 GTGGGGAAGA CCGCTCCGTT CCTGGTGTGT GCCGCCCTGG TACTCTTGGG TGGAGCTATT 900  
 CAGCTCTTTG TGCTCCAGCG GTCCCGGGTG CAGCCAGAGA CTCAGAAGGG GACACCCCTA 960  
 ACCAGCTGTC TGAAGGACCC GTACATCCTC ATTGTGTCAG GTCTCATCTC CTTTGCAAC1020  
 ATGGGCAATG CCATGCTGGA GCCAGCCCTG CCCATCTGGA TGTGTGAGAG CATGTGTTCC1080  
 CGAAAGATCG AGCTGGGCGT TGCCTTCTGT CCAGCTAGTA TCTCTTATCT CATTTGGAAC1140  
 AATATTTTGT GGATACTTGC ACACAAAATG GGGAGGTGGC TTTGTGCTCT TCGGGAATG1200  
 ATAATTTGTT GAGTCAGCAT TTTATGTATT CCAATTTCCAA AAAACATTTA TGGATCATAT1260  
 GTGCCGAATT TTGAGTTTGG TTTTGCAGAT GGAATGGTGG ATTCGCTCAAT GATGCCATAT1320  
 TGGGCTAACC TCGTAGACTT CGGGCAGCTG TCGGTCTATG GGAGTGTGTA CGCCATTGGC1380  
 GATGTGGCAT TTTGTATGGG GTATGCTATA GGTCTTCTGT CTGGTGGTGC TATTGCAAG1440  
 GCAATTTGAT TTTCCATGCT CATGACAAAT ATTGGGATAA TTGATATTTCT TTTGCCCTT1500  
 CTTGTGTTTT TTCTTCGAAG TCCACCTGCC AAAGAAGAAA AAATGGCTAT TCTCATGGAT1560  
 CACAACCTGCC CTATTAAACAA AAAAATGTAC ACTCAGATAA ATATCCAGTC ATATCCCATC1620  
 GGTGAAGATG AAGAATCTGA AAGTGACTGA GATGAGATCC TCAAAAATCT TCAAAAGT1680  
 TAATTTGTATA AAACAGTGTT TCCAGTGACA CAACCTATCC AGAACTGTCT TAGTCATAC1740  
 ATCCATCCCT GGTGAAGAGG TAAAACCAAA GGTATTATTAT TGTCTTCCAT GGTATTGTC1800  
 GATTGCCAAC AGGCTATTAA AGAAAAAGAA GCTTTTCTAG GGGTTTGTAT AAATAGTGT1860  
 GAACTTTTAT TTGATTTTAT TCATTTTATT AAATATCAT TCAATATATT TGATGAATA1920  
 GGTATTGTGT AAATCTATAA ATACTTGAAT CCAAACCAAA TATAATTTTT TAACCTACAT1980  
 TAACAACATC TTGGGCAAAA ATCATATTGG TAATGAGTGT TTAATAATTA AGCACACATT2040  
 ATCTCTGAGA CTCTTCCAAAC AAAGAGAAAC TAGAATGAAG TCTGAAAAAC AGAATCAAGT2100  
 AAGACAGCAT GTTATATAGT GACACTGAAT GTTATTTAAC TTGTAGTTAC TATCAATATA2160  
 TTTATGCGTT AAACAGCTAG TTCTCTCAAG TGTAGAGGAC AAGAACCTGT GTCAGTTATC2220  
 TTTTGATATC ATAAATCTTA GCTGGCAITTA GTTTTCTATG TAATCACTTA CTAATCAGCA2280  
 GTTGTAATTT ATATGTTAAC ATGTTATCTG TTGGGAGCA AACACTAAAG CCAATAAAG2340  
 AAAACAGCTA AATGTTCCGA AAGCAGAGAA AAGCAACCAA ACATATTGTT AGTCACTAA2400  
 AGCTTTCCCT TTAAGATGCA TACTTGTCTT ACTGGATGAA GAAATTTGAG GTACATGT2460  
 CCTTATACTG TCAAGGTTGT TTAACATGTA TAAGGTTAAT CGCCATCTAC TTCAGTTT2520  
 AGAAAAGGAA ACAAGAGAGT AAAACAGCT GCTCTGACTT TAATATCTGA TATATCTTT2580  
 GATCTGTTTG CAGGTCATCC AAGTGTTTTC TAGGAATATA TTTATTTTGA GTTGCTGAA2640  
 ACTACTATTT TTAGACTCC TGAAAGTTGT TCACATCAAT GTGAAGACAA ATTTTAAAG2700  
 AAAATGAAGA ATGAAATTAT GTCTTGAATC ATATATTAAG AAGTAAAAAT AATAGTGATC2760  
 AGGCAGAAAA GAAAAATGGA ACATCTAAAA ATGATATGTC TAACATATC ATCCAGTGTG2820  
 CAGTGTGTGT TATTTTTCTA AGCATGACAA CTGATGTGT CCTTTTCAGT GTAACAGCA2880  
 ATACTGTTAG TGAACATTGT CAATTTATGT CATTTTGTTA AGAGATATGA CTGGAGTGTG2940  
 CAGTGTGGAA TGTCCTAAT ACTACTTGTG AATCCTGCGC TTTATATATC ATAAACAAA3000  
 ATACTTGTAG TTGCTTAAGC TAAGATTGTG TTTGTGTAA CTTCGACATC AAGGAGCAA3060  
 GAACTTTAGA ACAGACTCCT CAATCTTTGT ACTTTCTTAT TCTCTAGGAA AGTAACACT3120  
 CGTTTCTAGA AGCTTTCTGT TGGGGCTTCC ATATTTCGAA GTCTGGTTTC TAAGTCAGT3180  
 GTGTTTGAAG CAACAGAACT TCCAACCTAC TTTTGTGGCA TTGGGCAACT TGGCCAGCT3240  
 TGCTACTTTG AAGATGGCT CTGGAGGAAA AGCCTTAAAA ATATACTTTA TTGCAATTTT ATTTTCTCT3300  
 TCTTACTTCT ACAGGGGTAG CCCCATAACC ATATACTTGA TTGCAATTTT ATTTTCTCT3360  
 GGGTTTCTGT TTCTCCCTGC CCAAGAGAGG CTGGCAAAAG TATGCTCTGT TTGTGCGCT3420  
 GTTGCAGCTT GTGTCTTTCT TTAACACCTT CAGAACTGTT TTGACAGCAA AGATAGCTG3480  
 CCGGATAAGA TAAATATATA TAAAAACCTT CAGAACTGTT AGATAGCTG3540

09673395.122700

TACTTGGGGA AAAAAATTCT AAGTCTTTT ATATGACTAA TATTCTTGGT TAGCAAGACT3600  
 GGAAAGAGGT GTTTTTTTAA AATGTACATA CCAGAACAAA GAACATACAG CTCTCTGAAC3660  
 ATTTATTTTT TGAACAGAGG TGCTTTTAT GTTTGGACCT GGTAAATACAG ATACAAAAAC3720  
 TTTAATGAGG TAGCAATGAA TATTCAACTG TTTGACTGCT AAGTGTATCT GTCCATATTT3780  
 TAGCAAGTTT ACTTAATAAA TCTTCTGAAC CATGTTTTGT GCCTGTTTGT ATTCCTTTAT3840  
 AAACCAATG TTGTGGAAT AAAATACATA AGGTATCATT TTGACCGT 3888

(2) INFORMATION ON SEQ ID NO. 539:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3304 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cdna library

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

AAACCCCTCTT GGCTGTCTGC TGTCCAGGGA GTCCGCACTC CCTTCATTAT AGCCTTGCTC 60  
 AGAGTGCAGC GGCAGGCGCT GGGATGGCCT CGGGAGAGGG ACCACAGAGC ACCAGCCTGC 120  
 ATGGAACTTC CTTCCTCACT CAGCTTCCCA CGTTGCCAGC TGGGACAGGG AGCATGGAGT 180  
 AATTTTGTCTG TGGAAAGACT TCACGTCTTG CCGAATGAAA GTCCCGCCTG TCTGTCAAGC 240  
 TGATGCGGTG CGAGCTGTCT GAGCACCCGG AATGGRATGA TCTATGCAC TCCCTCCGGA 300  
 TCAGTGTGGG GGGCCTTCCT GTGCTGGCGT CCAATGACCA GGGCCGGGAC CCCCCTGCTC 360  
 GCGCCGCTGC GAAGGTGATC CTGACGTTCT TTGTGGGTGC TGCCATCTCT TGGCTGCTCT 420  
 TCTCCACCCG CCGCGGCCCC GGCAGGCCCC CCACCCACAA TGCACACAA TGGAGGCTCG 480  
 GCCAGGCGCC CGCCAACCTG TACATGACA CCTACCCCTC GTCTCCCCCA CAAAGGACAC 540  
 CGGCTGGGAT TCGGTATCGA ATCGCAGTTA TCGCAGACCT GGACACAGAG CCAACCGCCC 600  
 AAGACGAAAA CACCTGGCGC AGCGACCTGA AAAAGGGCTA CCTGACCCCTG TCAGACAGTG 660  
 GGGACAAGGT CGGCTGGGAA TGGGACAAG ACCATGGGGT CTTGGAGTCC CACCTGGCGG 720  
 AGAAGGGGAG AGGCAATGGAG CTATCCGACC TGATTGTTTT CAATGGGAAA CTTTACTCCG 780  
 TGGATGACCG GAGCGGGGTC GTCTACCAGA TCGAAGCGAG CAAAGCCGTG CCTGGGTGA 840  
 TTCTGTCCGA CGCGCAGCGC ACCGTGGAGA AAGGCTTCAA GGGCCAGTGG CTGGCAGTGA 900  
 AGGACGAGCG TCTGTACCTG GCGCGCCTCG GCAGGAGTGG GAGCACCATT ACGGGTGATG 960  
 TGGTGAACGA GAACCCGGAG TGGGTGAAGG TGGTGGGCTA CAAGGCGAGC TGGAGCACAG 1020  
 AGAATCTGGT GTCCAATAC AACGCCCTGC GGGCTGCTGC CGGCATCCAG CGCCAGCAT1080  
 ACCCTACCCA TGAGTCTGCC TGCTGGAGTG ACACGCTGCA GCGCTGGTTC TTCTTCCGCT1140  
 GCGCGCCGAC CAGGAGCGC TACAGCGAGA AGGACGACGA GCGCAAGGGC GCCAATCTGC1200  
 TCTTGAGCGC TCCGCTGAC TTCCGCGACA TCGCTGTGAG CCACGTCGGG CGGGTGGCT1260  
 CCACTCAGCG CTTCCTGCTC TTCAAGTTCA TCCCCAACAC CGACGACAGC ATCATTTGG1320  
 CCTCAAAATC CAGGAGGAGC AGCGGACGAG TCGCCTCTTA CATCATCTCT TACCGCTGC1380  
 ACGGGCGGCT CTTGTTGCCG GAGACCAAGA TCGGAAGCGT GAAATACGAA GGCATCGAGT1440  
 TCATTTRAAT CAAAACGGAA ACACGTGAGCA AGGCCATCAG GACTCAGCTT TTATAAAAC1500  
 AAGAGGAGTG CACTTTTGTG TTGTTTTGTT CTTTGTGGAA CTGTGCGCTG GTTGGAGTGC1560  
 TGGACAGGGA GCCCAGTCCC GGGCCCCATA GTGGTGGCGG CACTGGAACC CCGGGCCCCA1620  
  
 CGGAGGCCCG GGTCTGAAT GCTTTCATG CTGCCATCTG GTGGTGATTT CGGTCACTTC1680  
 AGGCATTGAC TCAAGGCCCT CCTAACTGGC TGGGTGTTTT CTTCATCCCG ACCTCGTTTC1740  
 TTTTCTTTTC TATGTTCTTT TGTTCACTGA ATATCCCTAG AGCTCCTACC ATATGTCAGG1800  
 CCCTATGCCT CACCTCAGA ACGCAGTGAG CATGAGGTGG ACCTGTTTTC TGGGAACCC1860  
 AGGTCAACCC CTTTTCTTCC CAAACTTGGT GCCTTGGAAG AATCAGGTCC AGCCCTGAAG1920  
 ATCCTCGGGG AAGAAAATGT TTATGTTGCA GGGTATTGCA TGGTCACGAG TAGGGGGCAG1980  
 GCGCCTGGGG GACACACTCG CCCACAGCTG CACAGGCCAG GGGCACAGGC ACATCTGTT2040  
 GTTCTCAGCG TCTAGATAAA ACCATCTCCG CATCATGAG CCACTGACCG CTTCCTCTG2100  
 TCAAGAAAAA TCTGTGGCTG TGCAGTACTT TGAAGTTTTA ATTTATTAAC TGCTTTAAT2160  
 AAAGCAGTTT CCTTCTTAT AAAGTGAAT CACCAAATCT TATCACACAG AGGCAGTCC2220  
 TGTAGTTACC CAGCGCCGCT CAGCAGTGGG GGAGATTGTA AGGAAGCCGT GGGCGCTGG2280  
 GAAGCAAGTC TCACATGTGC GCGTCTTGCG CCAATGGATA CAAAGATAAA GAAATGTT2340  
 CCTTTTCTA GGAATGTGCA GAAATCTCA TGCCTTTCAA GACTTCTGTG AATGACTTGA2400  
 ATTTTITATT CCCTGCCTAG GGTCTGTGAA CGAGGCTGT CTCTTCCCTG GGGTTCTTT2460  
 CCATGGGCTT TATTCTCTCT CTTCAGTGGG GAGTTTGTCA GGCCTTCTCT GGTGAAACT2520  
 TCACGAGCGT TGGCTGGGCG TCGGCTTCG TGGAGTGTAC TCCAGGGTGA AGCCAGAGTG2580  
 GGATTGAGA CCGAGGTTAG GCACGACCCA GGCTGAGAAG GGACGTTTCC ATGCTCACAA2640  
 GTGCCCTCCC CACAGCAACT ACCTCACCCC GACCCCCACC CTCACTCTCA CCCACCCCG2700  
 GAGTGTCAG GGGTGCACAG GTGGGCGCGA GGGTGCCGCG TCTGGCTGTC CCGTGGCGG2760  
 TCCCTCACAA ACCTCTCCCC CTTTGAACCT CAAGCACAGC TGGGAGGAGG CAGCGAGGA2820  
 GGGAGCCCTC CACTCATGGT GTCTCTTTCC CCGCTATGTG CATAGGTGAT GAGGAGAGCG2880  
 AAGGAAGTGA AGCTGAATG TGACGCAATT CTGAAGAGCT CAGCTGTACG CGGGCAATAG2940  
 CTGGAAGCCC CAAGTCTGTT CTGACTTTGC CTGGCTGTCT CCTTGACCCG CTCTCTAGAT3000  
 CATTTGCTCT ATGTCACAGC CTGGGTCAAT TAAATAGAG ATGCAATCAG GAAGGTGGG3060  
 GGAATCTGGG CTGTGGCTGA ATTGAGACCT TGCTGATGTA TTCAATGTCAG CACTGAGTG3120  
 ACAGCCCAAG TGGCCGGAAG CAGCCTCTTC GCTATAGGCG TGATTTTGCA TTACTTTAAA3180  
 GCTCACCTTT TTTCTTCCCC TCTCTGTTCC GTGCTGTCAG CATAATGATT GTGTTCTCT3240  
 CCTATGGGAT CCATCTGTTT TGTAAACAAT AAAGCGTCTG AGGGAGTGTA AAAACAGAT3300  
 GGAT

## (2) INFORMATION ON SEQ ID NO. 540:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 863 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

CAGGATTGAA ACAAGATGGC GGGTTCGTGG TGAGAAGCCG TCAAGGAGTA GAAATTGGTA 60  
 TGCTTAGAAG CAGATTCTAA AAGCAGTTTC TCCTCAGAAC ATCTTTTTTC ATACCACTTG120  
 ATAAGCATCT TGAACACCA TGGCTGTAGC TGCAGTAAAA TGGGTGATGT CAAAGAGAAC180  
 TATCTTGAAA CATTATTTTC CAGTCCAAAA TGGAGCTTTA TATTGTGTTT GTCATAAATC240  
 TACGTATTCT CCTCTACCAG ATGACTATAA TTGCAACGTA GAGCTTGCTC TGACTTCTGA300  
 TGGCAGGACA ATAGTATGCT ACCACCTTTC TGTGGACATT CCATATGAAC ACACAAAACC360  
 TATCCCTCGG CCAGATCCTG TGCATAATAA TGAAGAAACA CATGATCAAG TGCTGAAAAC420  
 CAGATTGGAA GAAAAAGTTG AACACCTTGA GGAAGGACCT ATGATAGAAC AACTTAGCAA480  
 AATGTTCTTT ACTACTAAGC ACCGTTGGTA TCCTCATGGA CGGTATCACA GATGTCGTAA540  
 GAATCTGAAT CCTCCAAAAG ACAGATGATG CGGAGGTTCC TGGGGGAATC AAAGAGAAAT600  
 GTGCCCTATT TGCCATTTGA GAAATGCGAC TCTGGTGTAT TCAGTAATAT ATAGTAAAGT660  
 AATAATGATA AAATATCTTT TCATATATTA GAATGTGTAC TTTTATATAA AGTAATTCGT720  
 GATTTGACAT TCCTCATTTAG AGAGACCTAT TCCTTTTTTC GTTTTCTATT TTAGTGTTC780  
 ATTTATGTGC GGTCTCCAAT TTAGGACTTT TCCATAGTGC CAAAGCCATA CATATTCACT840  
 AGAACATCAA TAAAAAAA AAA 863

0067305.1.22701

## (2) INFORMATION ON SEQ ID NO. 541:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1962 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

ACCGACGGCC GCCCCTTTTC GTCTTTTTTT TTTTACATT TCAATATAT TTTATTACTT 60  
 TCCATCTTAG AAAGAATATG AAACCTGCGT GCAATGCTAA TGGTTTCTGA CATGTACATA 120  
 GCATATAACA CAGCAGTACA ATGCGGCATA TACTGGGGGG CAGTGTGTGG AGGGGGCGTT 180  
 CTTAAGGGTA TATGTACAGA GGAAGGGGCG CATGTGTCATC TTAGCTTTTCG AAAGAGGACT 240  
 GCACCTGTTTA ACATTGAAGA ATTACATGGG GAATCACAAA TATATTGCTT TAGTACTGCA 300  
 TGTGTCTGTG TGGTGAAGGA AAGAAACATG CTTTGAAGGT TTTCCCTTGT CAACAGAAATG 360  
 TGTGTCTGTG GCTGTGTATT GCGCATGTAT TCATATATTT TTAAGTTTTT TCCTAAGGTT 420  
 TTTGCTGACA GTGTTGGGAA CCTCACATGC TTTGAAAGCA TTAATATTGT AACCTGTGAA 480  
 CCTTTCAGAA ATCCTCAGGT TGGGAAAGAC CCCACACCTT CTTTAAGGAT CATTTGTCTC 540  
 GCCATCACAG GATCTTGGAA ATGTTTCTTA GGGTGTGTA AAATTAACCA GGGGGGAATG 600  
 AAGCACATTT TTCTGGCAAC CAAACTTGAG TTCTCAGAG AACAGATGCA GAGAGACCTG 660  
 CTCCTGCTTG CCCGGCTACA GGGGCCACTG TGGAGTCACA CTGAGGCTGT GACCGGCCAT 720  
 AAGCCGAGGA GAGCCCGTGG CAGCTGTGCC GAGGCGCCAG GCACCTTAAG CGGAAGCTTC 780  
 CCAAGCTAGG AATGGAGCAA CACTGCAATG AAATGTGTCC ACCAAGCTCA TTGTTCTCTC 840  
 CGGGCGCTTA TAAAGCTCAG ATGTATAGTG ACGTATGGAC AAATACAAAA AAAAAAAAAA 900  
 AAAAAAAAAA AAAAAAGCC TTTCTTTCTC ACAGGCATAA GACACAAATT ATATATTGTT 960  
 ATGAAGCACT TTTTACCAC GGTCTGTTT TACATTTTAT AGCTGCGTGC GAAAGGCTTC1020  
 CAGATGGGAG ACCCATCTCT CTTGTGCTCC AGACTTCATC ACAGGCTGCT TTTTATCAAA1080  
 AAGGGGAAAA CTCATGCCTT TCCTTTTTTA AAAATGCTTT TTTGTATTGT TCCATACGTC1140  
 ACTATACACT TGAGCTTTAT AAGCGCCCGG GAGGAACAAAT GAGCTTGGTG GACACATTTT1200  
 ATTGCAGTGT TGCTCCATTG CTAGCTTGGG AAGCTTCGCG TTAGAGGTTCC TGGCGCTCG1260  
 GCACAGCTGC CACGGGCTCT CCTGGGCTTA TGGCCGTCAT CAGCCTCAGT GTGACTCCAC1320  
 AGTGGCCCTC GTAGCCGGCG AAGCAGGAGC AGGCTCTCTC GCATCTGTTC TCTGAGGAAC1380  
 TCAAGTTTGG TTGCCAGAAA AATGTGCTTC ATTCCCCCTC GGTAAATTTT TACACACCTT1440  
 AGGAACATTT TCTAGATGCT TGTGTGGGCG AGACAAATGA TCCTTAAAGA AGGTGTGGGG1500  
 TCTTTCCCAA CCTGAGGATT TCTGAAAGGT TCACAGGTTT AATATTTAAT GCTTCAGAA1560  
 CATGTGAGGT TCCCAACACT GTGAGCAAAA ACCTTAGGAG AAAACTTAAA AATATATGAA1620  
 TACATGCGCA ATACACAGCT ACAGACACAC ATTTGTTTGA CAAGGGAAAA CCTTCAAAGC1680  
 ATGTTTCTTT CCTTCAACC ACAGAAACAT GCAGTACTAA AGCAATATAT TTGTATTTC1740  
 CCATGTAATT CTTCAATGTT AAACAGTGCA GTCTCTTTTC GAAAGCTAAG ATGACCATGC1800  
 GCCCTTTTCT CTGTACATAT ACCCTTAAGA ACGCCCCCTC CACACACTGC CCCCAGTAG1860  
 TACCGAGGCA TTGGTACCGG CTGGTGTAA AATGGCTATG GACATGGTTC AGGAACCAT1920  
 TTAGGCATTG GCATTGAGGG TTCCATAATC CGTTTCTAAG GA 1962

0673395.12708

## (2) INFORMATION ON SEQ ID NO. 542:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1772 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

TGGGGCGTGT AGTCCGGCCG GAACCTGTTT GCGACCCCGA GTCCCATGAC ACCGCTTCTC 60  
 CTCACACCCC AGTCCGCAGT GCCCTCCCCC AGCCTCGGCC GGGGCTCCCC GGAGCCGGGC 120  
 GTGGCGTTCC AGCTAGTGAG CCGTTTCTCC CCTGGGCTCG GAGGCGGAAG CTTGAGGGGC 180  
 GCGGGGAGGA GCTTCGCGTG CGGGGTGAAC GCCCGCTCTA CGTSGCTCGT CTCTTCGGCA 240  
 CCGCTCGCGC CGAGCCCCGT GTCCCCACGG CGGGCAGCAG CGCCGGCGGC GCGGCGTGAA 300  
 CGCGAGGGGG CGCGAGGGAG CCGCGGGCGG CGGCAGCAGC TACAGCGAAA TGGCGGAGAC 360  
 CGTGGCTGAC ACCCGGGCGC TGATCACCAA GCGCAGAAC CTGAATGACG CCTACGGACC 420  
 CCCCAGCAAC TTCTTCGAGA TCGATGTGAG CAACCCGCAA ACGGTGGGGG TCGGCGGGGG 480  
 CGGCTTCACC ACTTACGAAA TCAGGGTCAA GACAAATCTT CCTATTTTCA AGCTGAAAGA 540  
 ATCTACTGTT AGAAGAAGAT ACAGTGACTT TGAATGGCTG CGAAGTGAAT TAGAAAGAGA 600  
 GAGCAAGGTC GTAGTTCCCC CGCTCCCTGG GAAAGCGTTT TTGCGTCAGT TCCTTTTAGA 660  
 GGAGATGATG GAATATTTGA TGACAATTTT ATTGAGGAAA GAAAACAAGG GCTGGAGCAG 720  
 TTTATAAACA AGGTCGCTGG TCATCCTCTG GCACAGAACG AACCTTGTCT TCACATGTTT 780  
 TTACAGATAG AAATAATAGA TAAAGCTAT ACTCCATCTA AATAAGACA TGCCTGAAT 840  
 TTGGCAAGAA GGGGCAAAAA CGTGACTATT AATGATTGAT AAGCACCAGT GAAGAAGTC 900  
 TAACTTTTAG CATGCTGCAC AGAACTGGT ATAACATGCC TTCAGTATAC TAACACTCAT 960  
 ATGCTCAGTT TTGTTTGTGT TTGGCAGTTG ACAAGAAGTT AATTTGCTTT AGTAAAAATC1020  
 CCTCATTCGA GCCCTTCTAT ATAAATAGCT CTTTCTTGCT TGTTTAATGT AGTGCACACT1080  
 ATAGCCTCAC AAACCTGTGA TTCCAGTGTA ATCTGCAGTG TCGTGAACAT AAGTTCTGGC1140  
 TTGGCTCTAT TTGCAGGTTT TTGCGCTCTT GTTTGCTTCT TGCATCTGAT TAACTAGAA1200  
 ATTTCTCTAT CCCCCTTTAT ATTTGTGATG TCACCTTGACC CCATTTATGT GTAGGAGCAC1260  
 TACACCATTG GTTCCAATAA CTGCACACAT AAGATACATA CTTGTGTGCA GAAAGTATCT1320  
 TCCTCCAGGC TTGTAATACC CTTACATGGS AAGATTAATG AGGGAAATCT TTATATCTG1380  
 TATAAAAAAC AAGACAAATT TATATACTAA AATCATTTGT CTAAAAATTT AAGTTGTTTT1440  
 CAAATAAAAA TTAATATGCA TTTCTGATAT GCACGTATTG TGTTCGCTCC AGCTTTTTTT1500  
 GCTCTCTATG AGTGCTACT TAAGTCACTT GTTGAGAGGG ATTATTACT AATTATATAC1560  
 TTCTCATTCC TGTAACCTCA TTCCCTTTAA ACAGTGGTGA TATCAAATAT ACTTCCATCC1620  
 ATTGAATGAG GTATTTTTTA CAACAACAAA AGTGATATAC TAAAAAATGT ATTGCTAAG1680  
 GCTTATTGAA TCATTTTGAA GCACCTTTGT TATTTGAAAA CTGCTTTATA ATCTCATTTA1740  
 TTAAGAGGAC TTTCAAAGAT AAAACCAAAA AA 1772

06673395.122706



## (2) INFORMATION ON SEQ ID NO. 543:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1009 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

CTCGTGGGGT GATGTTGAGC AGAAGATACA ATTCAAAAGA GAAACAGCCA GTTTGAAACT 60  
 GTTACCCAC CAGCCCCGAA TTGTGGAGAT GAAGAAAGGA AGCAATGGCT ATGGTTTCTA 120  
 TCTGAGGSCA GGCTCAGAAC AGAAAGGTCA AATCATCAAG GACATAGATT CTGGAAGTCC 180  
 AGCAGAGGAG GCTGGCTTGA AGAACAATGA TCTGGTAGTT GCTGTCAACG GCGAGTCTGT 240  
 GGAACCCCTG GATCATGACA GTGTGGTAGA AATGATTAGA AAGGGTGGAG ATCAGACTTC 300  
 ACTGTTGGTG GTAGACAAAG AGACGGACAA CATGTACAGA CTGGCTCATT TTTCTCCATT 360  
 TCTCTACTAT CAAGAGTCAAG AACTGCCCAA TGGCTCTGTC AAGGAGGCTC CAGCTCCTAC 420  
 TCCCCTTCT CTGGAAGTCT CAAGTCCACC AGATACTACA GAGGAAGTAG ATCATAAGCC 480  
 TAAACTCTGC AGGCTGGCTA AAGGTGAAAA TGGCTATGGC TTTCACTTAA ATGCGATTGG 540  
 GGGTCTGCCA GGCTCATTCA TCAAAGAGGT ACAGAAGGGC GGTCTCTGCTG ACTTGGCTGG 600  
 GCTAGAGGAT GAGGATGTCA TCATTGAAGT GAATGGGGTG AATGTGCTAG ATGAACCTTA 660  
 TGAGAAGGTG GTGGATAGAA TCCAGAGCAG TGGGAAGAAT GTCACACTTC TAGTCTGTGG 720  
 AAGAAGGCC TATGATTATT TCCAAGCTAA GAAATCCCT ATTGTTCCCT CCCTGGCTGA 780  
 TGCCAGTTGA CAGCCCTGCA GGTCTTAAG AAGGAATAGT GGTGGAGTCA AACCATGACT 840  
 CGCACATGGC AAAAGAACGG GCGGCTATTG CAGACGGCTA ATTTATGCTT AACTTAGGAA 900  
 GAGATAAGGT TCCTTGAGCA CCAAAGATGA TTCATAACTC TGTATAGGTG ACAGCTGCTT 960  
 ATAAAAGCAT CTTAGCAGAT AAGCCTATTA AAATTGTGCT TTTGTAACA 1009

0967395.12700

## (2) INFORMATION ON SEQ ID NO. 544:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2834 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

00672395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

CACTTTGCGG GCGGCACCTTT TTCCAGGTTG TTAATCCAGC TAATGGAGAA GGATAGATGC 60  
 ACGCTACTTTG GTTTAGAAAA AAAAAACAAA ATGAGCAAAAC GAGACGCCCC TTCCGTTTTTA 120  
 TGATAACTAA GCTGCAGGAA AATAAATCGG CTGGCCCTAC TGCAATCTAC TGCATCGAG 180  
 AAACATCACA GAAATTTCTT TGATTTATCT TAATAGTGAC AAGTGAGCCT GCTTCTGTCA 240  
 ATTACTGAAG CTATAAGGAG ATTTTAAAA AATTAACCTT CAACACAATG AGGTGTTCGC 300  
 ACATCTGCAA ACTTCCTGGG AGAGTAATGG GGATTCGAGT GCTTCGATTA TCTTTGGTGG 360  
 TCATCCTCGT ATTATTACTG GTAGCTGGTG CTTTGACTCG CTTCCTTCCC AGTGTAAAG 420  
 AAGACAAGAT GCTCATGTTG CTGAGGGAAA TAAATTCCTA GGGCAAGTCC ACCATGGACT 480  
 CCTTTACTCT CATATGCGAG ACGTACAACA GAACAGATCT CTTATTGAAA CTTTAAATC 540  
 ATTATCAGCG TGTACCAAAAT CTGCACAAAG TGATTGTGGT ATGGAAACAAT ATTGGAGAGA 600  
 AGGCACCAGA TGAGTTATGG AATTCCTTAG GGGCCACCCC TATCCTGTGT ATCTTCAAC 660  
 AACAGACAGC AAACAGGATG AGAAATCGAC TCCAGGTCTT TCCTGAACGT GAAACCAATG 720  
 CAGTGTGTAT GGTAGATGAT GACACACTCA TCAGCACCCC AGACCTTGT TTTGCTTTCT 780  
 CAGTTTGGCA GCAATTTCTT GATCAAAATG TAGGATTTGT TCCTAGAAAG CACGCTCTCTA 840  
 CTTCATCAGG TCTACACAGT TATGGAAAGT TTGAATAGCA AGCACCAGGG TCTGGAATG 900  
 GTGACCAGTG CTCTATGGTG CTGATTGGAG CCTCATCTCT CAATAGCAAA TATCTTGAAT 960  
 TATTTGAGAG GCAACCTGCA GCTGTCCATG CTTTGATAGA TGATACTCAA AACTGTGATG1020  
 ATATTGCCAT GAATTTTATC ATTGCCAAGC ATATTGGCAA GACTTCAGGG ATATTGTGA1080  
 AGCCTGTAAA CATGGACAAT TTGAAAAAAG AAACCAACAG TGGCTATTCT GGAATGTGGC1140  
 ATCCAGGTGA GCACGCTCTG CAGAGGTCTT ATTGTATAAA TAAGCTTGT TATATCTATG1200  
 ATAGCATGCC CTTAAGATAC TCCAACATTA TGATTTCCTA GTTTGGTTTT CCATATGCCA1260  
 ACTACAAAAG AAAAAATATA AAGTAAACAA AAAAAACAA AACCTGAAAA CTGCTTGGCA1320  
 TTTGAGTAGC TTCTCCATGC TATCTATTTT TTAAGCAAC ATCATGAAT TATCTACTC1380  
 CAGAAGTCTC TACAATAGAA AAAAAAGTGC AGTGCTTCTA GGATATAAAA TTCACATTAC1440  
 TTTTGAAGAG CAAGAAGTTG GTCTTATCCA TGTAGGTCTT CTTATGAAGA GTTTTCATCC1500  
 AGGGATATAA CTCCTTGGTC AGTGATTTTA TTGTTTACAT CCTGAGACGT TTCTACAGTT1560  
 TCTTTGACTC CTGGCATTGT CCTTAAGGAC CTATAGCAAG CTGTTTCTAG GATCAGAAAC1620  
 TCAAGAGAGG CATTTCCTCT CTTTTTCACT AAAGGTCAAG TGTTTTAATT TGAACCTGA1680  
 AATGCCTCTT TAGCAAAAGC CTGTGGTATG GGGTAAAGCC ATGTAAGAG AGAATAGTCT1740  
 CAGTCACATA TGAAGAGGAA AATTGTCAGC TGCCAGTGCT TTCCCTGTGG CCTGCCAAC1800  
 CAGCTCTTTC AGGACGAACT CAGTCCAGCA TGGTTTTGAT GTAACCATCC ATGCTTTTAT1860  
 TTTTGTAAAG CTTTGTGGA CTGGGACAGT TAATTTTAGT AGCTGAAGTA CGTCTATGTG1920  
 TTTGCTTGAT ATTTGTGAAC ATTTACTGCA TGGATCACAA AACAATATAC CCTGTATTCT1980  
 TTACACGCCA CTTATATGCA GCAAGGAGTA AATGTGTTAC TAGATTCCGG TAGTGCATT2040  
 TGTCACTGAA TCTGACCTTG AGAATGTACA TTAATCTTA TATTTTACAT AATGTATGTG2100  
 TTGTTTAAAG AATGTATAAA AAACCTGAAA AAAATGAGTA AGRAACTGGCA GAAGTAAAAA2160  
 CCCCTTTGAT CAAGAAGTCT TTATTGTTAG AGCACTGGTT ATCTTCTGGA TACTAAAAAG2220  
 TTGTATTACA AAGCCAAACA CTTGCATTCA CAACTTTAAA AAAAGATCCA AGGAACATT2280  
 CATATATGAT AAATTTCAAC TACATACAAG GAGGAGAAAA TAAGAACCCA GTCATAACAG2340  
 AGGAATTCTA TAGGAGTCTG CATCAATCA TTCTTAAGTG TGCTACTCT CTGTTATGTG2400  
  
 AATTAGCGTC TGTGTTTCAC CCATTGCTGT TGTTTAGTCC TTGTTTACCA CTAAGGCAAG2460  
 GAATTCCTAA CTAGGCCCTCT GTTTACCAAC TTCTCTTTCT CCTCCTTTTC CTCTTATCC2520  
 TCCTCTCTCT CTCTCTCTCT ATATAATGCT AGTATATCTT CAAAATTGCA AAGCTGTGAG2580  
 AATATTAAAA TAATCATGGC TAATGTTCCA ATATGAGGT CTTTGTGGT TTAGTTCGCG2640  
 ATATGATGGT TTTTTTTTTA CATTAAGAGC TATATGTGTC TTAATGCAAT CAGATTGTGA2700  
 AAAACAAAAA CAAAGAAACT AAGAATCTTA CTAAAAATCG ATAATGTGAC TATCTGTTT2760  
 TGTCCAATAT TGGTAGTACT TTTTGGCTCT TTATGATTCC TCTAGCAGAT AAATAAAGA2820  
 AACTTTTGGC ATCC

2834

0967395-12700

## (2) INFORMATION ON SEQ ID NO. 545:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2319 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

AACGTCATTG GTAACAGCAA GTCCAGACACA CCAGCCCCCA GTTCCGAAGT GGTTTTGAT 60  
 TCAAAGAGAC AAGTTGAGAG AGAGGAAACC AACCATGAGA TCCAGGAGGG GAAAGAAGAG 120  
 CCTCAGAGGG ACAGGCTGCC GCAGGAGCCA GGCCGGGAGC AGGTNGTGGG AGACAGACCT 180  
 GTAGGTGGAA GAGGCTTCGG GGGAGCCGGA GAATGGGGCC AGACCCCAAG GGTGCAGGCT 240  
 CCCTCTCAG TGAGMCCAGG AAAATCCAGA GATGGAGGGC CCTGAGCGAG ACCAGCTTGT 300  
 CATCCCCGAC GGACAGGAGG AGGAGCAGGA ACCTGCCCGG GAAGGGAGAA ACCAGCAGAA 360  
 ACTGAGAGGA GAAGATGACT ACAACATGGA TGAATATGAA GCAGAACTCTG AGACAGACAA 420  
 GCAAGCAGCC CTGGCAGGGA ATGACAGAAA CATAGATGTT TTTAATGTTG AAGATCAGAA 480  
 AAGAGACACC ATAAATTTAC TTGATCAGCG TGAAAAGCGG AATCATACAC TCTGAATTGA 540  
 ACTGGAAATCA CATATTTTAC AACAGGGCCG AAGAGATGAC TATAAAATGT TCATGAGGGA 600  
 CTGAATCTAG AAAACTCTGA AATGTACTAA ATAAATGTGA CATCTGAANG ATGATTATTG 660  
 TGNAAATTTT AGTATGCACT TTGTGTAGGA AAAAATGGNA ATNGGTCCTT TAAACAGCTT 720  
 TTGGGGGGNT ACTTTNGGAA GTGTCTNAAT AANGGTGTCA CNAATTTTGT GNTAGTANGG 780  
 TATTTCTGTA GNAAGNNNTC AACACCAAAA CTNGGAACAT AGTTCTCTCT CAAGTGTGGT 840  
 CGACANCGGG NNGGCTTCCTG ATTCTGGAAT ATAACCTTGT GTAAATTAAC AGCCACCTAT 900  
 AGAAGAGTCC ATCTGCTGTG AAGGAGAGAG AGAGAATCTT GGGTTCGGTC GTCTCTCCA 960  
 CGTGCTGTAC CAAGTGCTGG TGCCAGCCTG TTACCTGTTC TCACTGAAA TAGCTGCTAA1020  
 TGCTCTTTGT TAGTCACTTC TGATTCTGAC AATCAATCAA TCAATGNGNC GTANGCACT1080  
 GACTGTCTAAC ACAAGGCTCA CTAGNCAAGG TAGNCAACNA GCTTTAAGTC TAAATACAA1140  
 GCTGTTCTGT TGAGAAATTT TTTAAAGGCG TACTTGTATA ATAACCCCTG TCATTTTAA1200  
 TGTACAAAAA GCTATTAAGT GGCTTAGAAT TTGAACATTT GTGGNTCTTT ATTTACTTTG1260  
 TCTNCGTGTG TGGGCAAGCG AACATCTTCC CTAATATAT ATTACCAAGA AANGCAAGA1320  
 AGCAGATTAG GNTTTTGTAC NNAACACANA ACAGGCCNNA AAAGGGGGCN TGNACCTGGA1380  
 GAGCAGAGCTG GTGNAGAGGC AAGGCATGNA GAGGGCRAGT TTGTTGTGGA CAGATCTGG1440  
 CCTACTTTAT TACTGGAGTA AAANGAAAAA AAGTTNCAT TGATGTCGNA AGGATATATA1500

CAGTGTNAG AAATNNNAGG NACTNGTTTN AGAAAAACAG GAATACNNAA TGGNTTGN1560  
 TTTATCATAN GTGNTACACA TTTAGCTTGT GGNATAATNG ACTCACAAAA CTGAN1620  
 AAATCAAGTT AATGTGAATT TTGAAATTA CTAATTAATC CTAATTCACA ATAACAATGG1680  
 CATTAAGGTT TGACTTGTAG TTGTTCTTAG TATTATTAT TACTTAATAGG CTCTTACCAC1740  
 TTGCAAAATA ACTGNNCCAC ATCATTAATG ACTGACTTCC CAGTAATANG CTCTCTAAGG1800  
 GGTAAGTNAG GAGGATCCAC AGGATTTGAG ATGCTAGGAT CCAGAGATCT GTTTGATNCC1860  
 AACCCCTTTA TTTTNCNAGAG GGGAAAATGG GGCCTNAGNA AGTTACANGA GCATCNTNAG1920  
 CNTGGTGCAG TGGNCCACCC NTGGCCNTCN ACACNAGACT CCNGAGATG TCGGGANCTA1980  
 CAGGCACACA GTCACTGAGG CAGGCCCNTG TTTCGAATTC AGGTTGGCNA CTNCCACN2040  
 TTAACAGTNN CTTCACTATGT GATGTCCTTA GTCACTAAG GTTAAANCTT TNCCCACCA2100  
 GAAAGGCCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC TCTTCTAANG TCTCTTCCA2160  
 GGCTCACTTT GAGTCTCTCT TNGGGGTTGA TNNNAGGAAT TTTCTCTTGC TTTCTCAAT2220  
 AACCTCTCAT TCATCTCATG TTTAATTTGT ACGCATAGAA TTGCTGAGAA ATAAATGTT2280  
 CTGTTCAACT TANNNNNAAA AAAAAANAA AAAAAAAA 2319

09673395 "122700

## (2) INFORMATION ON SEQ ID NO. 546:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2456 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

TGCAACTGTG CACCCAGCTT GCCAGATTTT TCCCCATTAC ACCCCCAAGTG TGGCATATCC 60  
 TTGGTCCCCA GAGGCACACC CTTGATCTG TGGACCTCCA GGCCTGGACA AGAGGCTGCT 120  
 ACCAGAAACC CCAGGCCCTT GTTACTCAA TTACAGGCCA GTGTGGTGTG GCCTGACTCC 180  
 TCGCCAGGCC CTGGAACAC ATCCACCTGG GGAGGGCCCT TCTGAATGGA GTTCTGGACAC 240  
 CGCAGAGGGC AGGCCATGCC CTTATCCGCA CTGCCAGGTG CTGTCCGCCCC AGCCTGGCTC 300  
 AGAGAGAGAA CTCGAGGAGC TGTGTGAACA GSCGTGTGGA GATGTTTCAGG CCTAGCTCCA 360  
 ACCAAGAGTG TGCTCCAGAT GTGTTGGGGC CCTAAGTTGG CACAGAGTCC TGCTCCTGGG 420  
 AAAGGAAGAG ACCACAGCAA ACACCATCTT TTTTGCCGTA CTTCCTAGAA GCAGTGGGAA 480  
 AGGAGCTGGT ATGTTGGGAG GGTGAGAGGG TGCCGTTTTC CTGCTCCAGC TCCAGACCTT 540  
 GTCTCGAGAA AACATCTGCA GTGCAGCAAA TCCATGTCCA GCCAGGCAAC CAGCTGCTGC 600  
 CTGTGGCGTG TGTGGGCTGG ATCCCTTGAA GGCTGAGTTT TTGAGGGCAG AAAGCTAGCT 660  
 ATGGGTAGCC AGGTGTTACA AAGGTGCTGC TCCTTCTCCA ACCCCTACTT GGTTCCTCTC 720  
 ACCCCAAGCC TCACTGTTCA ACCAGCCAGT GGGTTCAGCA GAACGCATGA CACCTTATCA 780  
 CCTCCCTCCT TGGGTGAGCT CTGAACACCA GCTTTGGCCC CTCACAGTA AGGCTGCTAC 840  
 ATTCAGGGGC AACCTGGGC TCTATCATTT TCCTTTTTTG CTCAAAGGAC CAGTAGCATA 900  
 GGTGAGCCCT GACCACTAAA AGGAGGGGTC CCTGAAGCTT TCCCACTATA GTGTGGAGTT 960  
 CTGTCCCTGA GGTGGGTACA GCAGCCTTGG TTCTCTGGG GGTTGAGAA ATGAATAGTG 1020  
 GGGAGGGAAA AACTCCTCCT TGAAGATTTC CTGTCTCAGA GTCCAGAGA GGTGAAGAGG 1080  
 AGGAATTTCT GCTGCACTTC ATCTGGGCAG AGGAAGGATG GAATGAAGTG AGAAGGCA 1140  
 GAATTAACAG TGAGCGGGGA CAACAAGAG TTTCTCTCTG TGCTTTAGAG 1200  
 CAAGGATGGA AATGCGGAC AACAAAGGAA AAGCAAGGTG TGACCTTGG GTTGGACAG 1260  
 CCCAGAGGCC CAGCTGCCCA GTATAAGCCA TACAGGCCAG GAGCCACAG GAGAGTGGAT 1320  
 TAGACACAA GTCTGGCCTC ACTGAGTGGA CAAGAGCTGA TGGGCCATCAT GAGGGTGACA 1380  
 TTACCCCCAG GGCAGCCTGA CCACTCTTGG CCCCTCAGGC ATTTATCCCAT TTGGAATGTG 1440  
 AATGTGTGTG CAAAGTGGGC AGAGGACCCC ACCTGGGAAC CTITTTCCCT CAGTTAGTGG 1500  
 GGAGACTAGC ACCTAGGTAC CCACATGGGT ATTTATATCT GAACACAGCA GACGCTTGA 1560  
 TCAGGCACTA TGTTAAGAAA TATATTTATT TGCTAATATA TTTATCCACA AATGTGGTCT 1620  
 TGCTCTGTGT TTTTGTCTGT TCGTGAAGT CACTCAGGGT AACACAGTCA TCTCTTCTA 1680  
 CATCAAGAGA AGTAATTTAT TTATGTTATC AGAGGCTAGG CTCCGATTCA TGAAGGATA 1740  
 GGGTGAAGTA GAGGGCTTGG CAATAAGAAC TGGTTGTAA GCGCCATAAA GTGTGGCTTA 1800  
 GTGAGATCAG GGAAGGATGA AGCATGACTG GATTCTTACT GTCCCTTCACT CATTATTATT 1860  
 ATACTGTTC ATTACACATT TATCATACTT CAGTGAAGTCA GACCTTGGGC AAATACTCTG 1920  
 TGCCCTCGCT TTTCAAGTCA TAAATGGGC CTACTTAATA GTTGTGACG GACTTACATG 1980  
 AGATAATAGA GTGTAGAAAA TATGTTCCAA AGTGGAAAGT TTTATTCAG GATAGAAAAC 2040  
 ATCCAAACCT GTACAGAGAG CCATCTGAAC ACAGCATGGG ACCGCCAACA AGAAGAAAGC 2100  
 CGCGCCGGAA GCAGCTCAAT CAGGAGGCTG GGCTGGAATG ACAGCGCAGC GGGGCTGAA 2160  
 ACTATTTATA TCCCAAAGCT CCTCTCAGAT AACACAAAT GACTCGCTTC TGCCCTGACT 2220  
 CGGGCTATTG CGAGGACAGA GAGCTGGTGC TCCATTTGCG TGAAGTCTCC AGGCGCAGAA 2280  
 GGGGCCCTTG TCGCTTCCCT ACAAGGCACA AGTTCCTCTT CTGCTTCCCC GAGAAGGTT 2340  
 TGGTAGGGGT GGTGGTTTAT TGCCATAGA ACAAGGCATT TCGCTTCCCTA GACGGTGA 2400  
 TGAAAGGGAA AAAAAGGACA CCTAATCTCC TACAATGTGT CTTTAGTAAA GGAACC 2456

09673395.12700

## (2) INFORMATION ON SEQ ID NO. 547:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2218 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

GAGGAAAAAG AACATGAAC AGCAACGATC TTGACTGTGC AACTCAGACA TTCCTGCAGA 60  
 AAAGACATAT GTTGCTTTAC AAGAAGGCCA AAGAAGCTATG GGGCCTTCCC AGCATTTGAC 120  
 TGTTCATTGC ATAGAATGAA TTAATATACC AGTTACTTGA ATGGGTATAA CGCATGATG 180  
 TGTTCATCAT CTAAGGAGGC TAGATCCTTC GCTGACTTCA CCATTCCCTCA AACCTGTAAG 240  
 TTTTCTCACTT CTTCCAAATT GGCTTTGGCT CTTTCTTCAA CCTTCCCATT CAAGAGCAAT 300  
 CTTTGCTAAG GAGTAAGTGA ATGTGAAGAG TACCAACTAC AACAAATCTA CAGATAATTA 420  
 GTGGATTGTG TTGTTTGTGT AGAGTGAAGG TTTCTTGCCA TCTGGTGCCT GATTAAAGCT 480  
 TGAGTATTAA GTTCTCAGCA TATCTCTCTA TTGCTTTGAC TTGAGTTTGC TGCATTTTCT 540  
 ATGTGCTGTT CGTGACTTGG AGAACTTAAA GTAATCGAGC TATGCCAATC TGGGTGGTGA 600  
 ACAGAGTACT TCCCACCACA GTGTTGAAAG GGAGAGCAAA GTCTTATGGA TAAACCCCTC 660  
 TTTCTTTTGG GGACCATGCG CTCTCACTTG AGAAGCTCAC CTGTGCTGAA TGTCCACATG 720  
 GTCACATAAC ATGTTATCCT TAAACCCCCC GTATGCCTGA GTTGAAAGGG CTCTCTCTTA 780  
 TTAGTGTTC ATGGGAACAT GAGGCGAGCA ATCTATTGCT AAGACTTTAC CAGGCTCAAA 840  
 TCATCTGAGG CTGATAGATA TTTGACTTGG TAAGACTTAA GTAAGGCTCT GGCTCCCAGG 900  
 GGCATAAGCA ACAGTTTCTT GAATGTGCCA TCTGAGAAGG GAGACCCAGG TTATGAGTTT 960  
 TCCTTTGAAC ACATTGGTCT TTTCTCAAAG TTCTCGCTTT GCTAGACTGT TAGTCTTTG1020  
 AGGACAGGGA CTATGCTCTA TCAATCACTA TTATTTTCTT GTTACCATGC ATGGGACAAG1080  
 TACACACAC ATATTTTGTG AGTCTTCTAA AAGACTCTCT TGATTGGGAG ACCATATCTA1140  
 TAATTTGGAT GTGAATCATT TCTTCAGTGG AATAAGAGCA CAACGGGCACA ACCTTCAAGG1200  
 ACATATTATC TACTATGAAC ATTTTACTGT GAGACTCTTT ATTTTGCCTT CTACTTGGCG1260  
 TGAATGAA CAACAAACAGG CCGTTGGGTT CCACAAAGTCA ATATATGTTG GATGAGGATT1320  
 CTGTTGCCTT ATTGGGAACCT GTGAGACTTA TCTGGTATGA GAAGCCAGTA ATAAACCTTT1380  
 GACCTGTMTT AACCAATGAA GATTATGAAT ATGTTAATAT GATGTAATTT GCTATTAAAG1440  
 TGTAAAGCAG TTCTAAGTTT TAGTATTGGG GGGATTGGTT TTTATTATTG TTTTCCCTTT1500  
 TGAAAATATC TGAGGAGTCT TTTGATAAAG TTAGTAAATG ATGTTAGATT TTAGTTTGGC1560  
 AAGCATGTGT TTTTTCAAAT ATATCAAGTA TAGAAAAAGG TAAACAGATT AAGAAGGAG1620  
 GCAATTATAT TATTTCTCTG TAGTTAAGCA AACACTTGTG GAGTGCCTGC TATGTGCACG1680  
 GCATGGGCCC ATATGTTGTG GGAGCTTGTG TAATTATGTA GGAAGCAATA GATCTCGTA1740  
 GTTACGTTAT GGGCAGATAC TTACTGTATG ATGGAAGAA CATCACAGTA ATCACAAAT1800  
 CAGAGCTGAG TTATCCCCAG TGTAGCTTCG TTGGGGATTG CAGTTTCTGG AACCGAGAGT1860  
 TAGGGCCATT TTATTTAAAA GAAACTCCCG GTTGAGACCG GTCTTATAGA ACCTCTGAAA1920  
 CGTACAAGCC TTACAGAAGT TAACTAAATT GGGATTAAAT TTTCTGTATG TATCTGCATA1980  
 ATTCTTGTGT TTCTTTCCAT CTGGCTCCTG GGTTGACAAT TTGTGGAAAC AACTCTATTG2040  
 CTACTATTAT AAAAAATACA GAAATCTTTC CCTTTAAGCT ATGTTAAATT CAAACTATTC2100  
 CTGCTATTCC TGTTTTGTCA AAGAATTATA TTTTCAAAA TATGTTTATT TTGTTGATG2160  
 GTCCACAGAA ACACATAATA AAACCACAGA GACCAGCCCC AAAAAAAAAG AAGTTTGTG 2218

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 548:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2196 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

```

CGGCGCGGATG CGCGCGAGACC CGGCGGGGGG CGGCGGGGGG CGTGAGCCCC GATGAGGCCC 60
GAGCGTCCCC GGGCGCGCGG CGAGCGGCCC GGGCCGATGG AGACCCCGCC GTGGGAGCCCA 120
GCCCGCAACG ACTCGCTGGC GCCCAGCTG ACCCGGGCGG TGCCCCCTCA CGTGAAGCTT 180
GGCCTCACCG TCGTCTACAC CGTGTCTTAC GCGCTGCTCT TCGTGTTCAT CTACGTGCAG 240
CTCTGGCTGG TGCTGGCTTA CCGCCACAAG CGGCTCAGCT ACCGAGCGGT CTTCCTCTTT 300
CTCTGCCTCT TCTGGGCTCT CCGCGGACC GTCTCTTCT CTCTCTACTT CAAAGACTTC 360
GTGGCGGCCA ATTGCCTCAG CCCCTTCGTC TTCTGGCTCG TCTACTGCTT CCCTGTGTGC 420

CTGCAGTTTT TCACCCCTCAC GCTGATGAAC TTGTACTTCA CGCAGGTGAT TTTCAAAGCC 480
AAGTCAAAAT ATTCTCCAGA ATTACTCAAA TACCGGTTGC CCCTCTAGCT GGCCTCCCTC 540
TTATCAGACC TTGTTTTCTC GTTGGTGAAT TTAACCTGTG CTGTGCTGGT AAAGACGGGA 600
AATTGGGAGA GGAAGGTTAT CGTCTCTGTG CGAGTGGCCA TTAATGACAC GCTCTCTCGT 660
CTGTGTGCCG TCTCTCTCTC CATCTGTCTC TACAAAATCT CTAAGATGTC CTTAGCCAA 720
ATTACTTGG AGTCCAAAGG CTCCTCGGTG TGTCAAAGTA CTGCCATCGG TGTCACCGTG 780
ATACTGTTTT ACACCTCTCG GGCCTGCTAC AACCTGTTC TCTGTCTACT TTCTCAGAAC 840
AAGAGCGTCC ATTCCCTTGA TTATGACTGG TACAATGTAT CAGACCAGGC AGATTTTGA 900
AATCAGCTGG GAGATGCTGG ATACGTATTA TTTGGAGTGG TGTATTATTG TTGGGAAC 960
TTACCTACCA CTTAGTCTGT TTATTTCTTC CGAGTTAGAA ATCCTACAAA GGACCTTACC 1020
AACCTCGGAA TGGTCCCCAG CCATGGATTG AGTCCAGAT CTATTTTCTT TGACAAACCT 1080
CGAAGATATG ACAGTGATGA TGACCTTGCC TGGAAACATT CCCCTCAGGG ACTTCAGG 1140
GGTTTTGCTC CAGATTTACTA TGATTGGGGA CAACAAACTA ACAGCTTCTC GGCACAAG 1200
GGAACCTTGC AAAGACTCAA CTTTGGATCC TGACAAACCA AGCCTTGGGT AGCATCAG 1260
AACAGTTTTA TGGACGATTG CTCAGATGAA AAGCTTCAGA AAGCATAGT GACAGCTGA 1320
TTTTTAGGGC ACTTTTCTCT AAGAAATAGA ACTTGATTTT TATTTTGTAC AGGTTTCCA 1380
TGGCCCCATA GGAATGACGA ATAATGTAGA CTGATAAACC CTATTTTTAG TACTAAAG 1440
GGAGCCTTGC TATTTCAGTG GGTATAATTT AAACCTTTTA AAGAAATCT GTACTTTT 1500
AAAGATGTAT TTTGTATAAC TTAATAATA ATGCTAAAGT ATACTAGGTT TTTTTCCT 1560
TGAGAAATGTT ACTGCAATCA TGTGTAGTT TGCAACGACT TTTATGCTA ATTCACTTT 1620
AAATATAGTA ATATATGGTC TAATAGTTTT TTAAGCTTTT TGGCATTAAG TATTCAC 1680
ATCTTACCTC TTTAGGTTCA TGATGGTCAC TCCGATTCTG ATGCGCATAG TGGTAGACT 1740
CTAAAAATACA GTTGACAACT TAGCCAAATTG CAACCTCAGT GTTGATAATT AAAATG 1800
GGTAAAGCAG CAGACTGTAA GGTCTTTAGA GATTTTCTT TTAAGGTTAG GCGCCTAG 1860
TCCCTCAAGG ATCTCTTAAG TTTTGGCCAA AGACTGGTAT TTCTTTTAC TAGGGCGC 1920
ATGTATACAC ATTAATGATA AGTTGATAAC ATTAATAAAT TAGCTTACTT ATCCTATT 1980
AOCCTCTCTG CTATGTTTAC AGAACCCTCA TAACTTTTTT TCAGCCTAAT GAAATCT 2040
ATGCATTACC TCAGGGCCAC ATCAAGAATA CACCCTTCT CTACTCTACT GAATGTT 2100
TACATTCAAG GAGAAAATAA GAGGGTCCAT AAAGGCGATT AATAACAAAT ACCCCAAG 2160
GTTGAGCTAA GACTATGTGG AATCCTAATA GTTTTTT 2196

```

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 549:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 701 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

AATTAAATA AATAGAAACA TACGGAGATT CTTTATGTT GSATTATTA TACCTCCAC 60  
 CATTTTGGTC CCGAAAAGG GAAAAGATAC ACGGTCGAGT AGTACAGGA TGTGTTCCC120  
 ACTACACATT ATGGCTATAA TGGAGTTGAA TTGCAACAG TAARATTTTG TTTGGATTG180  
 GTTCCCTCG ATCCCCCAG ACAGGAGCTT CCTCTCCAC CCTACCTGCC TGCCCTTAAG240  
 TTGTGTCCTA TTAAACTGGA CACAATCTC ACCGGCTTTT AGTCTAATAA TTGAATCATA300  
 GCTACACACA GTGACACCAG AATAGCTACT TGTTTTTTGA TGTACCAGT GAGTAACCTG360  
 TTTATCCTTG TATGTAGAAA CTAATTTTAC CATGATCACA GATCTGTGTA ACATCTCTAG420  
 TTTGAATTTT CACACAATTT TAAAATGTCT ACTAGAAAAC TTACACCTTT TTGTCCAAAG480  
 GTGCTCTTCA TCTATAAAAC CGTGGGCATA CTTCAAGTGT CTTCTGAGGC CAAATTTTGT540  
 GGGTCGTGGG GGACAATTTT GTATTAAACAT ACGTTATTTT GTAATTCATT CTCCAAATTT600  
 GAAGCTTTAT TAAAGGTATT CTATTTCCAC TGGCTTCCCT TAACCTTGAAT AAAATTTACT660  
 CCCAGTGCCG TGGCTCATGC CTGCTGCAAT CCCAGCCCTT T 701

## (2) INFORMATION ON SEQ ID NO. 550:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2214 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

00073945.1.2700



(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GCTAAAGAGG AGGATGCTAT ACTTTTCTAA ATGGCAAGAG ATGGGGAGAG AAGGGGATTA 60  
 AGAGTTGACC CGCAACCTCC CGGTGGATTCT TTTGTTCTTA CCAGATCTCT TGCCCACTCC 120  
 CCTATTCTGA AGTCGCTCTG GCTCTCTTGA CTGCTCCCTC ATTCTGAAGT CGTCTTGGCT 180  
 CTCTTGACTA CTCCTCTATT CTGAAGTCGT CTTGGCTCTC CTGACTACAC TATTTCAAGG 240  
 AATGATCACC AAGACACACA AAGTAGACCT TGGGCTCCCA GAGAAGAAAA AGAAGAAGAA 300  
 AGTGGTCAAA GAACCAAGAGA CTCGATACTC AGTTTAAAC AATGATGATT ACTTTGCTGA 360  
 TGTTCCTCCT TTAAGAGCTA CATCCCCCTC NTAAGAGTGT GGCCCATGGG CAGGCACCTG 420  
 AGATGCCTCT AGTGAAGAAA AAGAAGAAGA AAAAGAAGGG TGTCAGCACC CTTTGCAGGG 480  
 AGCATGTAGA ACCTGAGACC ACGCTGCCTG CTAGACGGAC AGAGAAGTCA CCCAGCCTCA 540  
 GGAAGCAGGT GTTTGGCCAC TTGGAGTTCC TCAGTGGGGA AAAGAAAAAN TAAGAAGTCA 600  
 CCTCTAGCCA TGTCCCATGC CTCTGGGGTG AAAACCTCCC CAGNACCCNT AGACAGGGTG 660  
 AGGAGGAAAC CAGAGTTGGC AAGAAGCTCA AAAAANCACA AGAAGGAAAA AAAGGGGGNC 720  
 CCAGGACCCC ACNAGCCTTC TCGGTCCAGG ACCCTTGGTT CTGTGAGGCC AGGGAGGCCA 780  
 GGGATGTTGG GGACACTTGC TNCAGTGGGG AAGAAGGATG AGGAACAGGC AGCCTTGGGG 840  
 NCAGAAACGG AAGNCGGAAG AGCCCCAGAG AACACAATGG GAAGGTGAAG AAGAAAAAAA 900  
 AATCCACCA GGAGGGAGAT GCCCTCCAG GCCACTCCAA GCCTCCAGG TCCATGGAGA 960  
 GCAGCCCTAG GAAAGGAAGT AAAAAGAAGC CAGTCAAAGT TGAGGCTCCG GAATACATCC1020  
 CCATAAGTGA TGACCCTAAG TCCTCCGCCAA AGAAAAGAT GAAGTCCAAA AAGAAGTAG1080  
 AGCAGCCAGT CATCGAGGAG CCAGCTCTGA AAAGGAAGAC GAGGAAGAAG AGGAAGAAGA1140  
 GTGGGGTAGC AGGAGACCCCT TGGAGGGGAG AAACAGACAC GAGCTTAGAG GTGGTGTGG1200  
 AAAAAAAGG CAACATGGAT GAGGCGCACA TAGACCAGGT GAGGCGAAG GCCTTGCAAG1260  
 AAGAGATCGA TCGCGAGTCA GCGAAAACGG AAGCTTCTGA AACCAGAAA TGGAAGGGAA1320  
 CCCAGTTTGG CCAGTGGGAT ACTGCTGGTT TTGAGAACGA GGACCAAAAA CTGAATTT1380  
 TCAGACTTAT GGGTGGCTTC AAAAACCTGT CCCCTCGTT CAGCGCCGCC CCGACGACGA1440  
  
 TTGCAAGGCC CAACATGGCC CTCGGCAAGA AGCGGCTGA CAGCCTGCAG CAGAATCTGC1500  
 AGCGGGGACTA CGACCGGGCC ATGAGCTTGG AAGTACAGCC GGGGAGCCGG CTTGCGGTGT1560  
 TCTCCACCGC CCCCACCAAG ATCTTTTACA TTGACAGGAA CGTTTCCAAG TCACTCAAGC1620  
 TGGAAAGTAA AACTCTAGAG TTTTGTCCCC CCAAACCTGC CACAATTGCT TTGATTATTC1680  
 CATTTATGCT GGAGATTACA AATTTTTTTT GGTGAACAAA TCAGATCTTG GTGAGGACCT1740  
 CGAGCAGTAA GATATAAATA ACTCCCNATA ACCTTACNCG TTCCCACTAA TGGAACTA1800  
 GGCATAAANT GTTTTATTNC AGTTGTGCAA ATGAAAAGCCA TCTGACAGT GGCTNCACAT1860  
 TGAACACCTG TGGAGATTAAG GGACGAGGAC AACTATTATT ATGGGCTTGG ATGAACCTGGG1920  
 CGAGGGCAGC TCATATTTCG GGAGCCAGGA GAACGAGTGA GTGCTAAAA CTCTGTTTT1980  
 CTGTGTAAAC CATTCCTGCC CTGTTTGAGA CATCAGTATG TACAGTTAAC TTTTGTGAG2040  
 TGTTTAGCAG GTACTAGGGA CATACTAGTG TTTTCCTTAA TGTATTTAAT CTCATTAATT2100  
 ATGAAATGGG TGCTATTATT AGCCCCATCT TATAGATGAG GCAACTGAGG TTCAGGGATA2160  
 AAGTAATAAA ATTGCTCTGG GTACCCAGC CACTAAAAAA AAAAAA AAAA 2214

09673305-12270

## (2) INFORMATION ON SEQ ID NO. 551:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1434 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

GCGCGGCCGG CGCCTGCGGG GCGAGAGGGT CGGGGCGAAG GGAAGCTAC GTCCCGGAGG 60  
 TGCGGTGTGG GGCACCGGGC GGGGCCGCGG GAACCGGCGC CCCACGGAGC TGCTGTGTGT 120  
 AGACCAACCC CGGGCCCCCA TCATCACTGC GCGCGCTTT CAGGCGCCGA GAACCTACCGT 180  
 TCCCGCATG CCATGAAATT GGCTCGGGC CTGAGGCGGG GTCCGGCCCT CCACCCGCTC 240  
 CCGCCGCGCG CGAATCGCGG TCGCGAGCCA TGGAGGAGGA GGCATCGTCC CCGGGGCTGG 300  
 GCTCGAGCAA GCGSCACCTG GAGAAGCTGA CCTCGGGCAT CACGCGCATC CTAGAATCTT 360  
 CCCCAGGTGT GACTGAGGTG ACCATCATAG AAAAGCCTCC TGCTGAACGT CATATGATT 420  
 CTTCTGGGA ACAAAAGAAT AACTGTGTGA TGCCTGAAGA TGTGAAGAAC TTTTACCTGA 480  
 TGACCAATGG CTTCCCATG ACATGGAGTG TGAAGCTGGA TGAGCACATC ATTCACCTGG 540  
 GAAGCATGGC AATTAAACAG ATCTCAAAAC TGAATCAGCT CACCCAGTCT TCCATGTATT 600  
 CACTTCTCAA TGCACCCACT CTGGCAGACC TGGAGGACGA TACACATGAA GCCAGTGATG 660  
 ATCAGCCAGA GAAGCCTCAC TTTGACTCTC GCAGTGTGAT ATTTGAGCTG GATTCAATGA 720  
 ATGGCAGTGG GAAAGTTTGC CTTGTCTACA AAAGTGGGAA ACCAGCATTG GCAGGAAGACA 780  
 CTGAGATCTG GTTCTCTGAC AGAGCGTTAT ACTGGCATT TCTCACAGAC ACCTTTACTG 840  
 CCTATTACCG CCTGCTCATC ACCACCTGG GCCTGCCCA GTGGCAATAT GCCTTCACCA 900  
 GCTATGGCAT TAGCCACAG GCCAAGCAAT GTTTCAGCAT GTATAAACCT ATCACCTACA 960  
 ACACAAACCT GCTCACAGAA GAGACCGACT CCTTTGTGAA TAAGCTAGAT CCCAGCAAG1020  
 TGTTTAAGAG CAAGAACAAG ATCGTAATCC CAAAAAGAA AGGCCTGTG CAGCCTGCAG1080  
 GTGGCCAGAA AGGCCCCCA GACCCCTCCG GTCCCTCCAC TTCTCCACT TCTAAATCCT1140  
 CCTCTGCTCT TGGAAACCCC ACCCGGAAGT GAGCACCCT CCTTCCAAC CTCTACCAAG1200  
  
 TCCAGAGTGG TGGTTTCCAT GCACAGATGG CCTTAGGGGT GACCTCCAGT TTTGCGTGTG1260  
 GACCGTAGGC CTCCTTTCTAG TTGAATGACC AAAATTGTAA GGCTTTTAGT CCCACCGACA1320  
 TTAGCCAGGC TCGTAGTGAG GCCTCCAGAG CAGGTTGTGC TGTCCCTGTC CTCTGGAAGC1380  
 AATGGGGAAT GTGGAATCAA GACAATGCCC AAAAAATTT TAATGCAGCT GGTC 1434

09672395.122700

## (2) INFORMATION ON SEQ ID NO. 552:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2434 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

CCCGGAGAAG GTGGAGGGAG ACGAGAAGCC GCCGAGAGCC GACTACCCCTC CGGGCCCGAGT 60  
 CTGCTCTGCC GTGGTGGATC TAAGCCTCAT CTGTATCCTC TTGTGATGGC GTGAAGGAAA 120  
 GCCATGGCAG ATTTCCAGCC TGGTGATGCT GTACAGAAAC CAGGTGGCCT GCTTCCATGC 180  
 CTCCTCAGCT TCAAGAAACT AGAATGAACC GAAGCATTCG TGTGGAGGTT GATGAATCAG 240  
 AACCATACCC AACTCAGTTG CTGAACCAAA TCCCAGAATA TTCCCCGGAA GAGGAATCAG 300  
 AACCCACCTG TCCCAATATA AGGAACATGG CACCCAAACAG CTTGTCTGCA CCCACAATGC 360  
 TTCACAATTC TCCCGGAGAC TTTTCTCAAG CTCACCTCAAC CCTGAACTTT GCAAAATCACC 420  
 AGCGGCCTGT ATCCCGCGAG GTCACCTGCC TGGCGACTCA AGTTCTGGAG GACAGTGAAG 480  
 ACAGTTTCTG CAGGAGACAC CCAGGCTCTG GCAAAGCTTT CCCTTCTGGG TGCTCTGCAG 540  
 TCAGCGAGCC TGGCTCTGAG TCTGTGGTTG GAGCCCTCCC TGCAGAGCAT CAGTTTTCAT 600  
 TTATGGAAA ACGTAATCAA TGGCTGGTAT CTCAGCTTTC AGCGGCTTCT CTTGACACTG 660  
 GCCATGACTC AGACAATACA GACCAAAAGT TACCTAATGC CTCAGCAGAC TCCTTGGGGC 720  
 GTAGCAGGGA GATGGTGCAA CGGCCCCAGC CTNCAACAGGA ACCGAGCAGG CCGTGATCTG 780  
 CCAACCATAT ACACGGGATA TGATTCCAGC CCCAGGATG TCCTTGGGCAT CAGGCACGCTG 840  
 GAAAGGCCCC TGNCCCTCAC CTCGCTGTGT TACCCCCAGG ACCTCCCCAG ACCTCTCAGG 900  
 TCCAGGGAGT TCCCTCAGTT TGAACCTCAG AGGTATCCAG CATGTGCACA GATGCTGCCT 960  
 CCCAATCTTT CCCACATGTC TCCATGGAAC TATCATTACC ATTGTCTGG AAGTCCCGAT1020  
 CACCAGGTGC NCATATGGCC ATGACTACCC TCGAGCAGCC TACCACAAG TGATCCAGCC1080  
 GGCTCTGCCCT GGGNCAGCCC CTNNGCCTGG AGCCAGTGTG AGAGGCTCTG ACCCTGTGCA1140  
 GAANNNGTTA TCTGGAATTA TCCGACCCC TGGGACCAAG AAGAGAGGCC CGCACAGAGA1200  
 GACTGCTCCT TTCCGGGGCT TCCAAGGCAC CAGGACCAGC CACATACCCA GCCACCTAAT1260  
 AGAGCTGGTG CTCCTGGGGA GTCCCTGGAG TGCCCTGCAG AGCTGAGAGC ACAGGTTCCC1320  
 CAGCCTCCGT CCCCAGCTGC TGTGCCTAGA CCCCTAGCA ACCCTCCAGC CAGAGGAATC1380  
 CTAATAACAA GCAATTTGCC AGAAGAATTG CGGAAGTCT TTATCACTTA TTCGATGGAG1440  
 ACAGCTATGG AGGTGGTGA AATTCGTGAAC TTTTGTGTG TAAATGGCTT CCAAACTGCA1500  
 ATTGANCANT ATTTCAGGAT AGAATCCGAG GCATTGATAT CATTNAAATG GATGGAGCGC1560  
 TACCTTANGG GATAAGACCG TGATGATAAT CGTAGCAATC AGCCCCNAAA NTACAANNK1620  
 AGGACGTNGG NAAGNCGCTG GANGTCNGCA GCTGGACGAG GATGAGCATG GCTTACATAC1680  
 TAAGTACATT CATCGAATGA TGCAGATTGA GTTCATAAAA CAAGGAAGCA TGAATTTCA1740

ATTACCTCCCT GTGCTCTTCC CAAATGTCTAA GAAGGAGCAT GTGCCACCAT GGCTTCAGAA1800  
 CACNCTATGT CTACAGCTGG CCCAAGAATN AAAAAAACA CTCGTCTGGG GCTGCTNGAG1860  
 AGAGGAAGAG TATGTGGCTC CTCACCGGGG GCCTCTGCCC ACCNCTTACC GTGGTTCCCT1920  
 TGTGANCACC GTTCATCCCC AGATCACTGA GGCNAGGCC ATGTTTGGGN GCCTTGTCT1980  
 GNACAGCAIT CTGGCTGAGG CTNNGCTCGT AGCANNCTCC TGGCTGGTGT TTNTCTGTT2040  
 CCNTCCCCGA NGAAGCCCTC TGSNCCCCC ANGGAACCT GTTGTCGAGA GCTCTCCCC2100  
 GGAGACCTCC NACACANCCC TGSNCTTTGA AGTGGAGTCT GTGNACTGNC TCTGCTTNGA2160  
 TCTGCTTTN AAAAAACCA TTGCAAGTGN CCAAGTGTCCC ATATGTTNCC TCTTNGACAG2220  
 NTTTGATGNN GTNCCATTCT NGGGCTCTCT AGTGCCTAGC AAGTAGATAA TGTAAAGGAT2280  
 GTNGGCAGCA AATGGAATG ACTACAAACA CTCTCCTATC AATCACTTCA GGCTACTTTT2340  
 ATGACTTAGC CAGATGCTTG TGTATCTCTA NGACCAAACT GATTCAATGA CAAATAATAA2400  
 AATGTTTACT CTTTGTGAAA AAAAAAATA AAAA 2434

09673395.122700

## (2) INFORMATION ON SEQ ID NO. 554:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1457 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

ACTAACCCAG AGTTGTGGCA TTATTAATTA TCACCTGGTCT TCTTAATCGT AAAACGGGGG 60  
 ACCCCAGAGG CAAGGAAATT TCCATTACCC TATATTGGGC TTAACCTTAA AGGAGTATAT 120  
 CCACATATCAA GAGCTTAGTA CAAAGGCTGG GGTGAAGTTA CATTATACCT GGGCGTTTTA 180  
 CCATACCAGG GACCCCACTT CAACAATGAC TGTGGAAGAC CAAAGGAGAT ACCTAGGTTC 240  
 AGATTATAAT AAATCACCCA GCACCACTTG AATGTATTAT CCACAAGAT ATAGCAATAA 300  
 TAAAGGTTAT ATATACATAT ATTTATCTTG GTAACTGAG GGCTAAAAAC GTGGAATACG 360  
 ATAATTTCTT TCAAGAGGTC CATCTGTAAG AAAGGGACCC AAAAGGACAG TGTTTGTGTT 420  
 GCATAAAATA TGGGTAAAGT GAGTTGGGA ACAAGGGTG GTTCTTTAG CTCTTCCAC 480  
 ATCTCTCTTT GATAAGGACT GAAACCTGCT TGATTCATGA TAAACGTTTC CTTTTTTTTT 540  
 TTTTTTGGCA GCGGGGAGAG GGAAGAGGA GGAATGGGG TTTGAGGACC ATGGCTTACC 600  
 TTTCTGCTCT TTGACCCATC ACACCCCAT TCTCTCTCTT TCCCTCTCCC CGCTGCCAAA 660  
 AAAAAAATA AGGAACGTT TATCATGAAT CAACAGGTT TCAGTCTTTA TCAAGAGAG 720  
 ATGTGGAAAG AGCTAAAGAA ACCACCTTT GTTCCCACT CCACCTTACC CATATTTTAT 780  
 GCAACACAAA CACTGTCCTT TTGGGTCCTT TTCTTACAGA TGGACCTCTT GAGAAGAATT 840  
 ATCGTATTCC ACGTTTITAG CCCTCAGGTT ACCAAGATAA ATATATGTAT ATATAACCTT 900  
 TATTATTGCT ATATCTTTGT GGATAATACA TTCAGTGGT GCTGGGTGAT TTATTATAAT 960  
 CTGAACCTAG GTATATCTTT TGGTCTTCCA CAGTCATGTT GAGGTGGGCT CCCTGGTATG 1020  
 GTAAAAAGCC AGGTATAATG TAACTTCACC CCAGCCTTTG TACTAAGCTC TTGATAGTGG 1080  
 ATATACTCTT TTAAGTTTAT CCCCATAATA GGGTAATGGA AATTTCTCTG CCTCTGGGTT 1140  
 CCCCATTCTT ACTATTAAAG AGACCACTGA TAATTTAATA ATGCCACCAA CTCTGGCTTA 1200  
 GTTAAGTGAG AGTGTGAAC TGTGTGCAAG AGAGCCTCAC ACCTCACTAG GTGCAGAGAG 1260  
 CCCAGGCCCT ATGTTAAAT CATGCACCTG AAAAGCAAAC CTTAATCTGC AAAGACAGCA 1320  
 GCAAGCATT TACGGTCATC TTGAATGATC CCTTTGAAAG TTTTTTTTGT GTTGGTTGG 1380  
 TTTAAATCA AGCCTGAGGC TGGGTGAAA CAGGTAGCCT ACACACCCCA AATTGGGGGT 1440  
 GTTCCCGGGG GAATGTT 1457

06673395.122700

## (2) INFORMATION ON SEQ ID NO. 555:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 741 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

CCTCCTAAAA GACTGGGAAA GCAGCTTTGG GCTTTGGGTC CTCCTAAAAA AACCAAGGCG 60  
 GATGACTTGG GGTITGGATC CCCTTCGGAT GTCACTCGAA AAAGCCTTAG CAGACCTGAT120  
 TGAGAAGGAA CTGTCCCGTT CAAAGACCAA CCTTCCCTTT CGCCCCACAT CTCTTCAGAA180  
 CTCCTCTTCA CACACTACAA CGGCCAAAGG TCCCAGGCTC TGGATTCTCT CATCTGCTG240  
 CAGCTACAAA TGCCAACTCT CTAAATAGTA CCTTTTCAGT CTTGCCCCAG AGGTTCCCTC300  
 AATTTTCAGCA GCACCGAGCG GTTATAATT CATTCACTTT TCCAGGCCAG GCAGCCCGCT360  
 ATCCTTGGAT GGCTTTTCCA NCGCAATAGC ATCATGCNAC TTGAACCACA CAGCAAAACC420  
 CACCTCAAAT AGTAATTTCT TGGACTTGAA TCTCCCGCCA CAGCACAAAC CAGGTCTGGG480  
 AGGGATCCCT GTAGCAGGGG AAGAAGAGGT GAAGGTTTCG ACCATGCCAC TGTCAACCTC540  
 TTCCCATTTA TTACAACAAG GACAGCAGCC TACAAGTCTC CACACTACTG TGGCCTGACA600  
 ACAGAAGTGA GAGGAGAGGA TTAGACTCTG GGGTGCTTGC ATGGGCAACT GGAATTTTGC660  
 ATGATTCTTT TATGATTTTG CTTTAAATGT ATACACCCAG AAGAGCCAAT ATAAACGTTTC720  
 CTCATGCCTA AAAAAAAAAA A 741

## (2) INFORMATION ON SEQ ID NO. 561:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 470 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

00021-563796

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

TDQPNIQSVK IHSLEPLRNPN KGCECPPRRD GFGFIKCVDR DVRMFFHFSE ILDGNQLHIA 60  
 DEVEFTTVPD MLSAQRNHAI RIKKLPKGTV SFHSHSDHRF LGTVEKEATF SNPKTSPNK120  
 GKEKEAEDGI IAYDDCGVKL TIAFAQKDVE GSTSPQIGDK VEFISIDKQR PGQVATCVR180  
 LLGRNSNSKR LLGYVATLKD NFGFIETANH DKEIFFHYSE FSGDVSLEL GDMVEYSLSK240  
 GKGNKVSARE VNKTHSVNGI TEEADPTIYS GKVIPLRSV DPTQTEYQGM IEIVEEGDMK300  
 GEVYPFGIVG MANKGDCLQK GESVKFQLCV LGQNAQTMAY NITPLRRATV ECVKDQFGFI360  
 NYEVGDSKKL FFHVKEVQDG IELQAGDEVE FSVILNQRTG KCSACNVWRV CEGPKA AAP420  
 RPDRLVNRLK NITLDDASAP RLMVLRQPRG PDNSMFGGAE RKIRQAGVID 470

## (2) INFORMATION ON SEQ ID NO. 562:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 126 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

LNAILNFFHM EKELLAISYF IVNEAKLIFH TFHCGPAQGC DUVSHSLCIL AQDTQLELDA 60  
 LPFLQAIPIFV GHPNDKAWID LTFHIALLHN LNHSVLVSLC WINTPQGANY FARVNGGISF120  
 LSNAIH 126

## (2) INFORMATION ON SEQ ID NO. 563:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 85 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

KSHTSCNLLS RPLFVNTKTF NLISYLRRSR SFHILGLKSN SQFHPTVIIS NNAILSLLLF60  
 AFIWASGFRI GKSGFFFYRA QKTVI 85

00672395-122700

## (2) INFORMATION ON SEQ ID NO. 564:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 549 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

LYPNFLVNEL ILKQKQRFEE KRFKLDHSVS STNGHRWQIF QDWLGTDQDN LDLANVNLML 60  
 ELLVQKKKQL EAESHAAQLQ ILMEFLKVAR RNKREOLEQI QKELSVLEED IKRVEEMSGLI120  
 YSPVSEDSTV PQFEAPSPSH SSIIDSTEYS QPPGFSGSSQ TKKQWPWNST LASRRKRLTA180  
 HFEDLEQCYF STRMSRISDD SRTASQLODEF QECLSKFTRY NSVRPLATLS YASDLYNGSS240  
 IVSSIEFDRD CDYFAIAGVT KIKVVEYDT VIQDAVDIHY PENEMTCNSK ISCISSWSSYH300  
 KNLLASSDYE GTVILWDGFT GQRSKVYQEH EKRCWSVDFN LMDPKLLASG SDDAKVKLWS360  
 TNLDNSVASI EAKANVCCVK FSPSSRYHLA FGCADHCVRH YDLRNTKQPI MVFKGHRKAV420  
 SYAKFVSGEE IVSASTDSQL KLWNVKGKPYC LRSFKGHINE KNFVGLASNG DYIACGSENN480  
 SLYLYYKGLS KTLTLTKFDT VKSVLDKDRK EDDTNEFVSA VCWRALEPGE SNVLIANSQ540  
 GTIKVLELV 549

## (2) INFORMATION ON SEQ ID NO. 565:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 132 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

TLFYFYIDMC NSQRGWEIRT LQIIHCYIIV HICYFVTFVF SPVFFFFFFF FFCGSIINFYC 60  
 FVIYFYSKEF VLSLQKLDNT TKSSNVHGVT LMVESWLGP NVPKVIKEGK EKKKIKFKTN120  
 PKPMMTLGRD IT 132

## (2) INFORMATION ON SEQ ID NO. 566:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

GTVLSSLTGE YKPLISSTLL ISSSKTLSSF WICSSCSLLF LLATLRNSIR ICSWAACDSA60  
SSCFFECTSN SNIRLTLAKS RLSWSVPNQS 90

(2) INFORMATION ON SEQ ID NO. 567:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 331 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

SANHKLEVNG TDGLAPVEVE ELLRQASERN SKSPTEYHEP VYANPFYRPT TPQRETVPFG 60  
PNFQERIKIK TNGLGIGVNE SIHNMGNLS EERGNNFNHI SPIPPVPHPR SVIQQAEKL120  
HTPQKRLMTP WEESNVMDQK DAPSPKRLS PRETIFGKSE HQNSSPTCQE DEEDVRYNIV180  
HSLPPDINDT EPVTMIFMGY QQAEDSEEDK KFLTGVDGII HAELVVVIDE EEEDEGEAEK240  
PSYHPIAPHS QVYQPAKPTP LPRKRSEASP HENTNHKSPH KNSISLKEQE ESLGSPVHHS300  
PFDAQTTGOG TEDPSLTALR MRMAKLGKKV I 331

(2) INFORMATION ON SEQ ID NO. 568:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 216 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

0007305.120700



(vi) ORIGIN  
(A) ORGANISM: HUMAN

```
LSLSTRMEEA ELVKGRLOAI TDKRKIQEEI SQKRLKIEED KLKHQHLKKK ALREKWLDD 60
ISSGKEQEEM KKNQOQDDQAI IQVLEQSILR LEKEIQDLER AELQISTKEE AILKKLSTE120
RTTEDIIRSV KVEREEARAE SIEDIHANTP DLPGKSIYPSR LRKEINEEAE DDEQNRKALY180
AMEEKVEKDL KGETESTVLS NTSGJOMYIK LTKGVKV 216
```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 132 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

```
LEKLHICFPQ LFGNFSQIMT TTYSHGLIWY TVMIIFWTSE KINKISRREI CKCFLVSSSK 60
DVIYIGGTLR SPFFPALPFS SLKLLRMDPQ SHLQLSEHQM GNGGQGCLSF LLALSEIWNF120
CGGIYDLCFH ED                                     132
```

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 199 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

NEVTPSWFW WTKLTFFFL ALKKSSRVSS SHLPRIYQAF LMSATFNEDV QALKELILHN 60  
PVTLKIQESQ LQPGDQLQF QVVCETEEDK FLLEYALLKL SLIRGKSLF VNTLERSYRL120  
RLFLEQSFSL PTCVLNGELPL RSRCHIIISQ NQGIFYDCVIA TDAEVLGKPR QRAMRPRRA180  
KTGTMASSRL ERTVLVALGH  
199

## (2) INFORMATION ON SEQ ID NO. 571:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 195 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

QVRRAALLSS AMEDSEALGF EHMGLDPRLL QAVTDLGWSR PTLIQEKAIP LALEGKDLLA 60  
 RARTGSGKTA AYAIPLMLQLL LHRKATGPVV EQAVRGLVLV PTKELARQAQ SMIQQLATYCI20  
 ARDVRVANVS AAEDSVSQRA VLMEKPDVVV GTPSRILSHL QQDSLKLKRD LELLVVDEAD180  
 LLFSFGFEE LKSL 195

## (2) INFORMATION ON SEQ ID NO. 572:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

DIGHSDIPST VGSQLLNHGL CLPCQLLGRN KNKASHCLFY HRTCRLPMEQ QLQHRNSISG60  
 RLPGARAGPS QEVLFP 76

## (2) INFORMATION ON SEQ ID NO. 573:

- (i) SEQUENCE CHARACTERISTIC:

00672395.122700

- (A) LENGTH: 91 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

DSQVGRGPQR NSSLHTGRSV HWGEATGSLR HLOWGRAQPL LFLGGKLRFK LPGGKSMGRK60  
QALXLLRVSV SFFFPLCLIN KFHFHSPNS L 91

(2) INFORMATION ON SEQ ID NO. 574:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 89 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

EKWNLLIRHK GKKGETETLS KXRACFLMD FPPGSLNRSF PPRKRGWAL PHWRNRKLPV60  
ASPQCTLLPV CRLEFLWGPI PTWLSHCPL 89

(2) INFORMATION ON SEQ ID NO. 575:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

0967395.122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

LIRCLRLFSH HVMERKLSTS FLRLPATQLL IHIWSEPWYP STIHARKLDV YSLPFFPLFG60  
 DFLSSAEDG VLVCPMATKI 80

## (2) INFORMATION ON SEQ ID NO. 577:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

LLPLLLLLLIH GDTPXGPGPX XQEAPNHRH GLEEXRISXK SCMGXVDWNG PEGVEIYVDG 60  
 KEPHNKSQSS QLGFKTNGHX KSSEXVXHDV LDNRKEAGVK VKEGHEHQNQ QDPASELHVL120  
 FGGALTHGGD ARKHALPFRT GFSRSTQPP PRARFLPLCR T 161

## (2) INFORMATION ON SEQ ID NO. 578:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 160 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

QTDNLSEKQP XGKXVCRGCP QGECSWERAV LLXPGRPALS XTLLXKXAPC EVNWVXVRGS 60  
 XXCXGAPAKT PXPQQRXAAS AXAGLEXSXA XAGXAGCCCK GLPXVWSXLA LPTASLEASX120  
 XPRFAASPT SCPSTLPQAT KTRFVLNKKX XLGTXSXLIF 160

00673305-122700

## (2) INFORMATION ON SEQ ID NO. 579:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 437 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

SQGVLSDDGV WRVKSIPNGK GSSPLPTATT PKPLIPTEAS IRVWGTSGTS HLHPRISICMI 60  
 QKYNHDGEAG RLEAFSQGES VLKEPKYQEE LEDRLHFYVE ECDYLQGFQI LCDLHDGFGS120  
 VGAKAAELLQ DEYSGRGIIT WGLLPGPYHR GEQRNIYRL LNTAFGLVHL TAHSSSLVCPL180  
 SLGSGGLRLP EPPVSFPYLH YDATALPFHCS AILATALDTV TVPYRLCSPS VSMVHLADML240  
 SFCGKKVVTA GAIIPFPLAP GQSLPDSLMO FGGATPWTPL SACGEPGSTR CFAQSVVLRG300  
 YRQSMHPKPK NQRDTSTLCP SCMYHWGRNL GSVFTTAAAW SHEFFPSAAD SLQGGSSSLP360  
 PLLKLQSTGY GSGWFFQGR SSVLSLPQQ WRASQCLGHC VPLRPCTRPW KPWPETSPNS420  
 TCGAGFASWM LEWSTMT 437

## (2) INFORMATION ON SEQ ID NO. 580:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 277 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes.

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

TERLLDGGP PHSPETPQFP PTTGAVLYTV KRNQVGFEVR SCPKASPRQ KEREQGQKAVS 60  
 ESEALMLVWD ASETKLPQT VEPASFLSP VSSKTRDAGR RHVSGKPDQT ERWLPSSRAR120  
 VKTRDRTCPV HESPSGIDTS ETSPKAPRG LAKDSGTQAK GPEGEQQPKA AEATVCANNS180  
 KVSSTGEKVV LWTREADRV LTMQEQGAQ PQTFNIIQQ LGNKTPAEVS HRFRELMQLF240  
 HTACEASESD EDDATSTNSA DQLSDHGDLL SEEELDE 277

## (2) INFORMATION ON SEQ ID NO. 581:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 172 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

FFESHSSSSS SDRSPWSDS WSALLVLVAS SSSSELASQA VVKSCMSSRK RWETSAGVLF 60  
 PSCWEMMLKV CGCAPCSWHM VRITRSASLV HRTTFSPVEL TLLLLAHTVA SAAFGCCSPS120  
 GPLACVPLSL AKPPLGALGE VSEVSIPDGD SWTGHVLSLV FTLALLEGSH LS 172

(2) INFORMATION ON SEQ ID NO. 582:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 549 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

EFFPGLTEPT AVRALARARR TRAGSASDPE RSPGAMALSE LALVRWLQES RRSRKLILFI 60  
 VFLALLLDMN LLTVVVIPII SYLYSIKHEK NATEIQTARP VHTASISDSF QSIFSYDENS120  
 TMVTGNATRD LTLHQATQH MVTNASAVPS DCPSEDKDLL NENVQVGLLF ASKATVQLIT180  
 NFFIGLLTNR IGYPIPIFAG FCIMFVSTIM FAFSSSYAFL LIARSLOGGIG SSCSSVAGMG240  
 MLASVYTDEE ERGNVMGIAL GGLAMGVLVG PPFGSVLVEF VGKTAPFLVL AALVLLDGA1300  
 QLFVLQPSRV PQESQKGTPL TLLKDPYIL IAAGSISFAN MGIAMLEPAL PIWMMETMCS360  
 RKWQLGVAFI PASISYLIQT NIFGILAHKM GRWLCALLGM IIVGVLSICI FFPKNIYGLI420  
 APNFGVGFAN GMDVSSMMPI MGYLVOLRHV SVYGSVYAIA DVAFCMGYAI GPSAGGAIAK480  
 AIGFPWMTI IGIIDILFAP LCFFLRSPPA KEEKMAILMD HNCPIKTKMY TQNNIQSYPI540  
 GEDEESES 549

(2) INFORMATION ON SEQ ID NO. 583:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 121 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

YLLSHWNQYF WDTCTQNGEV ALCSSGNQNC WSQHFMYSSIS KKHLWTHSSE LWSWECKWNG 60  
 GFVNDAYHGL PRRPAARVRL WECVRHCGCG ILYGVCYRSF CWWCYCKGNW ISMAHDNYWD120  
 N 121

(2) INFORMATION ON SEQ ID NO. 584:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

DGGSVHWPGR LDFCSILLML NAVQITWDDG DHDSQHVQVQ QQRQEHDEQD ELPRAAALLQ 60  
 PADQRQLAQG HGSGAPLGVA CAACGPFPCP RQRPHRSGLR QSGREF 106

(2) INFORMATION ON SEQ ID NO. 585:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 409 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00673001-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

KSRLSVTLMP VQLSEHPewn ESMHSLRISV GGLPVLASMT KAADPRFRPR WKVILTFVVG 60  
 AAILWLCSH RPAPGRPPTH NAHNWRLGQA PANWYNDTYP LSPFQRTTAP IRYRIAVIAD120  
 LDTEPTAQDE NTWRSDLKKG YLTLSDSGDK VAVEWDKDHG VLESHLAELKG RGMELSDLIV180  
 FNGKLYSVD RTGVYQIEG SKAVFWVILS OGDGTVEKGF KAEWLAVKDE RLYVGGGLGKE240  
 WTTITGDVNN ENPEWVKVVG YKGSVDHENW VSNYNALRAA AGIQPPANLI HESACWSDTL300  
 QRWFFLPRA SQUERYSEKDD ERKGANLLES ASPDFGDIIV SHVGAUVVPH GFSSFKFIPN360  
 TDDQIIIVALK SEEDSGRVAS YIMAFITLQGR FLLPETRIGS VKYEGIEFI 409

## (2) INFORMATION ON SEQ ID NO. 586:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 249 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

KLSPDGLAQCFRFEINELDA FVFHASDLGL RQOEAPVQRE GHVDVGGDSAA VLLGFEGHND 60  
 LVVGVGDELE GREAVSGDHR PDVAHSDVAE VRGGAQQQVG ALALVVLAV ALLAGAAARQE120  
 EPALQRTVTPA GRLMDEVSWR LDAGSSPQVG VVGHVPLVVH AALVAHHLHP LRLVHVHITR180  
 SGRPLLAQAA HVQTLVLHCQ PFGLEAFLHG AVAVGQNHFG HGFAAFDLVD DPRPVIHGV240  
 FFIENNVQV 249

## (2) INFORMATION ON SEQ ID NO. 587:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

LEFFIPCLGS VNEACLPFGV SFHGLYFSSS SGSFAGSSSLW KLHERWLGLG FAGVYSRVKA 60  
 EWLRLPRLT TQAEKGRFHH SQCPPHSNYL TPTTLTPTP PRDRQGHGG FEGAGSGCPC120  
 AGPSQTSPL KLKHSCEEGS EEGPLSHGL FPPLCHR 157

09673395.122700



## (2) INFORMATION ON SEQ ID NO. 588:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

NTMAVAAVKW VMSKRTILKH LFPVQNGALY CVCHKSTYSP LPDDYNCNVE LALTS DGR TI 60  
VCYHPSVDIP YEHTKPIPRP DPVHNNEETH DQVLKTRLEE KVEHLEEGPM IEQLSKMFFT120  
TKHRWYPHGR YHRCRKNLNP PKDR 144

## (2) INFORMATION ON SEQ ID NO. 589:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

IQHTAFSQMA NEAHFSLIPP GTSASSVFWR IQILTTSVIP SMRIPTVLSS KEHFARLFYH 60  
RSFLKVFENF FQSGFQHLIM CFFIIMHRIW PRDRFCVFIW NVHRRVVAYY CPAIRSQSKLL120  
YVALIIVW 128

## (2) INFORMATION ON SEQ ID NO. 590:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

KLVCLEADSK SSFSSEHLFS YHLISILKHH GCSCSKMGDV KENYLETFIS SPKWSFILCL60  
S 61

(2) INFORMATION ON SEQ ID NO. 591:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 173 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSPSLFLP GAYKAQMYSD VWTNTKKKKK 60  
KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVLQ TSSQAAFYQK120  
GENSCLSLFK NAFYLSIRH YTSLEYKRPG GTMSLVDTFH CSVAPFLAWE ASA 173

(2) INFORMATION ON SEQ ID NO. 592:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00672995 122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

TCEFFRNQV GKOPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPs 105

## (2) INFORMATION ON SEQ ID NO. 593:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

TCEFFRNQV GKOPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPs 105

## (2) INFORMATION ON SEQ ID NO. 594:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

TPALRARSRL DRCARAPCPH GGQQRRLRL NAEGAEGARG GGSSYSEMAE TVADTRRLIT 60  
 KPQNLNDAYG PPSNFLEIDV SNPQTVGVGR GRFTTYEIRV KTNLPFKLK ESTVRRRYSID120  
 FEWLRSELER ESKVVVPPLP GKAFRLRQFL EEMMEYLMTI LLRKENKGWS SL 172

## (2) INFORMATION ON SEQ ID NO. 595:

09673395-122700

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 127 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

SAAGCQPRSP PFRSCCRER GLPPPPPRSA AAAGAAARRG DTGLARSGRE ENEHVERAFT 60  
 PHAKLLPAPL KLPPPSFGKE RLTSWNATPG SREARPLGR GTADWGVRRS GVMGLGVANR120  
 FRPDYSA 127

(2) INFORMATION ON SEQ ID NO. 596:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 123 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN  
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

FTSQPFKVTV SSSNSRFFQL ENRKICLDPD FVSGEAPAD PHRLRVAHID LEEVAGGSVG 60  
 VIQVLRLLGQ PPGVSHGLRH FAVAAAAAAG SLRPLRVQPP PPALLPAVGT RGSRAAVAKR120  
 TST 123

(2) INFORMATION ON SEQ ID NO. 597:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 262 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

00673395-122700

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

SCGDVEQKIQ FKRETASLKL LPHQPRIVEM KKGSGNGYGFY LRAGSEQKGQ IIKDIDSGSP 60  
 AEEAGLKNND LVVAVNGESV ETLDHDSVVE MIRKGGDQTS LLVVDKETDN MYRLAHFSPF120  
 LYYQSQELPN GSVKEAPAPT PTSLEVSSPP OTTEEVDHKP KLCRLAKGEN GYGPHLNAIR180  
 GLPGSFIKEV QKGGPADLAG LEDEDVIEV NGVNVLDEPY EKVDRIQSS GKNVTLLVCG240  
 KKAYDYFQAK KIPIVPSLAD AS 262

(2) INFORMATION ON SEQ ID NO. 598:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 65 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

KGWRSDFTVG GRQRDGQHVQ TGSFFSISLL SKSRTAQWLC QGGSSSYSHF SGSLKSTRYY60  
 RGRSS 65

(2) INFORMATION ON SEQ ID NO. 599:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 63 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

AEDTIQKRNS QFETVTPPAP NCGDEERKQW LWFLSEGRLR TERSNHQGHR FWKSSRGGL60  
 EEQ 63

09673395 122700

## (2) INFORMATION ON SEQ ID NO. 600:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 336 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

KLNFTMRCC HICKLPGRVM GIRVLRSLV VILVLLVAG ALTALLPSVK EDKMLMLRRE 60  
 IKSQGSTMD SFTLIMQTYN RTDLLKLLN HYQAVPNLHK VIVVWNNIGE KAPDELWNSL120  
 GPHPIPVIFK QQTANRMRNR LQVFELETN AVLMVDDDTL ISTPDLVFAF SVWQQFPDQI180  
 VGFVPRKHVS TSSGIYSYGS FEMQAPGSGN GDQYSMVLIG ASFFNSKYLE LFRQRPAAVH240  
 ALIDDTQNC DDIAMNFIK HIGKTSIGIFV KPVNMDNLEK ETNSGYSGMW HRAEHALQRS300  
 YCINKLVNIY DSMFLYSNI MISQGFPPYA NYKRKI 336

## (2) INFORMATION ON SEQ ID NO. 601:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes.

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

HALKILQHYD FFWVFSICQL QKXNIKVKQT KTNLKTAWHL SSFSMLCIFL SNIMNFIYSR 60  
 SLYNRRKSAV LLGYKIHITF ESQVGLIQL GLLMKSFPHG I 101

## (2) INFORMATION ON SEQ ID NO. 602:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein

00673305.122700

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

FKSFNKRSLV LYVCIMRVKE SMVDLPWDFI SLRNMSSILSS LTLGSKAVKA PATSNNTMT60  
TKDNRSTRIP ITPGSLQMW QHLIVLKFNF 90

(2) INFORMATION ON SEQ ID NO. 603:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 163 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

IYGVSFLLFN IKNIYVSVIP CQGCLLVCLR FCFIFIHVVV IFSSQFLVS PFPGSFLLLL 60  
LSVGDDKLVS LRALHLWIFL XSLTGQAPV GSGPVLRLRP SLFHLQVCLP XPAPGLAPAA120  
ACPSEALLSP PGSHGWFLPS QLVSLNPKPL RNWGLVSGTC CYQ 163

(2) INFORMATION ON SEQ ID NO. 604:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

09673395-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

PLSFLMYKTL LSGLEFEHLW XFIYFAXVCG QSNIFPKYIL PRXKKQIRX FDXKXNRPKK 60  
 GAXTWSRAWX RGKAXRGQVC GGQICAYFIT GVKKXQSKID VXRIYTVXRN XRXKXKNNRN120  
 ) TWXWXYFHXX YTFSLWXNL TKLXFKIKLM 150

## (2) INFORMATION ON SEQ ID NO. 605:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 108 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

LDFKXQFCES IXPQAKCVXX MIKXXPXXIP VFLKXVPXIS XHCIYPXDIN XTLFSFYSSN 60  
 KVGTDLSTTN LPSXCLASXP CSAPGXXPLX XPVXFXVKXP NLLLAFSW 108

## (2) INFORMATION ON SEQ ID NO. 606:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 203 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

GPSALVHSVR PDLCSNPLSC GSLACMAYTG ELGLWAVQTQ GSHFAFPLLS PFSILALRQN 60  
 FSQRTLCCP RSAVILPFLP SFHPSSAQMK SSRNSSFLPL WDSGTGNLQG GVFPSPFLFL120  
 STPRGTAAV PTSGTELEHTI VGKLQGPLLL VLRAHLCYWS FWQKRKMIEP RVAPECCSLT180  
 VEGPKLVFRA HPRREVIRCH AFC 203

0067305-12700



## (2) INFORMATION ON SEQ ID NO. 607:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 154 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

EVROKEWCLL WSFPFPGAGL CAKLGPQHIW STILLVGARPE HLTQPVHTAP RVPPLSQAGP 60  
 TAPGSADKGM ACPLRCQNSI QKAPPQVDVV PGAGEESGTT TLAVNLSNRG LGFLVAASCP120  
 GLEVHRSRGV PLGTKDMPHW GCNGEKSGKL GAQL 154

## (2) INFORMATION ON SEQ ID NO. 608:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

CGVLSLRWVQ QPWFLWGLRI RIVGREKLLL EDFLSQSPRE VERRNFCWTS SGQRKDGMMKV 60  
 EKAEIQLSGD NKEFFSGKSF VLEQGWMGT TKEKQSVTLG FGQPRGPAFQ YKPYRFGTHR120  
 RVD 123

## (2) INFORMATION ON SEQ ID NO. 609:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 88 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

0967395-122700

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

LVEFNGLEWF HFSASRRQNK ESHSKMFIVD NMSLKVVPVC SYSTEEMIHI PIIDMVSQSE60  
ESFRLRHKYV LCTCPMLGNNR KIIVIDKT 88

(2) INFORMATION ON SEQ ID NO. 610:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

SCFHKLSTQE PDGKKKNKNYA DNYRKINPNL VKLVKACTFQ RFIRTGLNRE FLLNKMALTL60  
VPRNWNPPQRS YTGDNALIL 80

(2) INFORMATION ON SEQ ID NO. 611:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

MGITHECVIL LGASANSITV VPSLTLPVHH LRRLDPSLTS PFLKPVSFSL LPNWLWFLQ60  
PFHSRAIFAK E 71

(2) INFORMATION ON SEQ ID NO. 612:

(i) SEQUENCE CHARACTERISTIC:

00673395-122700

- (A) LENGTH: 395 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

APMRPERPRP RGSAPGPMET PPWDPARND SLPPTLTPAVP PYVKLGLTVV YTVFYALLFV 60  
 FIYVQLWLVL RYRHKRLSYQ SVFLFLCLFW ASLRTVLFSS YFKDFVAANS LSPFVFWLLY120  
 CFPVCLQFFT LTLMLLYFTQ VIFKAKSKYS PELLKYRLPL YLASLFISLV FLLVNLTCAV180  
 LVKTGNWERK VIVSVRVAIN DTLFVLCASV LSICLYKISK MSLANIYLES KGSSVCQVTA240  
 IGVTVILLYT SRACYNLFIL SFSQNKSVHS FDYDWNVSD QADLKNQLGD AGYVLFQVVL300  
 FVWELLPTTL VVYFFVRVNP TKDLTNPGMV PSHGFSRPSY FFDNPRRYDS DDDLAWNIA360  
 QGLQGGFAPD YYDWGQQTNS FLAQAGTLQR LNFGS 395

(2) INFORMATION ON SEQ ID NO. 613:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 213 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

ARCAETPAGA AAASVPDEAR ASFAARQRPR PDGDPVAGPS PQRLLAAHAD PGRAPLREAW 60  
 PHRRRLHRVLR AALRVHLRAA LAGAALPPQA AQLPERLPLS LPLLGLPADR PLLLLQLRLR120  
 GGQFAQPLRL LAALLLPCVP AVFHPHADEL VLHAGDFQSQ VKIFSRTQI EVAPLPGPL180  
 HQPCFPVGEF NLCCAGKDGK LGEEGYRLCA SGH 213

(2) INFORMATION ON SEQ ID NO. 614:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00673395-122700

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

LGFNHLREV QVHQREGEKL QAHREAVEQP EDEGAERIGR HEVFEVEGEE DGPQGGPEEA 60  
 EKEEDALVAE PLVAVTQHQP ELHVDHEEEQ RVEHGVDDGE AKLHVGGHGR GQRGRQRVVA120  
 GWVPRRGLHR AGGAAARPPT LGPHRGRSPP PPRGSPRIA P 161

(2) INFORMATION ON SEQ ID NO. 615:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

HKKTSSYSYGV TVCSYDSIIR LKAGEICVQF NRTQLKGRQV GWERKLLSGG IRGNQSKTKF 60  
 YCLQFNSIIA IMCSGKHIPV LLDRVSFPFS GTKMVEGIIN PT 102

(2) INFORMATION ON SEQ ID NO. 616:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

VTCLSLYVET NFTMITDLN ISSLNFHTIL KCLLENLHLF VPRCSSSIKP WAYFSVLLRP60  
 NFVGRGGQFC INIRYFVIHS PNLKLY 86

00673305.12700

## (2) INFORMATION ON SEQ ID NO. 617:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

RMLIQNCPPR PTKFGLRRTL KYAHGFIDEE HLGTKRCKFS SRHFKIVWKF KLEMLHRSVI60  
 MVKLVSTYKD KQVTHW 76

## (2) INFORMATION ON SEQ ID NO. 618:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 378 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

SRCRFCCRLS AAFPLPRLMG LAIVLAGRLN EGDRLKPPPI SLRNFSFWSS FSKPAVSHWP 60  
 NNWVPVHFLVS EASVLPDSRS ISSCKAFRLT WSMCASSMLP FFSNTTSKSV SVSSLQGSPIA120  
 TPLSFLFFLV FLFRAGSSMT GCSTFFLDPI FFFAEDLGSS LMGMYSGAST LTGFLLPFL180  
 GLLSMDLEGL EWPGRASPSW WIFFFFFFFFP LCSLGLFLRLP FLXPRLPVPH PSSPLXQVSP240  
 TSLASLASQN QGSWTEKAXG VLGPPFFPSC XFLSFLPTLV SSSPCLXLVG RFSPPQRHGTW300  
 LEVTSXFFFS PLRNSKNPNT CFLRLGDFSV RLAGSVVSGS TCSSQRLVTP FFFFFFFFTR360  
 GISGACPWAT LLXGGCSS 378

## (2) INFORMATION ON SEQ ID NO. 619:

- (i) SEQUENCE CHARACTERISTIC:

0067395.122700

- (A) LENGTH: 269 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

GTGSLGXRNQ XRXSPREHNG KVKKKKKIHO EGDALPGHSK PSRSMESSPR KGSKKKPKVKV 60  
 EAPEYIPISD DPKSSAKKKM KSKKKVQPV IEPALKRKT RKKRKESGVA GDPWREETDT120  
 DLEVVLKKG NMDEAHIDQV RRKALQEEID RESGKTEASE TRKWTGTQFG QWDTAGFENE180  
 DQKLKFLALM GGFKNLSPSF SRPASTIARP NMALGKKAAD SLQQNLQRDY DRAMSLEVP240  
 GSRLAVFSTA PNKIFYIORN ASKSVKLED 269

(2) INFORMATION ON SEQ ID NO. 620:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 218 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

VRVCFLLPRV SCYPTLFLLL FRLPFQSWLL DDWLLYLLFG LHLFLCGGLR VITYGDVFRS 60  
 LNFDWLLFTS FPRALHGGG GLGVAWEGIS LLVDFFLLH LPVFGSALP XSVSXPKAAC120  
 SSSFFPTXAS VPNIPLPLGL TEPRVLDREG XWGPXGPFPS FLXFFELLAN SGFLTLXG180  
 XGEVFTPEAW DMARGDLFXF LFPTEELQVA KHLPEAG 218

(2) INFORMATION ON SEQ ID NO. 621:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 389 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual

00673905.120700

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

AAGACGARGS GRRGSYVPEV RCGAPGGAAG TGAPRSCCCQ TNPGPSSSLR RAFRRRELPF 60  
PACHEIGLGA EAGSGPPAP AARESRSRAM EEEASSPGLG CSKPHLEKLT LGITRILESS120  
PGVTEVTIIE KPPAERHMIS SWEQKNNCVM PEDVKNFYLM TNGFHMTWSV KLDEHIIPLG180  
SMAINSISKL TQLTQSSMYS LPNAPTLDL EDDTHEASDD QPEKPHFDSR SVIFELDSCN240  
GSGKVCLVYK SGKPALAEDT EIWFLDRLY WHFLTDFTTA YYRLILTHLG LPQWQYAFTS300  
YGISPQAKQW FSMYKPITYN TNLLTEETDS FVNKLDPISKV FKSKNKIVIP KKKGPVQFAG360  
GQKGPSPSG PSTSSTSKSS SSGSNPTRK 389

(2) INFORMATION ON SEQ ID NO. 622:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 109 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

ARPAPAGREG RGEGEATSRG CGVGHRAQPR EPAPHGAAV RPTPGPHHC AALSGAENYR 60  
SRHAMKLASA LRRGPALHPL PPRANRGREP WRRRRRPRGW AAASRTWRS 109

(2) INFORMATION ON SEQ ID NO. 623:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 96 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

0067395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

RSAGGFMMV TSVTPGEDSR MRVMPRVFS RCGLLQFSPG DDASSMARD RDSRAAGAGG60  
GPDPAAPRP ISWHAGNGSS RRLKARRSDD GGPGLV 96

(2) INFORMATION ON SEQ ID NO. 624:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 218 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

CCTEHRWPAS MPPQLQETRM NRSIPVEVDE SEPYPQLLK PIPEYSPEEE SEPPAPNIRN 60  
MAPNSLSAPT MLHNSSGDFS QAHSTLKLAN HQRPVSRQVT CLRTQVLEDS EDSFCRRHPG120  
LGKAFPSGCS AVSEPAESV VGALPAEHQF SFMEKRNOWL VSQLSAASPD TGHDSKSDQ180  
SLPNASADSL GGSQEMVQRP QPXQEPSRPG SANHRHGI 218

(2) INFORMATION ON SEQ ID NO. 625:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 212 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

00673395.122700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

NLQITSGLYP GRSPACALKF WRTVKTVSAG DTQAWAKLSL LGALQSASLR LSLWLEPSLQ 60  
 SISFHLWKNV INGWYLSFQR LLLTLAMTQT NQTKVYLMPO QTPWAVARRW CNGPSLHRNR120  
 AGLDLPTIDT GYDSQPQDVL GIRQLERPLX LTSVCYPQDL PRPLRSREFF QFEPQRYPAC180  
 AQMLPPNLSP HAPWNYHYHC PGSPDHQVXI WF 212

## (2) INFORMATION ON SEQ ID NO. 630:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 184 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

FMINVSFFFF LAAGRGKEEE MCGDGSKAGK VSHGPQTFFP PLSLSPLPKK KKKETFFIMNQ 60  
 QGFSPYQREM WKELKKPFV PNSTLPIFYA TQTLSEWVPF LQMDLLRRII VFHFVSPQVT120  
 KINICIYNLY YCYIEVDNTE RWCWVIYYNL NLGISFGLPQ SLLRWGWPYG KTPRYNVTSP180  
 QPLY 184

## (2) INFORMATION ON SEQ ID NO. 631:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 138 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

GPWLTFPAFD PSHPISSSFP LPAAKKKKKE TFIMNQGGFS PYQREMWKEL KKPFPVFNST 60  
 LPIFYATQTL SFWVPFLQMD LLRRIIVFHV FSPQVTIKINI CIYNLYCYI FVDNTRWCW120  
 VIYYNLNLGI SFGLPQSC 138

06673365.122700

## (2) INFORMATION ON SEQ ID NO. 632:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

WVKGRKGKFW SSNPISSEFP LPAAKKKKKG NVYHSTGFG SLSKRDVERA KETTLCSQLH60  
FTHILCNTNT VLLGPFLTDG PLEKNYRIPR F 91

## (2) INFORMATION ON SEQ ID NO. 633:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

RNHAKIQLPM QAPQSLILSS QFCCQATVWV RVGCGCPCCN EWEEVDSCMV ETFTSSSPAT 60  
GIPPRPVLCC GGRKFSKLL FEVGFAVWEK XHDAIAXERP SKDSGLPGLE N 111

## (2) INFORMATION ON SEQ ID NO. 634:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

0067395.122700

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

LRRNCPVQRP TFFFAPHLFR TPLHTLQPPK VPGSGFLHPA AATNANSLNS TFSVLPQRFPP60  
QFQQHRAVYN SFSFPGQAAR YPWMAFFXQ 89

(2) INFORMATION ON SEQ ID NO. 635:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 89 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

FIQFSRPGSP LSLDGLSXAI ASCXLNHTAN PTSNSNFLDL NLPPQHNTGL GGIPVAGEEEE60  
VKVSTMPLST SSHSLQQGQQ PTLHTTVA 89

0073305.12700

09/673395  
529 Rec'd PCT/PTC 17 OCT 2000  
PCT/DE99/01174

WO 99/54461

### Claims

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-126 and Seq. ID Nos. 531-552, 554, and 555 or a complementary or allelic variant thereof.

3. Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, characterized in that they are expressed elevated in uterus tumor tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

09/673395-122700

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

00673205.122700

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. An antibody according to claim 20, wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. Seq. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

006672305 122700

26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 as tools for finding active ingredients against uterus tumors.

28. Use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 for expression of polypeptides that can be used as tools for finding active ingredients against the endometrial tumor.

29. Use of nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 as pharmaceutical agents in gene therapy for treatment of the endometrial tumor.

31. Use of polypeptide partial sequences Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635 for the production of a pharmaceutical agent for treatment of the endometrial tumor.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 142-528 and Seq. ID Nos. Seq. 561-575, 577-625, and 630-635.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

006723061422700

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 141 and Seq. ID Nos. 531-552, 554, and 555.

36. Use of the genomic genes according to claim 35, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

06673385.122700



## Systematic Gene Search in the Incyte LifeSeq Database

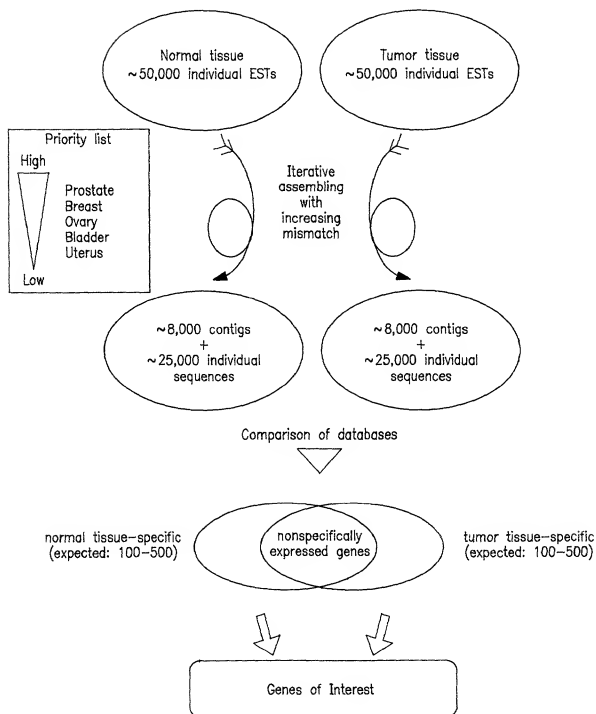


FIG. 1

## Principle of EST Assembly

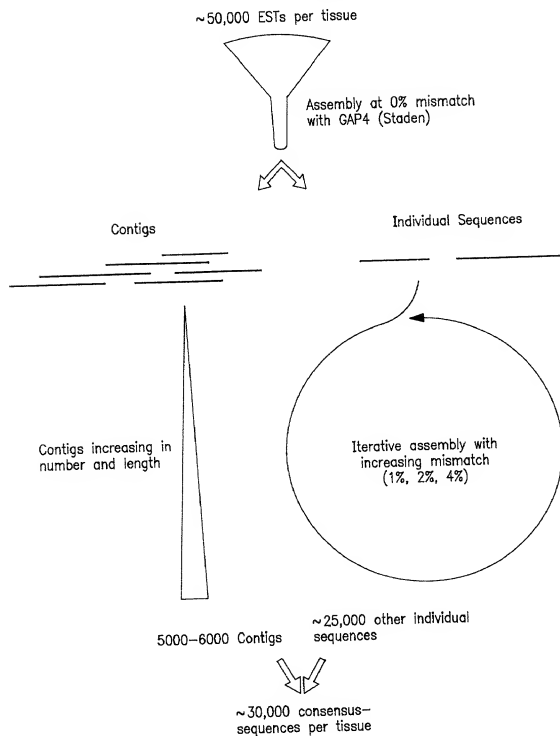


FIG. 2a

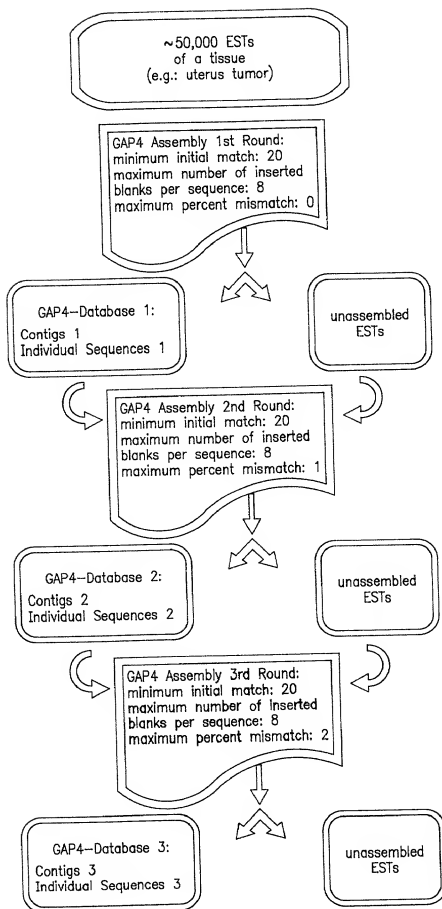


FIG. 2b-I

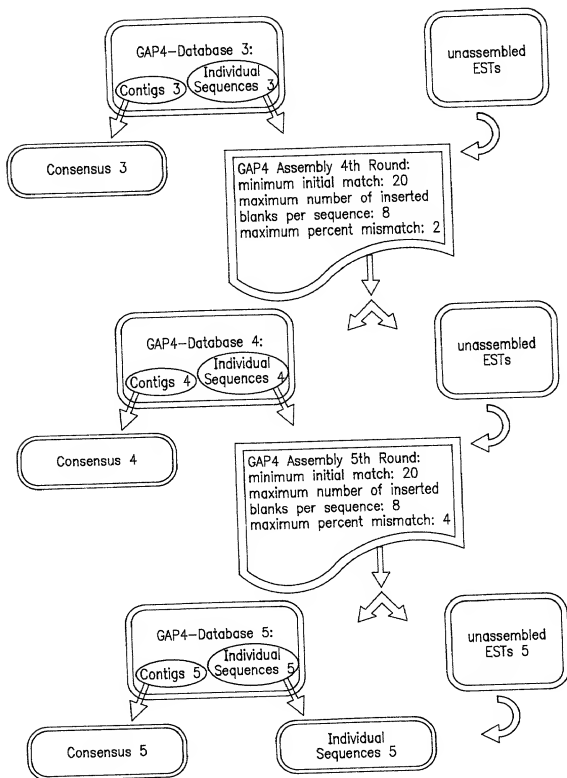


FIG. 2b-2

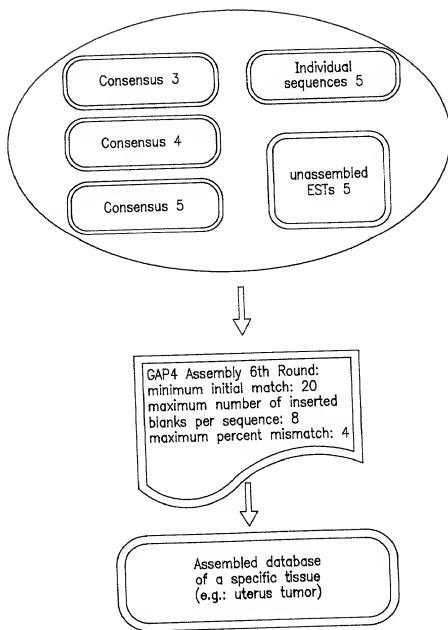


FIG. 2b-3

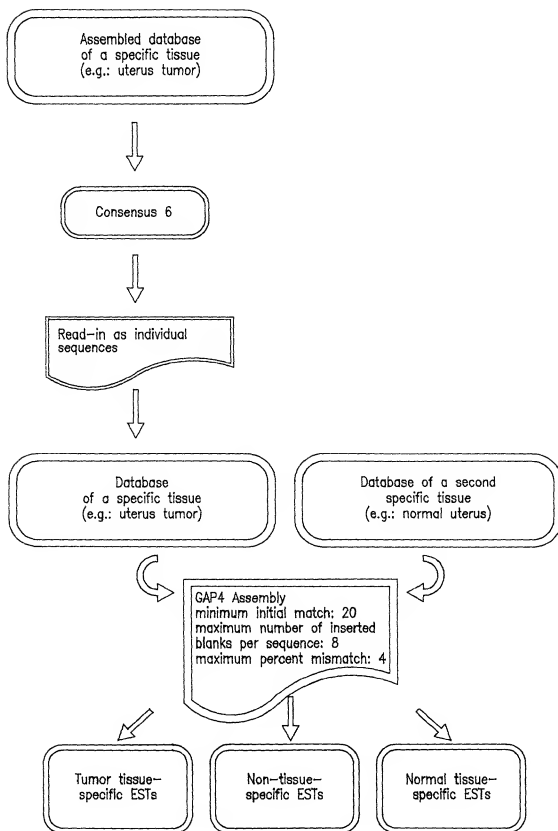


FIG. 2b-4

## In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

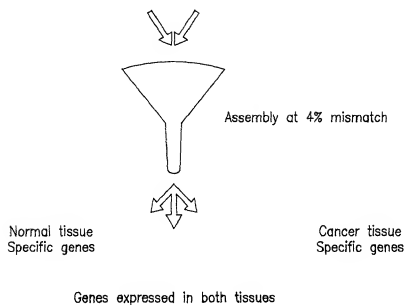


FIG. 3

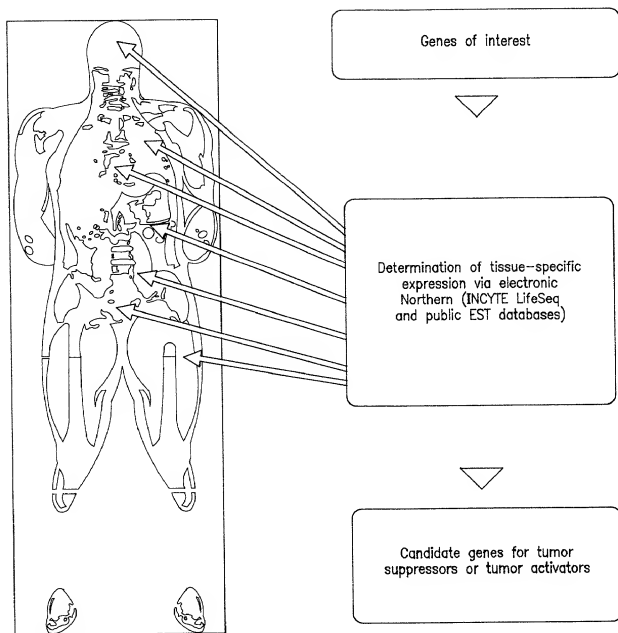


FIG. 4a



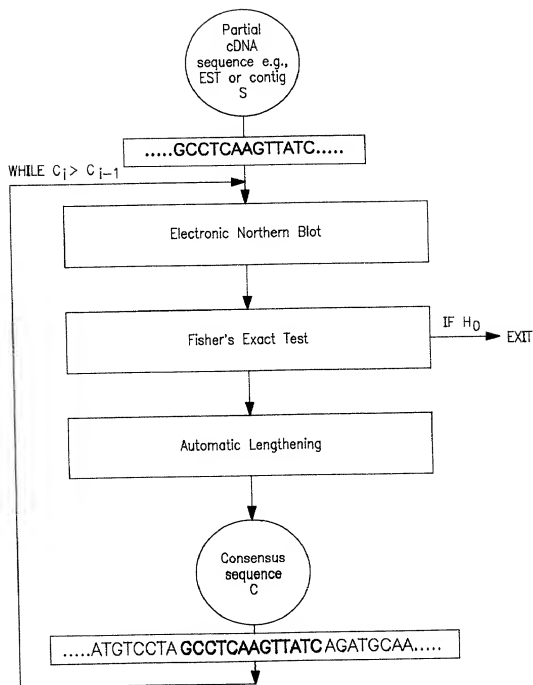


FIG. 4b

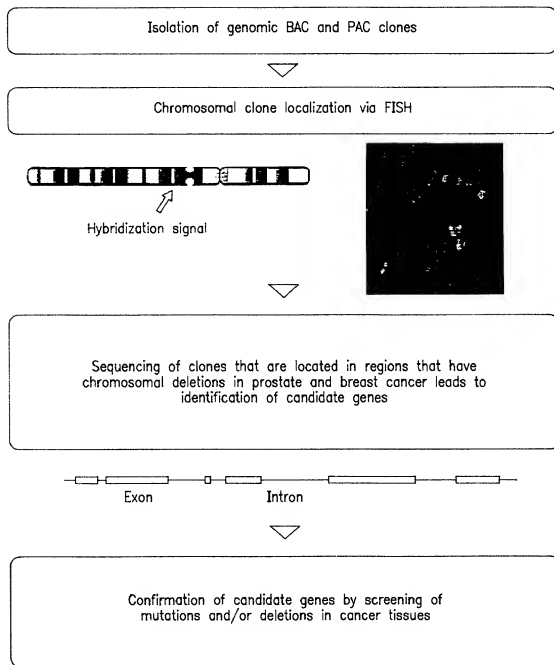


FIG. 5

Attorney Docket Number: SCH 1780**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN NUCLEIC ACID SEQUENCES OF ENDOMETRIUM TUMOR TISSUE**

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01174 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

**PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119**

APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 948.0	Germany	17 April 1998	X

by claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

**PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)**

APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

**PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120**

APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I, William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Aian E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Rutland (40,921) and Jennifer J. Branigan (37,432)

Attorney Docket Number: SCH 1780**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN NUCLEIC ACID SEQUENCES OF ENDOMETRIUM TUMOR TISSUE**

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01174 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 948.0	Germany	17 April 1998	X

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebowitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

## Declaration for Patent Application (Continued)

Full Name of additional joint inventor (given name family name)

André ROSENTHAL

Signature

Date

Residence

Berlin, Germany

Citizenship

Germany

Post Office Address Koppenplatz 10 D-10115 Berlin, Germany

00673395-122700

## Declaration for Patent Application (Continued)

**Correspondence Address:**  
**MILLEN WHITE ZELANO & BRANIGAN, P.C.**  
 Suite 1400  
 2200 Clarendon Boulevard  
 Arlington, VA 22201  
 TEL (703) 243-6333  
 FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name, family name)

**Thomas SPECHT**

Signature <i>Thomas Specht</i>	Date <i>17.10.00</i>
Residence <i>Berlin, Germany IEX</i>	Citizenship <i>Germany</i>

Post Office Address *Grabenstrasse 14, D-12209 Berlin, Germany*

Full Name of additional joint inventor (given name, family name)

**Bernd HINZMANN**

Signature <i>Bernd Hinzmann</i>	Date <i>17.10.2000</i>
Residence <i>Berlin, Germany IEX</i>	Citizenship <i>Germany</i>

Office Address *Parkstrasse 19, D-13127 Berlin, Germany*

Full Name of additional joint inventor (given name, family name)

**Amin SCHMITT**

Signature	Date
Residence <i>Berlin, Germany</i>	Citizenship <i>Germany</i>

Office Address *Laubacher Strasse 6/II, D-14197 Berlin, Germany*

Full Name of additional joint inventor (given name, family name)

**Stian PILARSKY**

Signature <i>Stian Pilarsky</i>	Date <i>17.10.00</i>
Residence <i>Schönfeld-Weissig, Germany IEX</i>	Citizenship <i>Germany</i>

Post Office Address *Heinrich-Lange-Strasse 13c, D-01474 Schönfeld-Weissig, Germany*

Full Name of additional joint inventor (given name, family name)

**Edgar DAHL**

Signature <i>Edgar Dahl</i>	Date <i>17.10.2000</i>
Residence <i>Potsdam, Germany IEX</i>	Citizenship <i>Germany</i>

Post Office Address *Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany*

■ Additional joint inventors are named on separately numbered sheets attached hereto

Declaration for Patent Application (Continued)

**Correspondence Address:**  
**MILLEN WHITE ZELANO & BRANIGAN, P.C.**  
 Suite 1400  
 2200 Clarendon Boulevard  
 Arlington, VA 22201  
 TEL (703) 243-6333  
 FAX (703) 243-6410

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name, family name)

**Thomas SPECHT**

Signature	Date
Residence <b>Berlin, Germany</b>	Citizenship <b>Germany</b>
Post Office Address <b>Grabenstrasse 14, D-12209 Berlin, Germany</b>	

Full Name of additional joint inventor (given name, family name)

**Bernd HINZMANN**

Signature	Date
Residence <b>Berlin, Germany</b>	Citizenship <b>Germany</b>
Post Office Address <b>Parkstrasse 19, D-13127 Berlin, Germany</b>	

Full Name of additional joint inventor (given name, family name)

**Amin SCHMITT**

Signature <i>Amin Schmitt</i>	Date <i>October 18, 2000</i>
Residence <b>Berlin, Germany DEX</b>	Citizenship <b>Germany</b>
Post Office Address <b>Laubacher Strasse 6/II, D-14197 Berlin, Germany</b>	

Full Name of additional joint inventor (given name, family name)

**Christian PILARSKY**

Signature	Date
Residence <b>Schönfeld-Weissig, Germany</b>	Citizenship <b>Germany</b>
Post Office Address <b>Heinrich-Lange-Strasse 13c, D-01474 Schönfeld-Weissig, Germany</b>	

Full Name of additional joint inventor (given name, family name)

**Edgar DAHL**

Signature	Date
Residence <b>Potsdam, Germany</b>	Citizenship <b>Germany</b>
Post Office Address <b>Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany</b>	

■ Additional joint inventors are named on separately numbered sheets attached hereto

## Declaration for Patent Application (Continued)

Full Name of additional joint inventor (given name, family name)

André ROSENTHAL

Signature

André Rosenthal

Date

17.10.2000

Residence

Berlin, Germany DEX

Citizenship

Germany

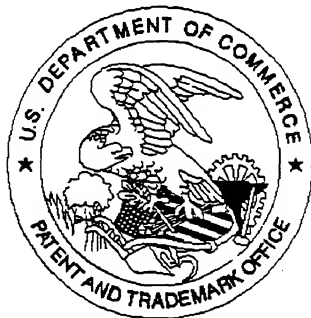
Post Office Address

Koppenplatz 10, D-10115 Berlin, Germany

09673395-122700



United States Patent & Trademark Office  
Office of Initial Patent Examination -- Scanning Division



Application deficiencies found during scanning:

☒ Page(s) \_\_\_\_\_ of Specification, claims were not present  
for scanning. (Document title)

☐ Page(s) \_\_\_\_\_ of \_\_\_\_\_ were not present  
for scanning. (Document title)

☒ Scanned copy is best available. Application pages numbered  
started on page 375.

00673395.122700